

SCORE OVER LENGTH SEARCHES

please scan  
into case #  
10/528631.  
R.R.

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 100%, maximum length 15nt,  
minimum length 10nt

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

This page blank (uspto)

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 17, 2007, 09:06:07 ; Search time 4 Seconds

(without alignments)

3.490 Million cell updates/sec

Title: US-10-528-631-1

Perfect score: 2517

Sequence: 1 gaatttagactgacgtga.....gaaacgacttgcctccagta 2517

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 241 seqs, 2773 residues

Total number of hits satisfying chosen parameters: 482

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 245 summaries

Database : pubmaindb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	0.5	13	1	US-10-257-017B-4121
2	13	0.5	13	1	US-10-257-017B-4122
3	13	0.5	13	1	US-10-257-017B-9699
4	13	0.5	13	1	US-10-257-017B-9700
5	13	0.5	13	1	US-10-257-017B-12355
6	13	0.5	13	1	US-10-257-017B-12356
7	13	0.5	13	1	US-10-257-017B-17287
8	13	0.5	13	1	US-10-257-017B-17288
9	13	0.5	13	1	US-10-257-017B-27007
10	13	0.5	13	1	US-10-257-017B-27008
11	13	0.5	13	1	US-10-257-017B-36977
12	13	0.5	13	1	US-10-257-017B-36978
13	13	0.5	13	1	US-10-257-017B-39519
14	13	0.5	13	1	US-10-257-017B-39520
15	13	0.5	13	1	US-10-257-017B-52161
16	13	0.5	13	1	US-10-257-017B-52162
17	13	0.5	13	1	US-10-257-017B-58001
18	13	0.5	13	1	US-10-257-017B-58002
19	13	0.5	13	1	US-10-257-017B-80329
20	13	0.5	13	1	US-10-257-017B-80330
21	13	0.5	13	1	US-10-257-017B-82965
22	13	0.5	13	1	US-10-257-017B-82966
23	13	0.5	13	1	US-10-257-017B-107917
24	13	0.5	13	1	US-10-257-017B-107918
25	13	0.5	13	1	US-10-257-017B-115749
26	13	0.5	13	1	US-10-257-017B-115750
27	13	0.5	13	1	US-10-257-017B-134105
28	13	0.5	13	1	US-10-257-017B-134106
29	13	0.5	13	1	US-10-257-017B-135813
30	13	0.5	13	1	US-10-257-017B-135814
31	13	0.5	13	1	US-10-257-017B-155745
32	13	0.5	13	1	US-10-257-017B-155746
33	13	0.5	13	1	US-10-257-017B-175099

13	0.5	13	1	US-10-257-017B-175100	Sequence 175100,
13	0.5	13	1	US-10-257-017B-226781	Sequence 226781,
13	0.5	13	1	US-10-257-017B-226782	Sequence 226782,
13	0.5	13	1	US-10-257-017B-229133	Sequence 229133,
13	0.5	13	1	US-10-257-017B-229134	Sequence 229134,
13	0.5	13	1	US-10-257-017B-230337	Sequence 230337,
13	0.5	13	1	US-10-257-017B-230338	Sequence 230338,
13	0.5	13	1	US-10-257-017B-239041	Sequence 239041,
13	0.5	13	1	US-10-257-017B-239042	Sequence 239042,
13	0.5	13	1	US-10-257-017B-245935	Sequence 245935,
13	0.5	13	1	US-10-257-017B-245936	Sequence 245936,
13	0.5	13	1	US-10-257-017B-256699	Sequence 256699,
13	0.5	13	1	US-10-257-017B-256700	Sequence 256700,
13	0.5	13	1	US-10-101-433A-36	Sequence 36, Appl
13	0.5	13	1	US-10-257-017B-268214	Sequence 268214,
13	0.5	13	1	US-10-257-017B-268215	Sequence 268215,
13	0.5	13	1	US-10-257-017B-269468	Sequence 269468,
13	0.5	13	1	US-10-257-017B-271155	Sequence 271155,
13	0.5	13	1	US-10-257-017B-271256	Sequence 271256,
13	0.5	13	1	US-10-257-017B-273021	Sequence 273021,
13	0.5	13	1	US-10-257-017B-273094	Sequence 273094,
13	0.5	13	1	US-10-257-017B-273359	Sequence 273359,
13	0.5	13	1	US-10-257-017B-275795	Sequence 275795,
13	0.5	13	1	US-10-257-017B-276042	Sequence 276042,
13	0.5	13	1	US-10-257-017B-276898	Sequence 276898,
13	0.5	13	1	US-10-257-017B-277817	Sequence 277817,
13	0.5	13	1	US-10-257-017B-278085	Sequence 278085,
13	0.5	13	1	US-10-257-017B-278485	Sequence 278485,
13	0.5	13	1	US-10-257-017B-287404	Sequence 287404,
13	0.5	13	1	US-10-257-017B-289853	Sequence 289853,
13	0.5	13	1	US-10-257-017B-289943	Sequence 289943,
13	0.5	13	1	US-10-257-017B-290100	Sequence 290100,
13	0.5	13	1	US-10-257-017B-293842	Sequence 293842,
13	0.5	13	1	US-10-257-017B-293989	Sequence 293989,
13	0.5	13	1	US-10-257-017B-296021	Sequence 296021,
13	0.5	13	1	US-10-257-017B-296971	Sequence 296971,
13	0.5	13	1	US-10-257-017B-298637	Sequence 298637,
13	0.5	13	1	US-10-257-017B-298693	Sequence 298693,
13	0.5	13	1	US-10-257-017B-299096	Sequence 299096,
13	0.5	13	1	US-10-257-017B-299809	Sequence 299809,
13	0.5	13	1	US-10-257-017B-300851	Sequence 300851,
13	0.5	13	1	US-10-257-017B-300951	Sequence 300951,
13	0.5	13	1	US-10-257-017B-302403	Sequence 302403,
13	0.5	13	1	US-10-257-017B-302732	Sequence 302732,
13	0.5	13	1	US-10-257-017B-303983	Sequence 303983,
13	0.5	13	1	US-10-257-017B-304010	Sequence 304010,
13	0.5	13	1	US-10-257-017B-305825	Sequence 305825,
13	0.5	13	1	US-10-257-017B-306706	Sequence 306706,
13	0.5	13	1	US-10-257-017B-307698	Sequence 307698,
13	0.5	13	1	US-10-257-017B-307725	Sequence 307725,
13	0.5	13	1	US-10-257-017B-311123	Sequence 311123,
13	0.5	13	1	US-10-257-017B-311282	Sequence 311282,
13	0.5	13	1	US-10-257-017B-311675	Sequence 311675,
13	0.5	13	1	US-10-257-017B-311721	Sequence 311721,
13	0.5	13	1	US-10-257-017B-313302	Sequence 313302,
13	0.5	13	1	US-10-257-017B-313534	Sequence 313534,
13	0.5	13	1	US-10-257-017B-313884	Sequence 313884,
13	0.5	13	1	US-10-257-017B-314036	Sequence 314036,
13	0.5	13	1	US-10-257-017B-316518	Sequence 316518,
13	0.5	13	1	US-10-257-017B-317853	Sequence 317853,
13	0.5	13	1	US-10-257-017B-318275	Sequence 318275,
13	0.5	13	1	US-10-257-017B-318945	Sequence 318945,
13	0.5	13	1	US-10-257-017B-318968	Sequence 318968,
13	0.5	13	1	US-10-257-017B-319068	Sequence 319068,
13	0.5	13	1	US-10-257-017B-319633	Sequence 319633,
13	0.5	13	1	US-10-257-017B-320634	Sequence 320634,
13	0.5	13	1	US-10-257-017B-325871	Sequence 325871,
13	0.5	13	1	US-10-257-017B-326780	Sequence 326780,
13	0.5	13	1	US-10-257-017B-327291	Sequence 327291,
13	0.5	13	1	US-10-257-017B-327799	Sequence 327799,
13	0.5	13	1	US-10-257-017B-327799	Sequence 327799,
13	0.5	13	1	US-10-257-017B-331385	Sequence 331385,
13	0.5	13	1	US-10-257-017B-332545	Sequence 332545,
13	0.5	13	1	US-10-257-017B-333439	Sequence 333439,

c 107	12	0.5	12	1	US-10-257-017B-334183	Sequence 334183,	c 180	10	0.4	10	1	US-09-986-718-25	Sequence 25, Appl
c 108	12	0.5	12	1	US-10-257-017B-334847	Sequence 334847,	c 181	10	0.4	10	1	US-09-979-593-57	Sequence 57, Appl
c 109	12	0.5	12	1	US-10-257-017B-335831	Sequence 335831,	c 182	10	0.4	10	1	US-10-033-145-1	Sequence 1, Appl
c 110	12	0.5	12	1	US-10-257-017B-337451	Sequence 337451,	c 183	10	0.4	10	1	US-10-033-145-175	Sequence 175, App
c 111	12	0.5	12	1	US-10-257-017B-337533	Sequence 337533,	c 184	10	0.4	10	1	US-10-033-145-223	Sequence 223, App
c 112	12	0.5	12	1	US-10-257-017B-337737	Sequence 337737,	c 185	10	0.4	10	1	US-10-033-145-414	Sequence 414, App
c 113	12	0.5	12	1	US-10-257-017B-337913	Sequence 337913,	c 186	10	0.4	10	1	US-10-033-145-528	Sequence 528, App
c 114	12	0.5	12	1	US-10-257-017B-338703	Sequence 338703,	c 187	10	0.4	10	1	US-10-033-145-592	Sequence 592, App
c 115	12	0.5	12	1	US-10-257-017B-339673	Sequence 339673,	c 188	10	0.4	10	1	US-10-033-145-761	Sequence 761, App
c 116	12	0.5	12	1	US-10-257-017B-340892	Sequence 340892,	c 189	10	0.4	10	1	US-10-033-145-767	Sequence 767, App
c 117	12	0.5	12	1	US-10-257-017B-341121	Sequence 341121,	c 190	10	0.4	10	1	US-10-033-145-929	Sequence 929, App
c 118	12	0.5	12	1	US-10-257-017B-341539	Sequence 341539,	c 191	10	0.4	10	1	US-10-033-145-929	Sequence 929, App
c 119	12	0.5	12	1	US-10-257-017B-342552	Sequence 342552,	c 192	10	0.4	10	1	US-10-033-145-1306	Sequence 1306, Ap
c 120	12	0.5	12	1	US-10-257-017B-344145	Sequence 344145,	c 193	10	0.4	10	1	US-10-033-145-1342	Sequence 1342, Ap
c 121	12	0.5	12	1	US-10-257-017B-344934	Sequence 344934,	c 194	10	0.4	10	1	US-10-033-145-1408	Sequence 1408, Ap
c 122	12	0.5	12	1	US-10-257-017B-346939	Sequence 346939,	c 195	10	0.4	10	1	US-10-033-145-1552	Sequence 1552, Ap
c 123	12	0.5	12	1	US-10-257-017B-348061	Sequence 348061,	c 196	10	0.4	10	1	US-10-033-145-1571	Sequence 1571, Ap
c 124	12	0.5	12	1	US-10-257-017B-350604	Sequence 350604,	c 197	10	0.4	10	1	US-10-033-145-1678	Sequence 1678, Ap
c 125	12	0.5	12	1	US-10-257-017B-351708	Sequence 351708,	c 198	10	0.4	10	1	US-10-033-145-1830	Sequence 1830, Ap
c 126	12	0.5	12	1	US-10-257-017B-355492	Sequence 355492,	c 199	10	0.4	10	1	US-10-033-145-1866	Sequence 1866, Ap
c 127	12	0.5	12	1	US-10-257-017B-355892	Sequence 355892,	c 200	10	0.4	10	1	US-10-033-145-2050	Sequence 2050, Ap
c 128	12	0.5	12	1	US-10-257-017B-357044	Sequence 357044,	c 201	10	0.4	10	1	US-10-238-732-3	Sequence 3, Appl
c 129	12	0.5	12	1	US-10-257-017B-357432	Sequence 357432,	c 202	10	0.4	10	1	US-10-010-802-286	Sequence 286, App
c 130	12	0.5	12	1	US-10-257-017B-357959	Sequence 357959,	c 203	10	0.4	10	1	US-10-223-765-294	Sequence 294, App
c 131	12	0.5	12	1	US-10-257-017B-358153	Sequence 358153,	c 204	10	0.4	10	1	US-10-390-045-20	Sequence 20, Appl
c 132	12	0.5	12	1	US-10-257-017B-358238	Sequence 358238,	c 205	10	0.4	10	1	US-10-390-045-36	Sequence 36, Appl
c 133	12	0.5	12	1	US-10-257-017B-358827	Sequence 358827,	c 206	10	0.4	10	1	US-10-390-045-56	Sequence 56, Appl
c 134	12	0.5	12	1	US-10-257-017B-359588	Sequence 359588,	c 207	10	0.4	10	1	US-10-330-627-63	Sequence 63, Appl
c 135	12	0.5	12	1	US-10-257-017B-362493	Sequence 362493,	c 208	10	0.4	10	1	US-10-330-627-172	Sequence 172, App
c 136	12	0.5	12	1	US-10-257-017B-364602	Sequence 364602,	c 209	10	0.4	10	1	US-10-330-627-313	Sequence 313, App
c 137	12	0.5	12	1	US-10-257-017B-365279	Sequence 365279,	c 210	10	0.4	10	1	US-10-330-627-687	Sequence 687, App
c 138	12	0.5	12	1	US-10-257-017B-367136	Sequence 367136,	c 211	10	0.4	10	1	US-10-330-627-988	Sequence 988, App
c 139	12	0.5	12	1	US-10-257-017B-367416	Sequence 367416,	c 212	10	0.4	10	1	US-10-330-627-1207	Sequence 1207, Ap
c 140	12	0.5	12	1	US-10-257-017B-369323	Sequence 369323,	c 213	10	0.4	10	1	US-10-154-890-28	Sequence 28, Appl
c 141	12	0.5	12	1	US-10-257-017B-375970	Sequence 375970,	c 214	10	0.4	10	1	US-10-186-950-25	Sequence 25, Appl
c 142	12	0.5	12	1	US-10-257-017B-376109	Sequence 376109,	c 215	10	0.4	10	1	US-10-160-358-103	Sequence 103, App
c 143	12	0.5	12	1	US-10-257-017B-376263	Sequence 376263,	c 216	10	0.4	10	1	US-10-298-796-57	Sequence 57, Appl
c 144	12	0.5	12	1	US-10-257-017B-377900	Sequence 377900,	c 217	10	0.4	10	1	US-10-293-222-322	Sequence 322, App
c 145	12	0.5	12	1	US-10-257-017B-378235	Sequence 378235,	c 218	10	0.4	10	1	US-10-293-222-367	Sequence 367, App
c 146	12	0.5	12	1	US-10-257-017B-379341	Sequence 379341,	c 219	10	0.4	10	1	US-10-293-222-399	Sequence 399, App
c 147	12	0.5	12	1	US-10-257-017B-379814	Sequence 379814,	c 220	10	0.4	10	1	US-10-293-222-430	Sequence 430, App
c 148	12	0.5	12	1	US-10-257-017B-380266	Sequence 380266,	c 221	10	0.4	10	1	US-10-434-479-20	Sequence 20, Appl
c 149	12	0.5	12	1	US-10-257-017B-380352	Sequence 380352,	c 222	10	0.4	10	1	US-10-434-479-36	Sequence 36, Appl
c 150	12	0.5	12	1	US-10-257-017B-380919	Sequence 380919,	c 223	10	0.4	10	1	US-10-434-479-56	Sequence 56, Appl
c 151	12	0.5	12	1	US-10-257-017B-380919	Sequence 380919,	c 224	10	0.4	10	1	US-10-034-350-15	Sequence 15, Appl
c 152	11	0.4	11	1	US-09-918-715-37	Sequence 381354,	c 225	10	0.4	10	1	US-10-821-568-55	Sequence 55, Appl
c 153	11	0.4	11	1	US-09-918-715-148	Sequence 37, Appl	c 226	10	0.4	10	1	US-10-149-109A-124	Sequence 124, App
c 154	11	0.4	11	1	US-09-943-115A-57	Sequence 148, App	c 227	10	0.4	10	1	US-10-149-109A-125	Sequence 125, App
c 155	11	0.4	11	1	US-09-943-115A-62	Sequence 57, Appl	c 228	10	0.4	10	1	US-10-901-415-15	Sequence 15, Appl
c 156	11	0.4	11	1	US-09-942-310-50	Sequence 62, Appl	c 229	10	0.4	10	1	US-10-755-118-60	Sequence 60, Appl
c 157	11	0.4	11	1	US-09-942-310-57	Sequence 50, Appl	c 230	10	0.4	10	1	US-10-755-118-73	Sequence 73, Appl
c 158	11	0.4	11	1	US-10-266-1388-8	Sequence 57, Appl	c 231	10	0.4	10	1	US-10-755-118-74	Sequence 74, Appl
c 159	11	0.4	11	1	US-10-265-5098-8	Sequence 8, Appl	c 232	10	0.4	10	1	US-10-805-292-153	Sequence 74, Appl
c 160	11	0.4	11	1	US-10-419-058-17	Sequence 8, Appl	c 233	10	0.4	10	1	US-10-661-398-4	Sequence 4, Appl
c 161	11	0.4	11	1	US-10-450-797-684	Sequence 17, Appl	c 234	10	0.4	10	1	US-10-661-398-5	Sequence 5, Appl
c 162	11	0.4	11	1	US-10-474-794-37	Sequence 1061, Ap	c 235	10	0.4	10	1	US-11-035-899-403	Sequence 403, App
c 163	11	0.4	11	1	US-10-474-794-148	Sequence 37, Appl	c 236	10	0.4	10	1	US-11-035-899-613	Sequence 613, App
c 164	11	0.4	11	1	US-10-979-159-37	Sequence 148, App	c 237	10	0.4	10	1	US-11-035-899-732	Sequence 732, App
c 165	11	0.4	11	1	US-10-979-159-148	Sequence 37, Appl	c 238	10	0.4	10	1	US-11-035-899-733	Sequence 733, App
c 166	10.4	0.4	12	1	US-10-257-017B-334847	Sequence 334847,	c 239	10	0.4	10	1	US-11-012-522-184	Sequence 184, App
c 167	10.4	0.4	12	1	US-10-257-017B-337451	Sequence 337451,	c 240	10	0.4	10	1	US-11-012-522-185	Sequence 185, App
c 168	10.4	0.4	12	1	US-10-257-017B-359588	Sequence 359588,	c 241	10	0.4	10	1	US-11-012-522-188	Sequence 188, App
c 169	10.4	0.4	12	1	US-08-935-377-15	Sequence 15, Appl	c 242	10	0.4	10	1	US-11-012-522-207	Sequence 207, App
c 170	10	0.4	10	1	US-09-772-105-83	Sequence 83, Appl	c 243	10	0.4	10	1	US-11-012-522-233	Sequence 233, App
c 171	10	0.4	10	1	US-09-822-250-15	Sequence 15, Appl	c 244	10	0.4	10	1	US-11-012-522-255	Sequence 255, App
c 172	10	0.4	10	1	US-09-816-763-55	Sequence 55, Appl	c 245	10	0.4	10	1	US-11-029-005-6	Sequence 6, Appl
c 173	10	0.4	10	1	US-09-371-900-25	Sequence 25, Appl							
c 174	10	0.4	10	1	US-09-951-133-8	Sequence 8, Appl							
c 175	10	0.4	10	1	US-09-951-133-11	Sequence 11, Appl							
c 176	10	0.4	10	1	US-09-955-410-28	Sequence 28, Appl							
c 177	10	0.4	10	1	US-09-983-210-6	Sequence 6, Appl							
c 178	10	0.4	10	1	US-09-970-820-25	Sequence 25, Appl							
c 179	10	0.4	10	1									

## ALIGNMENTS



```

; Sequence 4121, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 4121
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001541
US-10-257-017B-4121

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 AACAGTTGTTGAA 86
Db 1 AACAGTTGTTGAA 13

RESULT 2
US-10-257-017B-4122/c
; Sequence 4122, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 4122
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001541
US-10-257-017B-4122

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 AACAGTTGTTGAA 86
Db 13 AACAGTTGTTGAA 1

RESULT 3
US-10-257-017B-9699/c
; Sequence 9699, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

```

```

; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 9699
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002528
US-10-257-017B-9699

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 CAAATTTCGCAAAA 1093
Db 13 CAAATTTCGCAAAA 1

RESULT 4
US-10-257-017B-9700
; Sequence 9700, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 9700
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002528
US-10-257-017B-9700

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 CAAATTTCGCAAAA 1093
Db 1 CAAATTTCGCAAAA 13

RESULT 5
US-10-257-017B-12355/c
; Sequence 12355, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046

```

```

; SEQ ID NO 12355
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002930
US-10-257-017B-12355

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 TTTATTCAAAATA 203
Db 13 TTTATTCAAAATA 1

RESULT 6
US-10-257-017B-12356
; Sequence 12356, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 12356
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002930
US-10-257-017B-12356

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 TTTATTCAAAATA 203
Db 1 TTTATTCAAAATA 13

RESULT 7
US-10-257-017B-17287/c
; Sequence 17287, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 17287
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003734
US-10-257-017B-17287

```

```

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 CACCAAAACTAA 104
Db 13 CACCAAAACTAA 1

RESULT 8
US-10-257-017B-17288
; Sequence 17288, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 17288
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003734
US-10-257-017B-17288

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 CACCAAAACTAA 104
Db 1 CACCAAAACTAA 13

RESULT 9
US-10-257-017B-27007/c
; Sequence 27007, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 27007
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0007140
US-10-257-017B-27007

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1061 ATTACAAAAAT 1073
Db 1 ATTACAAAAAT 1073

```

Db 13 ATTACACAAAAAT 1

## RESULT 10

US-10-257-017B-27008  
; Sequence 27008, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 27008

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0007340

US-10-257-017B-27008

Query Match

Best Local Similarity 0.5%; Score 13; DB 1; Length 13;

Mismatches 0; Pred. No. 30;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1061 ATTACACAAAAAT 1073

Db 1 ATTACACAAAAAT 13

## RESULT 11

US-10-257-017B-36977/C

; Sequence 36977, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 36977

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011557

US-10-257-017B-36977

Query Match

Best Local Similarity 0.5%; Score 13; DB 1; Length 13;

Mismatches 0; Pred. No. 30;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1896 ATCACAATAATTTA 1908

Db 13 ATCACAATAATTTA 1

## RESULT 12

US-10-257-017B-36978

; Sequence 36978, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 36978  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011557  
US-10-257-017B-36978

Query Match

Best Local Similarity 0.5%; Score 13; DB 1; Length 13;

Mismatches 0; Pred. No. 30;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1896 ATCACAATAATTTA 1908

Db 1 ATCACAATAATTTA 13

## RESULT 13

US-10-257-017B-39519/C

; Sequence 39519, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 39519

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012084

US-10-257-017B-39519

Query Match

Best Local Similarity 0.5%; Score 13; DB 1; Length 13;

Mismatches 0; Pred. No. 30;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AAAAAACCAACCAA 97

Db 13 AAAAAACCAACCAA 1

## RESULT 14

US-10-257-017B-39520

; Sequence 39520, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; FILE REFERENCE: E01/1193/WO

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 39520
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012084
US-10-257-017B-39520

Query Match          0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AAACACCCACCAA 97
DB 1 AAACACCCACCAA 13

RESULT 15
US-10-257-017B-52161/c
; Sequence 52161, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 52161
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014506
US-10-257-017B-52161

Query Match          0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 AAACACCCACCAA 100
DB 13 AAACACCCACCAA 1

RESULT 16
US-10-257-017B-52162
; Sequence 52162, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 52162
; LENGTH: 13
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014506
US-10-257-017B-52162

Query Match          0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 AAACACCCACCAA 100
DB 1 AAACACCCACCAA 13

RESULT 17
US-10-257-017B-58001/c
; Sequence 58001, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 58001
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015581
US-10-257-017B-58001

Query Match          0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1631 AAATACATCAAAAC 1643
DB 13 AAATACATCAAAAC 1

RESULT 18
US-10-257-017B-58002
; Sequence 58002, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 58002
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015581
US-10-257-017B-58002

Query Match          0.5%; Score 13; DB 1; Length 13;
```

Best Local Similarity 100.0%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1631 AAATACATCAAC 1643  
| | | | | | | | | |  
Db 1 AAATACATCAAC 13

## RESULT 19

US-10-257-017B-80329/c  
; Sequence 80329, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 80329  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020386  
US-10-257-017B-80329

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CCTCAACGTACAA 1491  
| | | | | | | | | |  
Db 13 CCTCAACGTACAA 1

## RESULT 20

US-10-257-017B-80330  
; Sequence 80330, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 80330  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020386  
US-10-257-017B-80330

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1479 CCTCAACGTACAA 1491  
| | | | | | | | | |  
Db 1 CCTCAACGTACAA 13

## RESULT 21

US-10-257-017B-82965/c  
; Sequence 82965, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 82965  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020912  
US-10-257-017B-82965

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2064 CACGACCGTTACC 2076  
| | | | | | | | | |  
Db 13 CACGACCGTTACC 1

## RESULT 22

US-10-257-017B-82966  
; Sequence 82966, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 82966  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020912  
US-10-257-017B-82966

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2064 CACGACCGTTACC 2076  
| | | | | | | | | |  
Db 1 CACGACCGTTACC 13

## RESULT 23

US-10-257-017B-107917  
; Sequence 107917, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek

```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 107917
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027021
US-10-257-017B-107917

Query Match          0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      157 AATATTAAAGATT 169
Db      1 AATATTAAAGATT 13

RESULT 24
US-10-257-017B-107918/c
; Sequence 107918, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 107918
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027021
US-10-257-017B-107918

Query Match          0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      157 AATATTAAAGATT 169
Db      13 AATATTAAAGATT 1

RESULT 25
US-10-257-017B-115749
; Sequence 115749, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
```

```
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 115749
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029020
US-10-257-017B-115749

Query Match          0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      371 AATTAATTAAAAA 383
Db      1 AATTAATTAAAAA 13

RESULT 26
US-10-257-017B-115750/c
; Sequence 115750, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 115750
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029020
US-10-257-017B-115750

Query Match          0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      371 AATTAATTAAAAA 383
Db      13 AATTAATTAAAAA 1

RESULT 27
US-10-257-017B-134105
; Sequence 134105, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 134105
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

;  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033436  
US-10-257-017B-134105

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 ATTAATTAAAAA 384  
|||||  
Db 1 ATTAATTAAAAA 13

## RESULT 28

US-10-257-017B-134106/c  
; Sequence 134106, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 134106  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033436  
US-10-257-017B-134106

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 ATTAATTAAAAA 384  
|||||  
Db 13 ATTAATTAAAAA 1

## RESULT 29

US-10-257-017B-135813/c  
; Sequence 135813, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 135813  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033918  
US-10-257-017B-135813

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1176 ATATAAAATATAC 1188  
|||||  
Db 13 ATATAAAATATAC 1

## RESULT 30

US-10-257-017B-135814  
; Sequence 135814, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 135814  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033918  
US-10-257-017B-135814

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1176 ATATAAAATATAC 1188  
|||||  
Db 1 ATATAAAATATAC 13

## RESULT 31

US-10-257-017B-155745/c  
; Sequence 155745, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 155745  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0039325  
US-10-257-017B-155745

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1060 AATTACACAAAA 1072  
|||||  
Db 13 AATTACACAAAA 1

## RESULT 32

```
US-10-257-017B-155746
; Sequence 155746, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 155746
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0039325
US-10-257-017B-155746

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1060 AATTACACAAAA 1072
Db      1 AATTACACAAAA 13

RESULT 33
US-10-257-017B-175099
; Sequence 175099, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 175099
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043520
US-10-257-017B-175099

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1428 ATATATAATAAGA 1440
Db      1 ATATATAATAAGA 13

RESULT 34
US-10-257-017B-175100/c
; Sequence 175100, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
```

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 175100
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0041512
US-10-257-017B-175100

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1428 ATATATAATAAGA 1440
Db      13 ATATATAATAAGA 1

RESULT 35
US-10-257-017B-226781/c
; Sequence 226781, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 226781
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055287
US-10-257-017B-226781

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      94 CCAAAAACTAAAC 106
Db      13 CCAAAAACTAAAC 1

RESULT 36
US-10-257-017B-226782
; Sequence 226782, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```



```
; NUMBER OF SEQ ID NOS: 382046;
; SEQ ID NO 226782
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055287
US-10-257-017B-226782

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 CCAAAACTTAAC 106
Db 1 CCAAAACTTAAC 13

RESULT 37
US-10-257-017B-229133
; Sequence 229133, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 229133
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055898
US-10-257-017B-229133

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 AAAAGATTAAAT 378
Db 1 AAAAGATTAAAT 13

RESULT 38
US-10-257-017B-229134/c
; Sequence 229134, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 229134
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055898
```

```
US-10-257-017B-229134

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 AAAAGATTAAAT 378
Db 1 AAAAGATTAAAT 1

RESULT 39
US-10-257-017B-230337/c
; Sequence 230337, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 230337
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009298
US-10-257-017B-230337

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 ATCAACGAAATC 2058
Db 13 ATCAACGAAATC 1

RESULT 40
US-10-257-017B-230338
; Sequence 230338, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 230338
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009298
US-10-257-017B-230338

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 ATCAACGAAATC 2058
```

Db 1 ATCAACGAAATC 13  
|||||

## RESULT 41

US-10-257-017B-239041/c

; Sequence 239041, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 239041

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0058284

US-10-257-017B-239041

## Query Match

Best Local Similarity 0.5%; Score 13; DB 1; Length 13;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1559 CTAATACATATTA 1571

Db 13 CTAATACATATTA 1

## RESULT 42

US-10-257-017B-239042

; Sequence 239042, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 239042

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0058284

US-10-257-017B-239042

## Query Match

Best Local Similarity 0.5%; Score 13; DB 1; Length 13;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1559 CTAATACATATTA 1571

Db 1 CTAATACATATTA 13

## RESULT 43

US-10-257-017B-245935/c

; Sequence 245935, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 245935

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0060095

US-10-257-017B-245935

## Query Match

Best Local Similarity 0.5%; Score 13; DB 1; Length 13;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1560 TAATACATATTTAT 1572

Db 13 TAATACATATTTAT 1

## RESULT 44

US-10-257-017B-245936

; Sequence 245936, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 245936

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0060095

US-10-257-017B-245936

## Query Match

Best Local Similarity 0.5%; Score 13; DB 1; Length 13;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1560 TAATACATATTTAT 1572

Db 1 TAATACATATTTAT 13

## RESULT 45

US-10-257-017B-256699/c

; Sequence 256699, Application US/10257017B

; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine

; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B

; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046

; SEQ ID NO 256699

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0060095

US-10-257-017B-256699

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 256699
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0062513
US-10-257-017B-256699

Query Match          0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 AAAATACATACCA 210
Db 13 AAAATACATACCA 1

RESULT 46
US-10-257-017B-256700
; Sequence 256700, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 256700
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0062513
US-10-257-017B-256700

Query Match          0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 AAAATACATACCA 210
Db 1 AAAATACATACCA 13

RESULT 47
US-10-101-433A-36/c
; Sequence 36, Application US/10101433A
; Publication No. US20030119726A1
; GENERAL INFORMATION:
; APPLICANT: Hanscon, Sara
; APPLICANT: Crespi, Charles
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G00307/70019
; CURRENT APPLICATION NUMBER: US/10/101,433A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/277,095
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 12
```

```
; TYPE: DNA
; ORGANISM: Macaca mulatta
US-10-101-433A-36

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1440 AGCTGAAATATAC 1451
Db 12 AGCTGAAATATAC 1

RESULT 48
US-10-257-017B-268214/c
; Sequence 268214, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 268214
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0000986
US-10-257-017B-268214

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 372 ATTAATTAAAAA 383
Db 12 ATTAATTAAAAA 1

RESULT 49
US-10-257-017B-268241/c
; Sequence 268241, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 268241
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0000998
US-10-257-017B-268241

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 369 AGAATTAATAA 380  
| | | | | | | | | |  
Db 12 AGAATTAATAA 1

## RESULT 50

US-10-257-017B-269468  
; Sequence 269468, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 269468  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001773  
US-10-257-017B-269468

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 TTATTCAAAATA 203  
| | | | | | | | | |  
Db 1 TTATTCAAAATA 12

## RESULT 51

US-10-257-017B-271155/c  
; Sequence 271155, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 271155  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002410  
US-10-257-017B-271155

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 ACCAAAAACTAA 104  
| | | | | | | | | |  
Db 12 ACCAAAAACTAA 1

## RESULT 52

US-10-257-017B-271256  
; Sequence 271256, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 271256  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001774  
US-10-257-017B-271256

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2162 AATTAAGATTAT 2173  
| | | | | | | | | |  
Db 1 AATTAAGATTAT 12

## RESULT 53

US-10-257-017B-273021  
; Sequence 273021, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 273021  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001774  
US-10-257-017B-273021

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 899 TTGATGAAGATA 910  
| | | | | | | | | |  
Db 1 TTGATGAAGATA 12

## RESULT 54

US-10-257-017B-273094  
; Sequence 273094, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 273094
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003043
US-10-257-017B-273094

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      240 ATATGATTATTA 251
Db      1 ATATGATTATTA 12

RESULT 55
US-10-257-017B-273359
; Sequence 273359, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 273359
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003150
US-10-257-017B-273359

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      961 ATTAACAAACAA 972
Db      1 ATTAACAAACAA 12

RESULT 56
US-10-257-017B-275795/c
; Sequence 275795, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 275795
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004002
US-10-257-017B-275795

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1174 AAATATAAAATA 1185
Db      12 AAATATAAAATA 1

RESULT 57
US-10-257-017B-276042
; Sequence 276042, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 276042
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004073
US-10-257-017B-276042

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      96 AAAAATAAACG 107
Db      1 AAAAATAAACG 12

RESULT 58
US-10-257-017B-276898
; Sequence 276898, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 276898
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004327
```

US-10-257-017B-276898

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 GAAATATTTTGTG 331  
|||||  
DB 1 GAAATATTTTGTG 12

RESULT 59

US-10-257-017B-277817  
; Sequence 277817, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 277817  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004978  
US-10-257-017B-277817

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 ACCAAAAACTAA 104  
|||||  
DB 1 ACCAAAAACTAA 12

RESULT 60

US-10-257-017B-278085  
; Sequence 278085, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 278085  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005590  
US-10-257-017B-278085

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AAATACAAAAC 2355

DB 1 AAATACAAAAC 12  
|||||

RESULT 61

US-10-257-017B-278485  
; Sequence 278485, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 278485  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0006051  
US-10-257-017B-278485

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 TTAATTAATAAAA 384  
|||||  
DB 1 TTAATTAATAAAA 12

RESULT 62

US-10-257-017B-287404  
; Sequence 287404, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 287404  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013078  
US-10-257-017B-287404

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1174 AAATATATAATA 1185  
|||||  
DB 1 AAATATATAATA 12

RESULT 63

US-10-257-017B-289853/c  
; Sequence 289853, Application US/10257017B

```
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 289853
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014119
US-10-257-017B-289853

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1164 TATCGTAGAGAA 1175
Db 12 TATCGTAGAGAA 1

RESULT 64
US-10-257-017B-289943
; Sequence 289943, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 289943
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014158
US-10-257-017B-289943

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1063 TACACAAAATC 1074
Db 1 TACACAAAATC 12

RESULT 65
US-10-257-017B-290100/c
; Sequence 290100, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290100
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014216
US-10-257-017B-290100

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 898 TTTGATCAAGAT 909
Db 12 TTTGATCAAGAT 1

RESULT 66
US-10-257-017B-293842/c
; Sequence 293842, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 293842
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015827
US-10-257-017B-293842

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 CAAAAACTAAAC 106
Db 12 CAAAAACTAAAC 1

RESULT 67
US-10-257-017B-293989/c
; Sequence 293989, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 293989
```

```

; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015906
US-10-257-017B-293989

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2034 CACCACCAACTC 2045
DB 12 CACCACCAACTC 1

RESULT 68
US-10-257-017B-296021
; Sequence 296021, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 296021
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016856
US-10-257-017B-296021

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2483 CCAAAAACAAAA 2494
DB 1 CCAAAAACAAAA 12

RESULT 69
US-10-257-017B-296971/c
; Sequence 296971, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 296971
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017373
US-10-257-017B-296971
```

```

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1177 TATAAATATATAC 1188
DB 12 TATAAATATATAC 1

RESULT 70
US-10-257-017B-298637/c
; Sequence 298637, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 298637
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018205
US-10-257-017B-298637

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 ATTAAACACAA 234
DB 12 ATTAAACACAA 1

RESULT 71
US-10-257-017B-298693
; Sequence 298693, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 298693
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018205
US-10-257-017B-298693

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 AAATTTATACCA 348
DB 1 AAATTTATACCA 12
```



```

RESULT 72
US-10-257-017B-299096/c
; Sequence 299096, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 299096
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018429
US-10-257-017B-299096

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 88 AACCCACCAAAA 99
Db 12 AACCCACCAAAA 1

RESULT 73
US-10-257-017B-299809/c
; Sequence 299809, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 299809
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018756
US-10-257-017B-299809

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1681 CCAACTATACAA 1692
Db 12 CCAACTATACAA 1

RESULT 74
US-10-257-017B-300851/c
; Sequence 300851, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 300851
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019272
US-10-257-017B-300851

```

```

; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 300851
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019272
US-10-257-017B-300851

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 TTAACACACAAT 235
Db 12 TTAACACACAAT 1

RESULT 75
US-10-257-017B-300951/c
; Sequence 300951, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 300951
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019272
US-10-257-017B-300951

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 AACCCACCAAAA 100
Db 12 AACCCACCAAAA 1

RESULT 76
US-10-257-017B-302403/c
; Sequence 302403, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B

```

```
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 302403
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019982
US-10-257-017B-302403

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 CCAGAAACTAAA 105
DB 12 CCAGAAACTAAA 1

RESULT 77
US-10-257-017B-302732/c
/ Sequence 302732, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 302732
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020136
US-10-257-017B-302732

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2300 TAAAGAACGGAA 2311
DB 12 TAAAGAACGGAA 1

RESULT 78
US-10-257-017B-303983/c
/ Sequence 303983, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 303983
/ LENGTH: 12
/ TYPE: DNA
```

```
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC002074
US-10-257-017B-303983

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2343 GAAATACAAAAA 2354
DB 12 GAAATACAAAAA 1

RESULT 79
US-10-257-017B-304010/c
/ Sequence 304010, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 304010
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC002074
US-10-257-017B-304010

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2048 CAACGAAATCA 2059
DB 12 CAACGAAATCA 1

RESULT 80
US-10-257-017B-305825/c
/ Sequence 305825, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 305825
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021654
US-10-257-017B-305825

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
```

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GTAAAAACAAA 75  
Db 12 GTAAAAACAAA 1

## RESULT 81

US-10-257-017B-306706/c  
; Sequence 306706, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 306706  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022137  
US-10-257-017B-306706

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1625 TCATACAAATAC 1636  
Db 12 TCATACAAATAC 1

## RESULT 82

US-10-257-017B-307698  
; Sequence 307698, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 307698  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022646  
US-10-257-017B-307698

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1175 AATATAAATAT 1186  
Db 1 AATATAAATAT 12

## RESULT 83

US-10-257-017B-307725/c  
; Sequence 307725, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 307725  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022655  
US-10-257-017B-307725

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2345 AATACAAAACC 2356  
Db 12 AATACAAAACC 1

## RESULT 84

US-10-257-017B-311123  
; Sequence 311123, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 311123  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0024322  
US-10-257-017B-311123

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 710 TCGTTAAGATAT 721  
Db 1 TCGTTAAGATAT 12

## RESULT 85

US-10-257-017B-311282  
; Sequence 311282, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 311282
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0024396
US-10-257-017B-311282

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1728 TTACACCATAC 1739
Db 1 TTACACCATAC 12

RESULT 86
US-10-257-017B-311675
; Sequence 311675, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 311675
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide-Primer
US-10-257-017B-311675

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2025 CCAATCCATCAC 2036
Db 1 CCAATCCATCAC 12

RESULT 87
US-10-257-017B-311721
; Sequence 311721, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
```

```
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 311721
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0024649
US-10-257-017B-311721

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 AAAATACATACC 209
Db 1 AAAATACATACC 12

RESULT 88
US-10-257-017B-313302
; Sequence 313302, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 313302
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0025647
US-10-257-017B-313302

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1176 ATATAAAATATA 1187
Db 1 ATATAAAATATA 12

RESULT 89
US-10-257-017B-313534/c
; Sequence 313534, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/MO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 313534
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0025826  
US-10-257-017B-313534

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 TCAAAATACATA 207  
Db 12 TCAAAATACATA 1

## RESULT 90

US-10-257-017B-313884/c  
; Sequence 313884, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 313884  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026008  
US-10-257-017B-313884

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 AAAATACATACC 209  
Db 12 AAAATACATACC 1

## RESULT 91

US-10-257-017B-314036/c  
; Sequence 314036, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 314036  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026081  
US-10-257-017B-314036

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 GGAATATTTTT 330  
Db 12 GGAATATTTTT 1

## RESULT 92

US-10-257-017B-316518/c  
; Sequence 316518, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 316518  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027477  
US-10-257-017B-316518

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1176 ATATAAATATA 1187  
Db 12 ATATAAATATA 1

## RESULT 93

US-10-257-017B-317853/c  
; Sequence 317853, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 317853  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028303  
US-10-257-017B-317853

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2483 CCAAAACAAAA 2494  
Db 12 CCAAAACAAAA 1

## RESULT 94

US-10-257-017B-318275

```
; Sequence 318275, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 2000-04-07
; SEQ ID NO 318275
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028556
US-10-257-017B-318275

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      86  AAAAAACCAACCA 97
Db      1  AAAAAACCAACCA 12

RESULT 95
US-10-257-017B-318945/c
; Sequence 318945, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 2000-04-07
; SEQ ID NO 318945
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028972
US-10-257-017B-318945

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1855 ATTGTAGAGGT 1866
Db      12  ATTGTAGAGGT 1

RESULT 96
US-10-257-017B-318968
; Sequence 318968, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
```

```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 318968
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028996
US-10-257-017B-318968

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      221  ATATTAAACAC 232
Db      1  ATATTAAACAC 12

RESULT 97
US-10-257-017B-319068/c
; Sequence 319068, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 319068
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028996
US-10-257-017B-319068

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2482 TCCAAAACAAA 2493
Db      12  TCCAAAACAAA 1

RESULT 98
US-10-257-017B-319633
; Sequence 319633, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
```

; SEQ ID NO 319633  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029334  
US-10-257-017B-319633

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2348 ACAAAACCGAT 2359  
Db 1 ACAAAACCGAT 12  
|||||

RESULT 99  
US-10-257-017B-320634/c  
; Sequence 320634, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 320634  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029824  
US-10-257-017B-320634

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 AAAACACCAAA 98  
Db 12 AAAACACCAAA 1  
|||||

RESULT 100  
US-10-257-017B-325871  
; Sequence 325871, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 325871  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0032776  
US-10-257-017B-325871

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 909 TACCTTTAACAT 920  
Db 1 TACCTTTAACAT 12  
|||||

RESULT 101  
US-10-257-017B-326780  
; Sequence 326780, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 326780  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033275  
US-10-257-017B-326780

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1127 TTGGAAGAATAT 1138  
Db 1 TTGGAAGAATAT 12  
|||||

RESULT 102  
US-10-257-017B-327291/c  
; Sequence 327291, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 327291  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033541  
US-10-257-017B-327291

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2161 GAATTAAGATTA 2172  
|||||

Db 12 GAATTAAGATTA 1

## RESULT 103

US-10-257-017B-327799  
; Sequence 327799, Application US/10257017B  
; Publication No. US20040241651A1

; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 327799

; LENGTH: 12  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033909  
US-10-257-017B-327799

## Query Match

Best Local Similarity 0.5%; Score 12; DB 1; Length 12;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 AATATTAAAGAT 168

Db 1 AATATTAAAGAT 12

## RESULT 104

US-10-257-017B-331385

; Sequence 331385, Application US/10257017B  
; Publication No. US20040241651A1

; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek

; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 331385

; LENGTH: 12  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036165  
US-10-257-017B-331385

## Query Match

Best Local Similarity 0.5%; Score 12; DB 1; Length 12;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 CCAAAAACCTAAA 105

Db 1 CCAAAAACCTAAA 12

## RESULT 105

US-10-257-017B-332545/C

; Sequence 332545, Application US/10257017B  
; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 332545

; LENGTH: 12  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036982  
US-10-257-017B-332545

## Query Match

Best Local Similarity 0.5%; Score 12; DB 1; Length 12;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 CCACCAAAACT 102

Db 12 CCACCAAAACT 1

## RESULT 106

US-10-257-017B-333439/C

; Sequence 333439, Application US/10257017B  
; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO

; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 333439

; LENGTH: 12  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0037546  
US-10-257-017B-333439

## Query Match

Best Local Similarity 0.5%; Score 12; DB 1; Length 12;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2017 TCTTCAAAACCAA 2028

Db 12 TCTTCAAAACCAA 1

## RESULT 107

US-10-257-017B-334183/C

; Sequence 334183, Application US/10257017B  
; Publication No. US20040241651A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock

; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO



; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 334183  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0037993  
US-10-257-017B-334183

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2032 ATCACCACCAAC 2043  
Db 12 ATCACCACCAAC 1

## RESULT 108

US-10-257-017B-334847/c  
; Sequence 334847, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 334847  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0038439  
US-10-257-017B-334847

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1324 CATAATAACGAA 1335  
Db 12 CATAATAACGAA 1

## RESULT 109

US-10-257-017B-335831  
; Sequence 335831, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 335831  
; LENGTH: 12

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039046  
US-10-257-017B-335831

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 239 TATATGATTATT 250  
Db 1 TATATGATTATT 12

## RESULT 110

US-10-257-017B-337451  
; Sequence 337451, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 337451  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039880  
US-10-257-017B-337451

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1324 CATAATAACGAA 1335  
Db 1 CATAATAACGAA 12

## RESULT 111

US-10-257-017B-337533/c  
; Sequence 337533, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 337533  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039915  
US-10-257-017B-337533

Query Match 0.5%; Score 12; DB 1; Length 12;

```

Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2095 GTCAAAATATAC 2106
Db 12 GTCAAAATATAC 1

RESULT 112
US-10-257-017B-337737/c
; Sequence 337737, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 337737
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040047
US-10-257-017B-337737

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 TTAATTAATAAAA 384
Db 12 TTAATTAATAAAA 1

RESULT 113
US-10-257-017B-337913
; Sequence 337913, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 337913
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040140
US-10-257-017B-337913

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1167 GGTAGAGAAATA 1178
Db 1 GGTAGAGAAATA 12

Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

RESULT 114
US-10-257-017B-338703
; Sequence 338703, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 338703
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040634
US-10-257-017B-338703

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GTAAAAACAAAA 75
Db 1 GTAAAAACAAAA 12

RESULT 115
US-10-257-017B-339673/c
; Sequence 339673, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylation
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 339673
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0041132
US-10-257-017B-339673

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 497 TATTGGAAGGA 508
Db 12 TATTGGAAGGA 1

RESULT 116
US-10-257-017B-340892/c
; Sequence 340892, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek

```

```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 340892
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonukleotid-Primer
US-10-257-017B-340892

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AAATACAAAAC 2355
DB 12 AAATACAAAAC 1

RESULT 117
US-10-257-017B-341121
; Sequence 341121, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341121
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0041869
US-10-257-017B-341121

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 ATTAATTAAAAA 383
DB 1 ATTAATTAAAAA 12

RESULT 118
US-10-257-017B-341539/c
; Sequence 341539, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
```

```
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341539
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042092
US-10-257-017B-341539

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 TTTAATACATCC 1010
DB 12 TTTAATACATCC 1

RESULT 119
US-10-257-017B-342552
; Sequence 342552, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 342552
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042596
US-10-257-017B-342552

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1562 ATACATATTATA 1573
DB 1 ATACATATTATA 12

RESULT 120
US-10-257-017B-344145
; Sequence 344145, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 344145
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0006614  
US-10-257-017B-344145

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1425 AGAATATATAAT 1436  
Db 1 AGAATATATAAT 12

## RESULT 121

US-10-257-017B-344934  
; Sequence 344934, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 344934  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043787  
US-10-257-017B-344934

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1059 CAATTACACAAA 1070  
Db 1 CAATTACACAAA 12

## RESULT 122

US-10-257-017B-346999/c  
; Sequence 346999, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 346999  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0044865  
US-10-257-017B-346999

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 933 AGGAAAGATT 944  
Db 12 AGGAAAGATT 1

## RESULT 123

US-10-257-017B-348061/c  
; Sequence 348061, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 348061  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC004454;/  
US-10-257-017B-348061

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 598 AATATCATTCAT 609  
Db 12 AATATCATTCAT 1

## RESULT 124

US-10-257-017B-350604/c  
; Sequence 350604, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylation  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 350604  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC004454;/  
US-10-257-017B-350604

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTTAGAGTG 12  
Db 12 GAATTTAGAGTG 1

## RESULT 125

US-10-257-017B-351708/c  
; Sequence 351708, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 351708  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0047446  
US-10-257-017B-351708

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 TGGATATTAATAA 229  
|||||  
Db 12 TGGATATTAATAA 1

## RESULT 126

US-10-257-017B-355492/c  
; Sequence 355492, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 355492  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049668  
US-10-257-017B-355492

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1347 AAGTGTATTAATT 1358  
|||||  
Db 12 AAGTGTATTAATT 1

## RESULT 127

US-10-257-017B-355892/c  
; Sequence 355892, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin

US-10-257-017B-351708/c  
; Sequence 351708, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 351708  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0047446  
US-10-257-017B-351708

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 TGGATATTAATAA 229  
|||||  
Db 12 TGGATATTAATAA 1

## RESULT 126

US-10-257-017B-355492/c  
; Sequence 355492, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 355492  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049668  
US-10-257-017B-355492

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1347 AAGTGTATTAATT 1358  
|||||  
Db 12 AAGTGTATTAATT 1

## RESULT 127

US-10-257-017B-355892/c  
; Sequence 355892, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin

US-10-257-017B-351708/c  
; Sequence 351708, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 355892  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049849  
US-10-257-017B-355892

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 627 AAATATAATGTG 638  
|||||  
Db 12 AAATATAATGTG 1

## RESULT 128

US-10-257-017B-357044  
; Sequence 357044, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 357044  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050448  
US-10-257-017B-357044

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1896 ATCACAATAATT 1907  
|||||  
Db 1 ATCACAATAATT 12

## RESULT 129

US-10-257-017B-357432  
; Sequence 357432, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 357432  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050448  
US-10-257-017B-357432

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 357432
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050613
US-10-257-017B-357432

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1427 AATATATAATAA 1438
DB 1 AATATATAATAA 12

RESULT 130
US-10-257-017B-357959/c
; Sequence 357959, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 357959
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050895
US-10-257-017B-357959

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 TATATAATAAGA 1440
DB 12 TATATAATAAGA 1

RESULT 131
US-10-257-017B-358153
; Sequence 358153, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 358153
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC005054
```

US-10-257-017B-358153

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 AAACCACCAAAA 99  
DB 1 AAACCACCAAAA 12

RESULT 132

US-10-257-017B-358238  
; Sequence 358238, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 358238  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051005  
US-10-257-017B-358238

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 627 AAATATAATGTG 638  
DB 1 AAATATAATGTG 12

RESULT 133

US-10-257-017B-358827/c  
; Sequence 358827, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 358827  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051333  
US-10-257-017B-358827

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 CAAATAATACATAC 208

```
Db      12 CAAATACATAC 1
|||||
RESULT 134
US-10-257-017B-359588
; Sequence 359588, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359588
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051670
US-10-257-017B-359588
Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      230 CACAATCCGAT 241
Db      1 CACAATCCGAT 12
|||||
RESULT 135
US-10-257-017B-362493
; Sequence 362493, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 362493
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053260
US-10-257-017B-362493
Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1064 ACACAAAAATCA 1075
Db      1 ACACAAAAATCA 12
|||||
RESULT 136
US-10-257-017B-364602/c
; Sequence 364602, Application US/10257017B
```

```
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 364602
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0007151
US-10-257-017B-364602
Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1175 AATATAAATAT 1186
Db      12 AATATAAATAT 1
|||||
RESULT 137
US-10-257-017B-365279
; Sequence 365279, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 365279
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0055022
US-10-257-017B-365279
Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      158 ATATTAAGATT 169
Db      1 ATATTAAGATT 12
|||||
RESULT 138
US-10-257-017B-367136
; Sequence 367136, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 367136
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0056184
US-10-257-017B-367136
```

```
Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 87 AAACCCACCAAA 98
Db 1 AAACCCACCAAA 12
```

## RESULT 139

```
US-10-257-017B-367416
; Sequence 367416, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 367416
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0056324
US-10-257-017B-367416
```

```
Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 319 GGAATATATTTT 330
Db 1 GGAATATATTTT 12
```

## RESULT 140

```
US-10-257-017B-369323
; Sequence 369323, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 369323
```

```
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057582
US-10-257-017B-369323
```

```
Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 92 CACCAAAACTA 103
Db 1 CACCAAAACTA 12
```

## RESULT 141

```
US-10-257-017B-375970
; Sequence 375970, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 375970
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061543
US-10-257-017B-375970
```

```
Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 91 CCACCAAAACT 102
Db 1 CCACCAAAACT 12
```

## RESULT 142

```
US-10-257-017B-376109/c
; Sequence 376109, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 376109
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061614
US-10-257-017B-376109
```



```
Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2018 CTTCAAACCAAT 2029
Db 12 CTTCAAACCAAT 1

RESULT 143
US-10-257-017B-376263/c
; Sequence 376263, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 376263
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061704
US-10-257-017B-376263

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2255 TTGTATGTAAG 2266
Db 12 TTGTATGTAAG 1

RESULT 144
US-10-257-017B-377900/c
; Sequence 377900, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 377900
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC006316
US-10-257-017B-377900

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 498 ATTGAAGCAT 509
Db 12 ATTGAAGCAT 1
```

```
RESULT 145
US-10-257-017B-378235/c
; Sequence 378235, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 378235
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0062683
US-10-257-017B-378235

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 TCGTAGAAGTAA 41
Db 12 TCGTAGAAGTAA 1

RESULT 146
US-10-257-017B-379341
; Sequence 379341, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 379341
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004827
US-10-257-017B-379341

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 TATTCAAAATAC 204
Db 1 TATTCAAAATAC 12

RESULT 147
US-10-257-017B-379814
; Sequence 379814, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
```

```
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ TITLE OF INVENTION: methylations
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ PRIOR FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 379814
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063728
US-10-257-017B-379814

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 AAAAAATTAGAG 142
Db 1 AAAAAATTAGAG 12

RESULT 148
US-10-257-017B-380266/c
/ Sequence 380266, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ TITLE OF INVENTION: methylations
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 380266
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063728
US-10-257-017B-380266

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 601 ATCATTCATTTA 612
Db 12 ATCATTCATTTA 1

RESULT 149
US-10-257-017B-380352/c
/ Sequence 380352, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ TITLE OF INVENTION: methylations
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
```

```
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 380352
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0064144
US-10-257-017B-380352

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 CGCTTAAACG 877
Db 12 CGCTTAAACG 1

RESULT 150
US-10-257-017B-380919/c
/ Sequence 380919, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ TITLE OF INVENTION: methylations
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 380919
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0064144
US-10-257-017B-380919

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 AATTAATTAAAA 382
Db 12 AATTAATTAAAA 1

RESULT 151
US-10-257-017B-381354
/ Sequence 381354, Application US/10257017B
/ Publication No. US20040241651A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexander Olek
/ APPLICANT: Christian Piepenbrock
/ APPLICANT: Kurt Berlin
/ TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
/ TITLE OF INVENTION: methylations
/ FILE REFERENCE: E01/1193/WO
/ CURRENT APPLICATION NUMBER: US/10/257,017B
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 382046
/ SEQ ID NO 381354
/ LENGTH: 12
/ TYPE: DNA
```

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0064302  
US-10-257-017B-381354

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 TGGAAATATTTT 329  
|||||  
Db 1 TGGAAATATTTT 12

RESULT 152  
US-09-918-715-37  
; Sequence 37, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-715-37

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 TGTTTATACA 1007  
|||||  
Db 1 TGTTTATACA 11

RESULT 153  
US-09-918-715-148  
; Sequence 148, Application US/09918715  
; Publication No. US20030017157A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/09/918,715  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 148  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-918-715-148

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 TGTGTGAAAAA 90  
|||||  
Db 1 TGTGTGAAAAA 11

RESULT 154  
US-09-943-115A-57  
; Sequence 57, Application US/09943115A  
; Publication No. US20030017469A1  
; GENERAL INFORMATION:  
; APPLICANT: SEQUENOM, Inc.  
; APPLICANT: Risinger, Carl  
; APPLICANT: Andersson, Maria  
; APPLICANT: Lewander, Tommy  
; APPLICANT: Olaisson, Erik  
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9  
; FILE REFERENCE: 52459-20021.00  
; CURRENT APPLICATION NUMBER: US/09/943,115A  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: UK 0021286.0  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 57  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 5'-sequence to the polymorphic sites on the coding  
; OTHER INFORMATION: strand  
US-09-943-115A-57

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 498 ATTTGAAAGCA 508  
|||||  
Db 1 ATTTGAAAGCA 11

RESULT 155  
US-09-943-115A-62/c  
; Sequence 62, Application US/09943115A  
; Publication No. US20030017469A1  
; GENERAL INFORMATION:  
; APPLICANT: SEQUENOM, Inc.  
; APPLICANT: Risinger, Carl  
; APPLICANT: Andersson, Maria  
; APPLICANT: Lewander, Tommy  
; APPLICANT: Olaisson, Erik  
; TITLE OF INVENTION: DETECTION OF CYP3A4 AND CYP2C9  
; FILE REFERENCE: 52459-20021.00  
; CURRENT APPLICATION NUMBER: US/09/943,115A  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: UK 0021286.0  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 62  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 5'-sequence to the polymorphic sites on the

```
; OTHER INFORMATION: non-coding strand
US-09-943-115A-62

Query Match          0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 498 ATTGGAAGCA 508
Db 11 ATTGGAAGCA 1

RESULT 156
US-09-942-310-50
; Sequence 50, Application US/09942310
; Publication No. US20030044797A1
; GENERAL INFORMATION:
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria K.
; APPLICANT: Lewander, Tommy
; APPLICANT: Olafsson, Erik
; TITLE OF INVENTION: Detection of CYP2D6 Polymorphisms
; FILE REFERENCE: GG119.1US
; CURRENT APPLICATION NUMBER: US/09/942,310
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: GB 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 11
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-942-310-50

Query Match          0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1125 ACTTGAAGCA 1135
Db 1 ACTTGAAGCA 11

RESULT 157
US-09-942-310-57/c
; Sequence 57, Application US/09942310
; Publication No. US20030044797A1
; GENERAL INFORMATION:
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria K.
; APPLICANT: Lewander, Tommy
; APPLICANT: Olafsson, Erik
; TITLE OF INVENTION: Detection of CYP2D6 Polymorphisms
; FILE REFERENCE: GG119.1US
; CURRENT APPLICATION NUMBER: US/09/942,310
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: GB 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 11
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-942-310-57

Query Match          0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1125 ACTTGAAGCA 1135
Db 1 ACTTGAAGCA 11

RESULT 158
US-10-266-138B-8
; Sequence 8, Application US/10266138B
; Publication No. US20030152964A1
; GENERAL INFORMATION:
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: URSCHITZ, Johann
; TITLE OF INVENTION: METHODS OF IDENTIFYING PHOTODAMAGE USING GENE
; FILE REFERENCE: J6664US(ED;EP/JVT)seq13Sep'02:51 84
; CURRENT APPLICATION NUMBER: US/10/266,138B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/338,272
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Seq # 1 of 1
US-10-266-138B-8

Query Match          0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CAATAAACTGA 2119
Db 1 CAATAAACTGA 11

RESULT 159
US-10-265-509B-8
; Sequence 8, Application US/10265509B
; Publication No. US20030170739A1
; GENERAL INFORMATION:
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: URSCHITZ, Johann
; TITLE OF INVENTION: GENE EXPRESSION FOR ANALYZING PHOTODAMAGE
; FILE REFERENCE: J6663US(ED;EP/JVT)seq13Sep'02:51-84
; CURRENT APPLICATION NUMBER: US/10/265,509B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/337,856
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Seq # 58 of 58
US-10-265-509B-8

Query Match          0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2109 CAATAAACTGA 2119  
 |||||  
 Db 1 CAATAAACTGA 11

## RESULT 160

US-10-419-058-17  
 ; Sequence 17, Application US/10419058  
 ; Publication No. US20040053366A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lo, Kin-Ming  
 ; APPLICANT: Zhang, Jinyang  
 ; APPLICANT: Gillies, Stephen D.  
 ; TITLE OF INVENTION: Expression and Export of Anti-Obesity Proteins as Fc  
 ; TITLE OF INVENTION: Fusion Proteins  
 ; FILE REFERENCE: LEX-008  
 ; CURRENT APPLICATION NUMBER: US/10/419,058  
 ; CURRENT FILING DATE: 2003-04-18  
 ; PRIOR APPLICATION NUMBER: US/09/479,508  
 ; PRIOR FILING DATE: 2000-01-07  
 ; PRIOR APPLICATION NUMBER: US 60/115,079  
 ; PRIOR FILING DATE: 1999-01-07  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 17  
 ; LENGTH: 11  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: EcoRI/AflII  
 ; OTHER INFORMATION: linker-adaptor  
 US-10-419-058-17

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 713 TTAGATATCG 723  
 |||||  
 Db 1 TTAGATATCG 11

## RESULT 161

US-10-450-797-684  
 ; Sequence 684, Application US/10450797  
 ; Publication No. US20040142335A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Petersohn, Dirk  
 ; APPLICANT: Conradt, Marcus  
 ; APPLICANT: Hofmann, Kay  
 ; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO  
 ; FILE REFERENCE: HENK-0041  
 ; CURRENT APPLICATION NUMBER: US/10/450,797  
 ; CURRENT FILING DATE: 2003-12-04  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/15178  
 ; PRIOR FILING DATE: 2001-12-20  
 ; PRIOR APPLICATION NUMBER: DE 101 00 121.5  
 ; PRIOR FILING DATE: 2001-01-03  
 ; NUMBER OF SEQ ID NOS: 1435  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 684  
 ; LENGTH: 11  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-450-797-684

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2109 CAATAAACTGA 2119  
 |||||  
 Db 1 CAATAAACTGA 11

## RESULT 162

US-10-450-797-1061/c  
 ; Sequence 1061, Application US/10450797  
 ; Publication No. US20040142335A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Petersohn, Dirk  
 ; APPLICANT: Conradt, Marcus  
 ; APPLICANT: Hofmann, Kay  
 ; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO  
 ; FILE REFERENCE: HENK-0041  
 ; CURRENT APPLICATION NUMBER: US/10/450,797  
 ; CURRENT FILING DATE: 2003-12-04  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/15178  
 ; PRIOR FILING DATE: 2001-12-20  
 ; PRIOR APPLICATION NUMBER: DE 101 00 121.5  
 ; PRIOR FILING DATE: 2001-01-03  
 ; NUMBER OF SEQ ID NOS: 1435  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 1061  
 ; LENGTH: 11  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-450-797-1061

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 660 TGTAAACTCA 670  
 |||||  
 Db 11 TGTAAACTCA 1

## RESULT 163

US-10-474-794-37  
 ; Sequence 37, Application US/10474794  
 ; Publication No. US20040213793A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carson-Walter, Eleanor  
 ; APPLICANT: St. Croix, Brad  
 ; APPLICANT: Vogelstein, Bert  
 ; APPLICANT: Kinzler, Kenneth  
 ; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
 ; FILE REFERENCE: 1107.00179  
 ; CURRENT APPLICATION NUMBER: US/10/474,794  
 ; CURRENT FILING DATE: 2003-10-14  
 ; PRIOR APPLICATION NUMBER: 60/282,850  
 ; PRIOR FILING DATE: 2001-04-11  
 ; PRIOR APPLICATION NUMBER: 60/308,829  
 ; PRIOR FILING DATE: 2001-08-01  
 ; NUMBER OF SEQ ID NOS: 359  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 37  
 ; LENGTH: 11  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-474-794-37

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 997 TGTAACTACA 1007  
 |||||  
 Db 1 TGTAACTACA 11

## RESULT 164

US-10-474-794-148  
 ; Sequence 148, Application US/10474794  
 ; Publication No. US20040213793A1

```

; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-474-794-148

```

```

Query Match          0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      80 TGTGAAAAAA 90
        |||||
Db       1 TGTGAAAAAA 11

```

## RESULT 165

```

US-10-979-159-37
; Sequence 37, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-979-159-37

```

```

Query Match          0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      997 TGTTTAATACA 1007
        |||||
Db       1 TGTTTAATACA 11

```

## RESULT 166

```

US-10-979-159-148
; Sequence 148, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix

```

```

; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-979-159-148

```

```

Query Match          0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      80 TGTGAAAAAA 90
        |||||
Db       1 TGTGAAAAAA 11

```

## RESULT 167

```

US-10-257-017B-334847
; Sequence 334847, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 334847
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC003H439
US-10-257-017B-334847

```

```

Query Match          0.4%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1225 TTCGTTATTAG 1236
        |||||
Db       1 TTCGTTATTAG 12

```

## RESULT 168

```

US-10-257-017B-337451/c
; Sequence 337451, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine

```

```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 337451
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039880
US-10-257-017B-337451

Query Match      0.4%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1225 TTGTTATTAAAG 1236
Db 12 TTGTTATTATG 1

RESULT 169
US-10-257-017B-359588/c
; Sequence 359588, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359588
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051670
US-10-257-017B-359588

Query Match      0.4%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1742 ATACGGATGTG 1753
Db 12 ATACGGATGTG 1

RESULT 170
US-08-935-377-15
; Sequence 15, Application US/08935377
; Publication No. US2003013917A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: T Cells Specific for Target Antigens and
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20005
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,377
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-935-377-15

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 TACCTATGGC 1458
Db 1 TACCTATGGC 10

RESULT 171
US-09-772-105-83/c
; Sequence 83, Application US/09772105
; Patent No. US20010029015A1
; GENERAL INFORMATION:
; APPLICANT: Ozellus, Laurie J.
; TITLE OF INVENTION: TORSIN, TORSIN-RELATED GENES, AND
; TITLE OF INVENTION: METHODS OF DETECTING NEURONAL DISEASES
; FILE REFERENCE: 0838.1001009
; CURRENT APPLICATION NUMBER: US/09/772,105
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/218,363
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/099,454
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/050,244
; PRIOR FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Exon/intron of TORB
US-09-772-105-83

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 CTGAGTTTGC 743
Db 10 CTGAGTTTGC 1

RESULT 172
US-09-822-250-15
```

```
; Sequence 15, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-15

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1449 TACCTATGCC 1458
Db       1 TACCTATGCC 10

RESULT 173
US-09-816-763-55/c
; Sequence 55, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor IAF
US-09-816-763-55

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      147 AGCAGATGCC 156
Db       10 AGCAGATGCC 1

RESULT 174
US-09-371-900-25/c
; Sequence 25, Application US/09371900
; Patent No. US20020137700A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP

; Sequence 15, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-15

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1449 TACCTATGCC 1458
Db       1 TACCTATGCC 10

RESULT 173
US-09-816-763-55/c
; Sequence 55, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor IAF
US-09-816-763-55

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      147 AGCAGATGCC 156
Db       10 AGCAGATGCC 1

RESULT 174
US-09-371-900-25/c
; Sequence 25, Application US/09371900
; Patent No. US20020137700A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP

; Sequence 8, Application US/09951133
; Patent No. US20020146714A1
; GENERAL INFORMATION:
; APPLICANT: LIEBER, CHARLES M.
; APPLICANT: WOOLLEY, ADAM T.
; APPLICANT: HAHM, JONG-IN
; APPLICANT: HOUSMAN, DAVID
; TITLE OF INVENTION: DIRECT
; FILE REFERENCE: HUV-042.01
; CURRENT APPLICATION NUMBER: US/09/951,133
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/231,608
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesis: PNA
```

```
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/371,900
; FILING DATE: 11-Aug-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/599,654
; FILING DATE: 09-FEB-1996
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-371-900-25

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2031 CATCACCACC 2040
Db       10 CATCACCACC 1

RESULT 175
US-09-951-133-8
; Sequence 8, Application US/09951133
; Patent No. US20020146714A1
; GENERAL INFORMATION:
; APPLICANT: LIEBER, CHARLES M.
; APPLICANT: WOOLLEY, ADAM T.
; APPLICANT: HAHM, JONG-IN
; APPLICANT: HOUSMAN, DAVID
; TITLE OF INVENTION: DIRECT
; FILE REFERENCE: HUV-042.01
; CURRENT APPLICATION NUMBER: US/09/951,133
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/231,608
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesis: PNA
```



```
; OTHER INFORMATION: label
US-09-951-133-8

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2505 CTTGCTCCA 2514
Db 1 CTTGCTCCA 10

RESULT 176
US-09-951-133-11/c
; Sequence 11, Application US/09951133
; Patent No. US20020146714A1
; GENERAL INFORMATION:
; APPLICANT: LIEBER, CHARLES M.
; APPLICANT: WOOLLEY, ADAM T.
; APPLICANT: HAHM, JONG-IN
; APPLICANT: HOUSMAN, DAVID
; TITLE OF INVENTION: DIRECT HAPLOTPYING USING CARBON NANOTUBE PROBES
; FILE REFERENCE: HUV-042.01
; CURRENT APPLICATION NUMBER: US/09/951.133
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/231,608
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-951-133-11

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2505 CTTGCTCCA 2514
Db 1 CTTGCTCCA 10

RESULT 177
US-09-955-410-28
; Sequence 28, Application US/09955410
; Patent No. US20020146718A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases
; FILE REFERENCE: ISIS4800
; CURRENT APPLICATION NUMBER: US/09/955.410
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 09/686,114
; PRIOR FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020146718A1el Sequence
US-09-955-410-28
```

```
Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAACAAAA 75
Db 1 AAAAACAAAA 10

RESULT 178
US-09-983-210-6
; Sequence 6, Application US/09983210
; Patent No. US20020160383A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/983.210
; FILING DATE: 2001-OCT-23
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150156
; FILING DATE: 1994-APR-05
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-09-983-210-6

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAACAAAA 75
Db 1 AAAAACAAAA 10

RESULT 179
US-09-970-820-25/c
; Sequence 25, Application US/09970820
; Patent No. US20020170077A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
```

```

; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/970,820
; APPLICATION NUMBER: US/09/970,820
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-970-820-25

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040
DB 10 CATCACCACC 1

RESULT 180
US-09-970-820-25/c
; Sequence 25, Application US/09986718
; Patent No. US20020178458A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/986,718
; FILING DATE: 09-No. US20020178458A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,573
; FILING DATE: <Unknown>

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-986-718-25

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040
DB 10 CATCACCACC 1

RESULT 181
US-09-979-593-57/c
; Sequence 57, Application US/09979593
; Publication No. US20030082555A1
; GENERAL INFORMATION:
; APPLICANT: Genesense Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y
; APPLICANT: Denton, R. Rex
; APPLICANT: Kliem, Stefanie E
; APPLICANT: Lee, Helen H
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
; FILE REFERENCE: MMH-0425 PCT ICAM2
; CURRENT APPLICATION NUMBER: US/09/979,593
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/14714
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: 60/201,946
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-979-593-57

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 444 CGAAGATGAA 453
DB 10 CGAAGATGAA 1

RESULT 182
US-10-033-145-1/c
; Sequence 1, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS

```

```
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      624 AGAAATATA 633
DB      10 AGAAATATA 1

RESULT 183
US-10-033-145-175/c
; Sequence 175, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 175
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-175

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      819 TCTTCTGAGT 828
DB      10 TCTTCTGAGT 1

RESULT 184
US-10-033-145-223/c
; Sequence 223, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 223
; LENGTH: 10
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-10-033-145-223

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      345 ACCAGTAGCA 354
DB      10 ACCAGTAGCA 1

RESULT 185
US-10-033-145-414/c
; Sequence 414, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 414
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-414

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1934 ATCAGCATCA 1943
DB      10 ATCAGCATCA 1

RESULT 186
US-10-033-145-528
; Sequence 528, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 528
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-528

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1132 AGAATATCAG 1141
DB      1 AGAATATCAG 10
```

```
RESULT 187
US-10-033-145-592
; Sequence 592, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 592
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-592
```

```
Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      933 AGGAAAGAT 942
Db      1 AGGAAAGAT 10
```

```
RESULT 188
US-10-033-145-761/c
; Sequence 761, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 761
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-761
```

```
Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1837 GAAACCAAGCT 1846
Db      10 GAAACCAAGCT 1
```

```
RESULT 189
US-10-033-145-767/c
; Sequence 767, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
```

```
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 767
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-767
```

```
Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      803 GTGCTTGGC 812
Db      10 GTGCTTGGC 1
```

```
RESULT 190
US-10-033-145-929
; Sequence 929, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 929
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-929
```

```
Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      420 ATTGATCAAT 429
Db      1 ATTGATCAAT 10
```

```
RESULT 191
US-10-033-145-929/c
; Sequence 929, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 929
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-929
```

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 420 ATTGATCAAT 429  
 Db 10 ATTGATCAAT 1

## RESULT 192

US-10-033-145-1306  
 ; Sequence 1306, Application US/10033145  
 ; Publication No. US2002015151A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GENZYME CORPORATION  
 ; APPLICANT: ROBERTS, BRUCE  
 ; APPLICANT: SHANKARA, SRINIVAS  
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES  
 ; FILE REFERENCE: GA0201C  
 ; CURRENT APPLICATION NUMBER: US/10/033,145  
 ; CURRENT FILING DATE: 2001-11-05  
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800  
 ; PRIOR FILING DATE: 1999-06-18  
 ; NUMBER OF SEQ ID NOS: 2137  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1306  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-033-145-1306

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2295 ATGGTTAAAG 2304  
 Db 1 ATGGTTAAAG 10

## RESULT 193

US-10-033-145-1342/c  
 ; Sequence 1342, Application US/10033145  
 ; Publication No. US2002015151A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GENZYME CORPORATION  
 ; APPLICANT: ROBERTS, BRUCE  
 ; APPLICANT: SHANKARA, SRINIVAS  
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES  
 ; FILE REFERENCE: GA0201C  
 ; CURRENT APPLICATION NUMBER: US/10/033,145  
 ; CURRENT FILING DATE: 2001-11-05  
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800  
 ; PRIOR FILING DATE: 1999-06-18  
 ; NUMBER OF SEQ ID NOS: 2137  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1342  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-033-145-1342

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 759 TGAAGAGAA 768  
 Db 10 TGAAGAGAA 1

## RESULT 194

US-10-033-145-1408  
 ; Sequence 1408, Application US/10033145  
 ; Publication No. US2002015151A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GENZYME CORPORATION  
 ; APPLICANT: ROBERTS, BRUCE  
 ; APPLICANT: SHANKARA, SRINIVAS  
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES  
 ; FILE REFERENCE: GA0201C  
 ; CURRENT APPLICATION NUMBER: US/10/033,145  
 ; CURRENT FILING DATE: 2001-11-05  
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800  
 ; PRIOR FILING DATE: 1999-06-18  
 ; NUMBER OF SEQ ID NOS: 2137  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1408  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-033-145-1408

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1582 AACGAAAGTG 1591  
 Db 1 AACGAAAGTG 10

## RESULT 195

US-10-033-145-1552/c  
 ; Sequence 1552, Application US/10033145  
 ; Publication No. US2002015151A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GENZYME CORPORATION  
 ; APPLICANT: ROBERTS, BRUCE  
 ; APPLICANT: SHANKARA, SRINIVAS  
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES  
 ; FILE REFERENCE: GA0201C  
 ; CURRENT APPLICATION NUMBER: US/10/033,145  
 ; CURRENT FILING DATE: 2001-11-05  
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800  
 ; PRIOR FILING DATE: 1999-06-18  
 ; NUMBER OF SEQ ID NOS: 2137  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1552  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-033-145-1552

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 508 ATCACTCAG 517  
 Db 10 ATCACTCAG 1

## RESULT 196

US-10-033-145-1571/c  
 ; Sequence 1571, Application US/10033145  
 ; Publication No. US2002015151A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GENZYME CORPORATION  
 ; APPLICANT: ROBERTS, BRUCE  
 ; APPLICANT: SHANKARA, SRINIVAS  
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES  
 ; FILE REFERENCE: GA0201C  
 ; CURRENT APPLICATION NUMBER: US/10/033,145  
 ; CURRENT FILING DATE: 2001-11-05

```
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1571
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1571
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1633 ATACATCAAA 1642
Db 10 ATACATCAAA 1
```

```
RESULT 197
US-10-033-145-1678
; Sequence 1678, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1678
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1678
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 999 TTATAATACAT 1008
Db 1 TTATAATACAT 10
```

```
RESULT 198
US-10-033-145-1830
; Sequence 1830, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1830
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1830
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
```

```
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 806 TCTTGGCATA 815
Db 1 TCTTGGCATA 10
```

```
RESULT 199
US-10-033-145-1866/c
; Sequence 1866, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1866
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1866
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 831 GCTGTCAACA 840
Db 10 GCTGTCAACA 1
```

```
RESULT 200
US-10-033-145-2050/c
; Sequence 2050, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2050
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-2050
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1754 TGATTACATT 1763
Db 10 TGATTACATT 1
```

```
RESULT 201
US-10-238-732-3/c
; Sequence 3, Application US/10238732
```

```

; Publication No. US20030077635A1
; GENERAL INFORMATION:
; APPLICANT: DAKO A/S
; TITLE OF INVENTION: DENDRIMERS AND METHODS FOR THEIR PREPARATION AND USE
; FILE REFERENCE: P65587US1
; CURRENT APPLICATION NUMBER: US/10/238,732
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 09/606,315
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: PA 1999 00934
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: linker sequence.
US-10-238-732-3

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      124 ACTGGCAAAA 133
Db      10 ACTGGCAAAA 1

RESULT 202
US-10-010-802-286
; Sequence 286, Application US/10010802
; Publication No. US20030078220A1
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Duda, Amy
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; APPLICANT: Windemuth, Andreas
; TITLE OF INVENTION: Drug Target Isogenes: Polymorphisms in the Interleukin
; TITLE OF INVENTION: 4 Receptor Alpha Gene
; FILE REFERENCE: MMH-0002US2 IL4R alpha
; CURRENT APPLICATION NUMBER: US/10/010,802
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/US00/19094
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 286
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-802-286

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1211 AAGCAGCTCC 1220
Db      1 AAGCAGCTCC 10

RESULT 203
US-10-223-765-294/c
; Sequence 294, Application US/10223765
; Publication No. US20030165997A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo

```

```

; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 294
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-223-765-294

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1211 AAGCAGCTCC 1220
Db      10 AAGCAGCTCC 1

RESULT 204
US-10-390-045-20/c
; Sequence 20, Application US/10390045
; Publication No. US20030170713A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POLYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/10/390,045
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US/09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-390-045-20

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      828 TGGGCTGTCA 837
Db      10 TGGGCTGTCA 1

RESULT 205

```





```

; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcription
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-313

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      345 ACCAGTAGCA 354
      |||||
DB      10 ACCAGTAGCA 1

```

## RESULT 210

```

US-10-330-627-687
; Sequence 687, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; TITLE OF INVENTION: Human Transcription
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 687
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-687

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1874 AAAGCCCAAGA 1883
      |||||
DB      1 AAAGCCCAAGA 10

```

## RESULT 211

```

US-10-330-627-988
; Sequence 988, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; TITLE OF INVENTION: Human Transcription
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 988
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-988

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2109 CAATAAACTG 2118
      |||||
DB      1 CAATAAACTG 10

```

## RESULT 212

```

US-10-330-627-1207/c
; Sequence 1207, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; TITLE OF INVENTION: Human Transcription
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1207
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1207

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      819 TCTTCTGAGT 828
      |||||
DB      10 TCTTCTGAGT 1

```

## RESULT 213

```

US-10-154-890-28
; Sequence 28, Application US/10154890
; Publication No. US20030180734A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/10/154,890
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US/08/108,591
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030180734A1e1 Sequence
US-10-154-890-28

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;

```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAAACAAA 75  
 Db 1 AAAAAACAAA 10

## RESULT 214

US-10-186-950-25/c  
 ; Sequence 25, Application US/10186950  
 ; Publication No. US20030188327A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FALB, DEAN A  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
 ; NUMBER OF SEQUENCES: 54  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS LLP  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/186,950

APPLICATION NUMBER: US/10/186,950

FILING DATE: 02-Jul-2002

CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/944,496

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/599,654

FILING DATE: 09-FEB-1996

APPLICATION NUMBER: US 08/485,573

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/386,844

FILING DATE: 10-FEB-1995

## ATTORNEY/AGENT INFORMATION:

NAME: CORUZZI, LAURA A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-104

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 750-9090

TELEFAX: (212) 869-8864

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic oligonucleotide"

HYPOTHETICAL: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-10-186-950-25

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040  
 Db 10 CATCACCACC 1

## RESULT 215

US-10-160-358-103

; Sequence 103, Application US/10160358

; Publication No. US20030198969A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genesee Pharmaceuticals, Inc.  
 ; APPLICANT: Bieglecki, Karyn  
 ; APPLICANT: Cappola, Gina-Marie  
 ; APPLICANT: Koshiy, Beena  
 ; APPLICANT: Monroe, Glen  
 ; TITLE OF INVENTION: HAPLOTYPES OF THE TACR2 GENE  
 ; FILE REFERENCE: TACR2 MMH-0225US  
 ; CURRENT APPLICATION NUMBER: US/10/160,358  
 ; CURRENT FILING DATE: 2002 05 30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/47194  
 ; PRIOR FILING DATE: 2001 11 09  
 ; PRIOR APPLICATION NUMBER: 60/247,649  
 ; PRIOR FILING DATE: 2000-11-09  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 103  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-160-358-103

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1400 ATAGAGCTAA 1409  
 Db 1 ATAGAGCTAA 10

## RESULT 216

US-10-298-796-57/c

; Sequence 57, Application US/10298796

; Publication No. US20030220490A1

; GENERAL INFORMATION:

; APPLICANT: KURIYAMA, Shinichi

; APPLICANT: HASEGAWA, Takashi

; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS

; FILE REFERENCE: 1110-253P

; CURRENT APPLICATION NUMBER: US/10/298.796

; CURRENT FILING DATE: 2002-11-19

; PRIOR APPLICATION NUMBER: US/09/311,793

; PRIOR FILING DATE: 1999-06-25

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 57

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Synthetic DNA Primers

; US-10-298-796-57

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 989 CTCACGAATG 998  
 Db 10 CTCACGAATG 1

## RESULT 217

US-10-293-222-322/c

; Sequence 322, Application US/10293222

; Publication No. US2004003932A1

; GENERAL INFORMATION:

; APPLICANT: Versteeg, Rogier

; APPLICANT: Caron, Hubertus N.

; TITLE OF INVENTION: MYC targets

; FILE REFERENCE: 2183-5580US

; CURRENT APPLICATION NUMBER: US/10/293,222

; CURRENT FILING DATE: 2002-11-12

```
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 322
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-322
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 188 ACATTATTC 197
Db 10 ACATTATTC 1
```

```
RESULT 218
US-10-293-222-367/c
; Sequence 367, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 367
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-367
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2344 AAATACAAA 2353
Db 10 AAATACAAA 1
```

```
RESULT 219
US-10-293-222-399
; Sequence 399, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
```

```
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 399
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-399
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 487 GGAGGAGGC 496
Db 1 GGAGGAGGC 10
```

```
RESULT 220
US-10-293-222-430
; Sequence 430, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 430
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-430
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 65 TAAAAACAAA 74
Db 1 TAAAAACAAA 10
```

```
RESULT 221
US-10-434-479-20/c
; Sequence 20, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMEPA1 GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-434-479-20

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 TGGGCTGTCA 837
DB 10 TGGGCTGTCA 1

RESULT 222
US-10-434-479-36/c
; Sequence 36, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMEPAL GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-434-479-36

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1837 GAAACCAGCT 1846
DB 10 GAAACCAGCT 1

RESULT 223
US-10-434-479-56
; Sequence 56, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMEPAL GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-434-479-56

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 TACCTATGGC 1458
DB 1 TACCTATGGC 10

RESULT 225
US-10-821-568-55/c
; Sequence 55, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-434-479-56

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 AAAGCCAAGA 1883
DB 1 AAAGCCAAGA 10

RESULT 224
US-10-034-350-15
; Sequence 15, Application US/10034350
; Publication No. US20040151730A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods of Selecting Polynucleotides Encoding Ant. Prot.
; FILE REFERENCE: 1821.0010002
; CURRENT APPLICATION NUMBER: US/10/034,350
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 08/945,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-034-350-15

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 TACCTATGGC 1458
DB 1 TACCTATGGC 10

RESULT 225
US-10-821-568-55/c
; Sequence 55, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
```

```
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor IAF
US-10-821-568-55

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      147 AGCAGATGGC 156
Db      10 AGCAGATGGC 1

RESULT 226
US-10-149-109A-124
; Sequence 124, Application US/10149109A
; Publication No. US20040248090A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method For The Parallel Detection Of The
; FILE REFERENCE: E01-1140-WO
; CURRENT APPLICATION NUMBER: US/10/149,109A
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Comment for artificial sequence: chemically
US-10-149-109A-124

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      371 AATTAATTAA 380
Db      1 AATTAATTAA 10

RESULT 227
US-10-149-109A-125/c
; Sequence 125, Application US/10149109A
; Publication No. US20040248090A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method For The Parallel Detection Of The
; FILE REFERENCE: E01-1140-WO
; CURRENT APPLICATION NUMBER: US/10/149,109A
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Comment for artificial sequence: chemically
US-10-149-109A-125

; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor IAF
US-10-821-568-55

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      147 AGCAGATGGC 156
Db      10 AGCAGATGGC 1

RESULT 226
US-10-149-109A-124
; Sequence 124, Application US/10149109A
; Publication No. US20040248090A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method For The Parallel Detection Of The
; FILE REFERENCE: E01-1140-WO
; CURRENT APPLICATION NUMBER: US/10/149,109A
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Comment for artificial sequence: chemically
US-10-149-109A-124

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      371 AATTAATTAA 380
Db      1 AATTAATTAA 10

RESULT 227
US-10-149-109A-125/c
; Sequence 125, Application US/10149109A
; Publication No. US20040248090A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method For The Parallel Detection Of The
; FILE REFERENCE: E01-1140-WO
; CURRENT APPLICATION NUMBER: US/10/149,109A
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Comment for artificial sequence: chemically
US-10-149-109A-125

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      149 TACCTATGGC 1458
Db      1 TACCTATGGC 10

RESULT 229
US-10-755-118-60/c
; Sequence 60, Application US/10755118
; Publication No. US20050009041A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
; FILE REFERENCE: ISIS-5427
; CURRENT APPLICATION NUMBER: US/10/755,118
; CURRENT FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: US 08/462,977
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: DN 510/92
; PRIOR FILING DATE: 1992-04-15
; PRIOR APPLICATION NUMBER: DN 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: DN 986/91
; PRIOR FILING DATE: 1991-05-24
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 10
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Lys-NH2
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: (2'-aminoethyl)glycine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: Hydrogen
US-10-755-118-60
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 66 AAAAAACAAAA 75
Db 10 AAAAAACAAAA 1
```

```
RESULT 230
US-10-755-118-73/c
; Sequence 73, Application US/10755118
; Publication No. US2005009041A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
; FILE REFERENCE: ISIS-5427
; CURRENT APPLICATION NUMBER: US/10/755,118
; CURRENT FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: US 08/462,977
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: DN 510/92
; PRIOR FILING DATE: 1992-04-15
; PRIOR APPLICATION NUMBER: DN 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: DN 986/91
; PRIOR FILING DATE: 1991-05-24
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Lys-NH2
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: Hydrogen
US-10-755-118-73
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 66 AAAAAACAAAA 75
Db 10 AAAAAACAAAA 1

RESULT 231
US-10-755-118-74
; Sequence 74, Application US/10755118
; Publication No. US2005009041A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR
; FILE REFERENCE: ISIS-5427
; CURRENT APPLICATION NUMBER: US/10/755,118
; CURRENT FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: US 08/462,977
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: DN 510/92
; PRIOR FILING DATE: 1992-04-15
; PRIOR APPLICATION NUMBER: DN 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: DN 986/91
; PRIOR FILING DATE: 1991-05-24
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 74
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deoxynucleotide
US-10-755-118-74
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 66 AAAAAACAAAA 75
Db 10 AAAAAACAAAA 1
```

```
RESULT 232
US-10-805-292-153
; Sequence 153, Application US/10805292
; Publication No. US20050026176A1
; GENERAL INFORMATION:
; APPLICANT: Yoshii, Hiroto
; APPLICANT: Fukui, Toshifumi
; TITLE OF INVENTION: DNA PROBE DESIGNING APPARATUS AND INFORMATION PROCESSING METHOD
; FILE REFERENCE: 03560.003438
; CURRENT APPLICATION NUMBER: US/10/805,292
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: JPA2003-099464
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 153
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: DNA exemplified in the drawing
US-10-805-292-153
```

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 AACTGGAAA 323  
 |||||  
 Db 1 AACTGGAAA 10

## RESULT 233

US-10-661-398-4  
 ; Sequence 4, Application US/10661398  
 ; Publication No. US2005069896A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horvitz, H. Robert  
 ; APPLICANT: Ceol, Craig  
 ; TITLE OF INVENTION: RB PATHWAY AND CHROMATIN REMODELING  
 ; TITLE OF INVENTION: GENES THAT ANTAGONIZE LET-60 RAS SIGNALING  
 ; FILE REFERENCE: 01997/548003  
 ; CURRENT APPLICATION NUMBER: US/10/661,398  
 ; CURRENT FILING DATE: 2003-09-12  
 ; PRIOR FILING DATE: 2003-01-02  
 ; PRIOR FILING DATE: 2003-01-02  
 ; PRIOR FILING DATE: 2002-09-12  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Caenorhabditis elegans  
 US-10-661-398-4

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 921 AGTTTCAGAC 930  
 |||||  
 Db 1 AGTTTCAGAC 10

## RESULT 234

US-10-661-398-5  
 ; Sequence 5, Application US/10661398  
 ; Publication No. US2005069896A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horvitz, H. Robert  
 ; APPLICANT: Ceol, Craig  
 ; TITLE OF INVENTION: RB PATHWAY AND CHROMATIN REMODELING  
 ; TITLE OF INVENTION: GENES THAT ANTAGONIZE LET-60 RAS SIGNALING  
 ; FILE REFERENCE: 01997/548003  
 ; CURRENT APPLICATION NUMBER: US/10/661,398  
 ; CURRENT FILING DATE: 2003-09-12  
 ; PRIOR FILING DATE: 2003-01-02  
 ; PRIOR FILING DATE: 2003-01-02  
 ; PRIOR FILING DATE: 2002-09-12  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Caenorhabditis elegans  
 US-10-661-398-5

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 921 AGTTTCAGAC 930

Db 1 AGTTTCAGAC 10  
 |||||

## RESULT 235

US-11-035-899-403/c  
 ; Sequence 403, Application US/11035899  
 ; Publication No. US20050196412A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nicholas J. Deacon  
 ; APPLICANT: Jennifer C. Learmont  
 ; APPLICANT: Dale A. McPhee  
 ; APPLICANT: Suzanne Crowe  
 ; APPLICANT: David Cooper  
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
 ; NUMBER OF SEQUENCES: 841  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
 ; STREET: 400 GARDEN CITY PLAZA  
 ; CITY: GARDEN CITY  
 ; STATE: NEW YORK  
 ; COUNTRY: U.S.A.  
 ; ZIP: 11530-0299  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/11/035,899  
 ; FILING DATE: 14-Jan-2005  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/477,464  
 ; FILING DATE: 07-JUN-1995  
 ; APPLICATION NUMBER: PM3864 (AU)  
 ; FILING DATE: 14-FEB-1994  
 ; APPLICATION NUMBER: PM4002 (AU)  
 ; FILING DATE: 21-FEB-1994  
 ; APPLICATION NUMBER: PM0284 (AU)  
 ; FILING DATE: 23-DEC-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: FRANK S. DIGICLIO  
 ; REFERENCE/DOCKET NUMBER: 9606Z-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (516) 742-4343  
 ; TELEFAX: (516) 742-4366  
 ; INFORMATION FOR SEQ ID NO: 403:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 403:  
 US-11-035-899-403

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 CACTGGATAT 224  
 |||||  
 Db 10 CACTGGATAT 1

## RESULT 236

US-11-035-899-613  
 ; Sequence 613, Application US/11035899  
 ; Publication No. US20050196412A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nicholas J. Deacon  
 ; APPLICANT: Jennifer C. Learmont  
 ; APPLICANT: Dale A. McPhee

```

;
; Suzanne Crowe
; David Cooper
;
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
;
; INFORMATION FOR SEQ ID NO: 613:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-11-035-899-613

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GAACTGCTGA 737
DB 1 GAACTGCTGA 10
|||||
;
; RESULT 237
; US-11-035-899-732
; Sequence 732, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
;
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
;
; INFORMATION FOR SEQ ID NO: 613:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-11-035-899-613

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GAACTGCTGA 737
DB 1 GAACTGCTGA 10
|||||
;
; RESULT 237
; US-11-035-899-732
; Sequence 732, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
;
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
;
; INFORMATION FOR SEQ ID NO: 613:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-11-035-899-613

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GAACTGCTGA 737
DB 1 GAACTGCTGA 10
|||||
;
; RESULT 237
; US-11-035-899-732
; Sequence 732, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
;
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
;
; INFORMATION FOR SEQ ID NO: 732:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 732:
US-11-035-899-732

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1232 TTAAGCCTCA 1241
DB 1 TTAAGCCTCA 10
|||||
;
; RESULT 238
; US-11-035-899-733
; Sequence 733, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
;
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
;
; INFORMATION FOR SEQ ID NO: 732:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 732:
US-11-035-899-732
```



```

; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PNO284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 733:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 733:
US-11-035-899-733

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1233 TAAGCCTCAA 1242
Db      1 TAAGCCTCAA 10

```

## RESULT 239

```

; US-11-012-522-184
; Sequence 184, Application US/11012522
; Publication No. US20060014264A1
; GENERAL INFORMATION:
; APPLICANT: Stowers Institute for Medical Research
; APPLICANT: Sauer, Brian Lee
; APPLICANT: Petyuk, Vladislav Aleksandrovich
; TITLE OF INVENTION: A CRE/LOX SYSTEM WITH LOX SITES HAVING AN EXTENDED SPACER REGION
; FILE REFERENCE: 097289
; CURRENT APPLICATION NUMBER: US/11/012,522
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/587,399
; PRIOR FILING DATE: 2004-07-13
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 184
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant lox sites
; US-11-012-522-184

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      371 AATTAATTAA 380
Db      1 AATTAATTAA 10

```

## RESULT 240

```

; US-11-012-522-185/c
; Sequence 185, Application US/11012522
; Publication No. US20060014264A1
; GENERAL INFORMATION:
; APPLICANT: Stowers Institute for Medical Research
; APPLICANT: Sauer, Brian Lee
; APPLICANT: Petyuk, Vladislav Aleksandrovich
; TITLE OF INVENTION: A CRE/LOX SYSTEM WITH LOX SITES HAVING AN EXTENDED SPACER REGION
; FILE REFERENCE: 097289
; CURRENT APPLICATION NUMBER: US/11/012,522

```

```

; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/587,399
; PRIOR FILING DATE: 2004-07-13
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 185
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant lox sites
; US-11-012-522-185

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      371 AATTAATTAA 380
Db      10 AATTAATTAA 1

```

## RESULT 241

```

; US-11-012-522-188
; Sequence 188, Application US/11012522
; Publication No. US20060014264A1
; GENERAL INFORMATION:
; APPLICANT: Stowers Institute for Medical Research
; APPLICANT: Sauer, Brian Lee
; APPLICANT: Petyuk, Vladislav Aleksandrovich
; TITLE OF INVENTION: A CRE/LOX SYSTEM WITH LOX SITES HAVING AN EXTENDED SPACER REGION
; FILE REFERENCE: 097289
; CURRENT APPLICATION NUMBER: US/11/012,522
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/587,399
; PRIOR FILING DATE: 2004-07-13
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 188
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant lox sites
; US-11-012-522-188

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      373 TTAATTAATAA 382
Db      1 TTAATTAATAA 10

```

## RESULT 242

```

; US-11-012-522-207
; Sequence 207, Application US/11012522
; Publication No. US20060014264A1
; GENERAL INFORMATION:
; APPLICANT: Stowers Institute for Medical Research
; APPLICANT: Sauer, Brian Lee
; APPLICANT: Petyuk, Vladislav Aleksandrovich
; TITLE OF INVENTION: A CRE/LOX SYSTEM WITH LOX SITES HAVING AN EXTENDED SPACER REGION
; FILE REFERENCE: 097289
; CURRENT APPLICATION NUMBER: US/11/012,522
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/587,399
; PRIOR FILING DATE: 2004-07-13
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 207
; LENGTH: 10

```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant lox sites
US-11-012-522-207

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1332 CGAAGAATTA 1341
Db 1 CGAAGAATTA 10

RESULT 243
US-11-012-522-233
; Sequence 233, Application US/11012522
; Publication No. US20060014264A1
; GENERAL INFORMATION:
; APPLICANT: Stowers Institute for Medical Research
; APPLICANT: Sauer, Brian Lee
; TITLE OF INVENTION: A CRE/LOX SYSTEM WITH LOX SITES HAVING AN EXTENDED SPACER REGION
; FILE REFERENCE: 097289
; CURRENT APPLICATION NUMBER: US/11/012,522
; PRIOR FILING DATE: 2004-12-15
; PRIOR FILING DATE: 2004-07-13
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 233
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant lox sites
US-11-012-522-233

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 585 TATGCATGAA 594
Db 1 TATGCATGAA 10

RESULT 244
US-11-012-522-255/c
; Sequence 255, Application US/11012522
; Publication No. US20060014264A1
; GENERAL INFORMATION:
; APPLICANT: Stowers Institute for Medical Research
; APPLICANT: Sauer, Brian Lee
; TITLE OF INVENTION: A CRE/LOX SYSTEM WITH LOX SITES HAVING AN EXTENDED SPACER REGION
; FILE REFERENCE: 097289
; CURRENT APPLICATION NUMBER: US/11/012,522
; PRIOR FILING DATE: 2004-12-15
; PRIOR FILING DATE: 2004-07-13
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 255
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant lox sites
US-11-012-522-255

Query Match      0.4%; Score 10; DB 1; Length 10;
```

```
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2288 AAATCACATG 2297
Db 10 AAATCACATG 1

RESULT 245
US-11-029-005-6
; Sequence 6, Application US/11029005
; Publication No. US20060046255A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; STREET: Langlandsvej 20 B 3 th
; CITY: Fredericksberg
; COUNTRY: Denmark
; ZIP: DK-2000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/029,005
; FILING DATE: 05-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/983,210
; FILING DATE: 2001-OCT-23
; APPLICATION NUMBER: US 08/150156
; FILING DATE: 1994-APR-05
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Berg, Rolf Henrik
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-11-029-005-6

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAACAAAA 75
Db 1 AAAAACAAAA 10

Search completed: January 17, 2007, 09:06:12
Job time : 5 secs
```

```

RESULT 1
US-11-148-303-479
; Sequence 479, Application US/11148303
; Publication No. US20060154886A1
; GENERAL INFORMATION:
; APPLICANT: Gruenenthal GmbH
; TITLE OF INVENTION: Regulatory elements in the 5' region of the VR1 gene
; FILE REFERENCE: GR01P003WO
; CURRENT APPLICATION NUMBER: US/11/148,303
; CURRENT FILING DATE: 2005-06-09
; NUMBER OF SEQ ID NOS: 781
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 479

```

; SEQ ID NO 792  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-158-209-792

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 758 TTGAAGAGAA 768  
Db 11 TTGAAGAGAA 1

## RESULT 4

US-09-966-746-5  
; Sequence 5, Application US/09966746  
; Publication No. US20060257849A1  
; GENERAL INFORMATION:  
; APPLICANT: Zauderer, Maurice  
; TITLE OF INVENTION: Method of Screening for Therapeutics for Infectious Diseases  
; FILE REFERENCE: 1821.0060001  
; CURRENT APPLICATION NUMBER: US/09/966,746  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: US 60/236,381  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer  
US-09-966-746-5

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 TACCTATGGC 1458  
Db 1 TACCTATGGC 10

## RESULT 5

US-10-524-432-196/c  
; Sequence 196, Application US/10524432  
; Publication No. US20060127902A1  
; GENERAL INFORMATION:  
; APPLICANT: Genzyme Corporation  
; APPLICANT: The Johns Hopkins University  
; TITLE OF INVENTION: BRAIN ENDOTHELIAL EXPRESSION PATTERNS  
; FILE REFERENCE: 003482.00010  
; CURRENT APPLICATION NUMBER: US/10/524,432  
; CURRENT FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: US 60/403,390  
; PRIOR FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 60/458,978  
; PRIOR FILING DATE: 2003-04-01  
; NUMBER OF SEQ ID NOS: 869  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 196  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-524-432-196

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1065 CACAAAATC 1074  
Db 10 CACAAAATC 1

## RESULT 6

US-10-524-432-837/c  
; Sequence 837, Application US/10524432  
; Publication No. US20060127902A1  
; GENERAL INFORMATION:  
; APPLICANT: Genzyme Corporation  
; APPLICANT: The Johns Hopkins University  
; TITLE OF INVENTION: BRAIN ENDOTHELIAL EXPRESSION PATTERNS  
; FILE REFERENCE: 003482.00010  
; CURRENT APPLICATION NUMBER: US/10/524,432  
; CURRENT FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: US 60/403,390  
; PRIOR FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 60/458,978  
; PRIOR FILING DATE: 2003-04-01  
; NUMBER OF SEQ ID NOS: 869  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 837  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-524-432-837

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1065 CACAAAATC 1074  
Db 10 CACAAAATC 1

## RESULT 7

US-10-691-012-28  
; Sequence 28, Application US/10691012  
; Publication No. US20060160731A1  
; GENERAL INFORMATION:  
; APPLICANT: Buchardt, Ole  
; APPLICANT: Egholm, Michael  
; APPLICANT: Nielsen, Peter Sigil  
; APPLICANT: Berg, Rolf Henrik  
; TITLE OF INVENTION: Peptide Nucleic Acids  
; FILE REFERENCE: ISIS0540  
; CURRENT APPLICATION NUMBER: US/10/691,012  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: US/08/108,591  
; PRIOR FILING DATE: 1993-11-22  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Novel Sequence  
US-10-691-012-28

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAACAAAA 75  
Db 1 AAAAACAAAA 10

## RESULT 8

US-10-511-841A-3/c

```
; Sequence 3, Application US/10511841A
; Publication No. US20070004047A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SASKATCHEWAN
; APPLICANT: LEE, Jeremy S.
; APPLICANT: WETTIG, Shawn D.
; APPLICANT: KRAATZ, Heinz-Bernhard
; TITLE OF INVENTION: METHODS AND APPARATUS FOR MOLECULAR DATA STORAGE, RETRIEVAL AND
; TITLE OF INVENTION: ANALYSIS
; FILE REFERENCE: 81527-37
; CURRENT APPLICATION NUMBER: US/10/511,841A
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: WO PCT/CA03/00574
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/373,644
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA strand referred to as MM1 Sequence
US-10-511-841A-3

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 CATGAAGTCC 1531
    |||||
DB 10 CATGAAGTCC 1

RESULT 9
US-11-452-925-20/c
; Sequence 20, Application US/11452925
; Publication No. US20060269546A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMPAL GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/11/452,925
; CURRENT FILING DATE: 2006-06-15
; PRIOR APPLICATION NUMBER: US/10/434,479
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-452-925-20

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 TGGGCTGTCA 837
    |||||
DB 10 TGGGCTGTCA 837

; Sequence 3, Application US/10511841A
; Publication No. US20070004047A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SASKATCHEWAN
; APPLICANT: LEE, Jeremy S.
; APPLICANT: WETTIG, Shawn D.
; APPLICANT: KRAATZ, Heinz-Bernhard
; TITLE OF INVENTION: METHODS AND APPARATUS FOR MOLECULAR DATA STORAGE, RETRIEVAL AND
; TITLE OF INVENTION: ANALYSIS
; FILE REFERENCE: 81527-37
; CURRENT APPLICATION NUMBER: US/10/511,841A
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: WO PCT/CA03/00574
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/373,644
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA strand referred to as MM1 Sequence
US-10-511-841A-3

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 CATGAAGTCC 1531
    |||||
DB 10 CATGAAGTCC 1

RESULT 9
US-11-452-925-20/c
; Sequence 20, Application US/11452925
; Publication No. US20060269546A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMPAL GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/11/452,925
; CURRENT FILING DATE: 2006-06-15
; PRIOR APPLICATION NUMBER: US/10/434,479
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-452-925-20

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 TGGGCTGTCA 837
    |||||
DB 10 TGGGCTGTCA 837

; Sequence 36, Application US/11452925
; Publication No. US20060269546A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMPAL GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/11/452,925
; CURRENT FILING DATE: 2006-06-15
; PRIOR APPLICATION NUMBER: US/10/434,479
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-452-925-36

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1837 GAAACCAAGCT 1846
    |||||
DB 10 GAAACCAAGCT 1

RESULT 11
US-11-452-925-56
; Sequence 56, Application US/11452925
; Publication No. US20060269546A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMPAL GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/11/452,925
; CURRENT FILING DATE: 2006-06-15
; PRIOR APPLICATION NUMBER: US/10/434,479
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 10
; TYPE: DNA
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-452-925-56

```

```

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1874 AAAGCCAAGA 1883
Db 1 AAAGCCAAGA 10

```

```

RESULT 12
US-11-297-134-10/c
; Sequence 10, Application US/11297134
; Publication No. US2006011297A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Roberts, Bruce
; TITLE OF INVENTION: BLOOD FACTOR DOMAINS
; FILE REFERENCE: 5270C
; CURRENT APPLICATION NUMBER: US/11/297,134
; PRIOR FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: PCT/US2005/018461
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/477,291
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-297-134-10

```

```

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 196 TCAAAATACA 205
Db 10 TCAAAATACA 1

```

```

RESULT 13
US-11-297-134-50
; Sequence 50, Application US/11297134
; Publication No. US2006011297A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Roberts, Bruce
; TITLE OF INVENTION: BLOOD FACTOR DOMAINS
; FILE REFERENCE: 5270C
; CURRENT APPLICATION NUMBER: US/11/297,134
; PRIOR FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: PCT/US2005/018461
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/477,291
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-297-134-50

```

```

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 999 TTTAATACAT 1008
Db 1 TTTAATACAT 10

```

```

RESULT 14
US-11-346-326-35
; Sequence 35, Application US/11346326
; Publication No. US20060148036A1
; GENERAL INFORMATION:
; APPLICANT: Hanna et al
; TITLE OF INVENTION: GABAA Receptor Epsilon Subunits
; FILE REFERENCE: PF374P1D1
; CURRENT APPLICATION NUMBER: US/11/346,326
; CURRENT FILING DATE: 2006-02-03
; PRIOR APPLICATION NUMBER: 09/030,832
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 08/888,012
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-346-326-35

```

```

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 506 GGATCACCTC 515
Db 1 GGATCACCTC 10

```

```

RESULT 15
US-11-148-303-177
; Sequence 177, Application US/11148303
; Publication No. US20060154886A1
; GENERAL INFORMATION:
; APPLICANT: Gruenenthal GmbH
; TITLE OF INVENTION: Regulatory elements in the 5' region of the VRI gene
; FILE REFERENCE: GROIP003WO
; CURRENT APPLICATION NUMBER: US/11/148,303
; CURRENT FILING DATE: 2005-06-09
; NUMBER OF SEQ ID NOS: 781
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 177
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: VSAP4 Q5
US-11-148-303-177

```

```

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1212 AGCAGCTCCA 1221
Db 1 AGCAGCTCCA 10

```

```

Search completed: January 17, 2007, 09:10:30
Job time : 0.001 secs

```

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2007, 20:59:06 ; Search time 14217 Seconds  
(without alignments)  
11321.352 Million cell updates/sec

Title: US-10-528-631-1  
Perfect score: 2517  
Sequence: 1 gaatttagtgtagctga.....gaaacgactgcctccagta 2517

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 1

Total number of hits satisfying chosen parameters: 12730834

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pi:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_uni:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_cm:\*  
15: gb\_pa:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	25	1.0	2800	13	CR855983	CR855983 Parametiu
2	25	1.0	110000	15	CP000102	Continuation (3 of
3	23	0.9	133896	12	CR936298	CR936298 Danio rer
4	23	0.9	147460	11	BX255929	BX255929 Zebrafish
5	23	0.9	152010	11	BX511002	BX511002 Zebrafish
6	23	0.9	211752	12	CT025902	CT025902 Danio rer
7	23	0.9	234428	12	AC113793	AC113793 Rattus no
8	22	0.9	4833	5	AK125056	AK125056 Homo sapi
9	22	0.9	5368	2	AX344691	AX344691 Sequence
10	22	0.9	23887	5	HSTITINN2	X90569 H.sapiens m
11	22	0.9	31876	13	AV656839	AV656839 Leishmani
12	22	0.9	37515	2	AX458481	AX458481 Sequence
13	22	0.9	44184	12	AC174086	AC174086 Strongylo
14	22	0.9	96951	12	AC177789	AC177789 Strongylo
15	22	0.9	103053	2	CQ848088	CQ848088 Sequence
16	22	0.9	104299	2	CS119317	CS119317 Sequence
17	22	0.9	153477	12	AC006278	AC006278 Plasmodiu
18	22	0.9	156702	12	AC084223	AC084223 Homo sapi

c 19	22	0.9	157927	5	AP006278	AP006278 Homo sapi
c 20	22	0.9	160356	12	AC177406	AC177406 Strongylo
c 21	22	0.9	166176	12	AC165302	AC165302 Mus muscu
c 22	22	0.9	171301	5	AC010859	AC010859 Homo sapi
c 23	22	0.9	173527	12	AC168365	AC168365 Strongylo
c 24	22	0.9	177476	5	AC010680	AC010680 Homo sapi
c 25	22	0.9	182455	6	AC136735	AC136735 Mus muscu
c 26	22	0.9	193489	6	AC158347	AC158347 Mus muscu
c 27	22	0.9	195546	6	AC127338	AC127338 Mus muscu
c 28	22	0.9	208618	12	AC102175	AC102175 Mus muscu
c 29	22	0.9	235590	12	AC106473	AC106473 Rattus no
c 30	22	0.9	251551	13	AE014844	AE014844 Plasmodiu
c 31	22	0.9	266598	12	AC106954	AC106954 Rattus no
c 32	22	0.9	294540	5	HS277892	AJ277892 Homo sapi
c 33	21	0.8	350	15	MHO251995	AJ251995 Mycoplasma
c 34	21	0.8	350	15	MHO279209	AJ279209 Mycoplasma
c 35	21	0.8	350	15	MHO279210	AJ279210 Mycoplasma
c 36	21	0.8	350	15	MHO279211	AJ279211 Mycoplasma
c 37	21	0.8	350	15	MHO279213	AJ279213 Mycoplasma
c 38	21	0.8	350	15	MHO279214	AJ279214 Mycoplasma
c 39	21	0.8	350	15	MHO279215	AJ279215 Mycoplasma
c 40	21	0.8	350	15	MHO279216	AJ279216 Mycoplasma
c 41	21	0.8	350	15	MHO279217	AJ279217 Mycoplasma
c 42	21	0.8	350	15	MHO279218	AJ279218 Mycoplasma
c 43	21	0.8	350	15	MHO279219	AJ279219 Mycoplasma
c 44	21	0.8	350	15	MHO279220	AJ279220 Mycoplasma
c 45	21	0.8	350	15	MHO279221	AJ279221 Mycoplasma

#### ALIGNMENTS

CR855983 2800 bp DNA linear INV 14-SEP-2005  
Parametiu tetraurelia macronuclear, putative gene for  
CGMP-dependent protein kinase 13, isoform 2, complete gene.

CR855983  
CR855983.1 GI:74832328

VERSION  
genomic DNA; INV.

KEYWORDS  
Parametiu tetraurelia

SOURCE  
Parametiu tetraurelia

ORGANISM  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;

REFERENCE  
1 (bases 1 to 2800)

AUTHORS  
Kissmehl R., Krueger, T., Treptau, T., Froissard, M. and Plattner, H.

TITLE  
Identification of a multigene family encoding CGMP-dependent

JOURNAL  
protein kinases in Parametium tetraurelia cells

REFERENCE  
2 (bases 1 to 2800)

AUTHORS  
Unpublished

JOURNAL  
Genoscope.

TITLE  
Direct Submission

JOURNAL  
Submitted (08-NOV-2004) Genoscope - Centre National de Sequencage :

COMMENT  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr

Sequencing was performed at Genoscope and annotations were obtained

by Roland Kissmehl (University of Konstanz, Department of Biology,

Germany).

FEATURES  
Location/Qualifiers

source  
1..2800

/organism="Parametium tetraurelia"

/macronuclear

/mol\_type="genomic DNA"

/db\_xref="taxon:5888"

/note="Genoscope sequence ID : SC 6060 255158 252358

one base has to be removed from this part of the

SuperContig sequence, 't' between t252524 and a252526"

join(53..256,282..675,705..815,842..1341,1376..1789,

1815..2078,2105..2488,2515..2697)

/gene="pkg13-2"

join(53..256,282..675,705..815,842..1341,1376..1789,

1815..2078,2105..2488,2515..2697)

/gene="pkg13-2"





complete sequence.

ACCESSION BX255929  
 VERSION BX255929.7 GI:42820876  
 KEYWORDS HTG.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 147460)  
 Heath, P.  
 Direct Submission  
 Submitted (26-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
 On Feb 25, 2004 this sequence version replaced gi:42661822.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: zfish-help@sanger.ac.uk  
 -----

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see [http://www.sanger.ac.uk/Projects/D\\_rerio/fishmask.shtml](http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml) CH211-271P5 is from a CHORI-211 BAC library

VECTOR: pTARBAC2.1.

FEATURES  
 source  
 1. 147460  
 /location=Qualifiers  
 /organism="Danio rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="CH211-271P5"  
 /clone\_lib="CHORI-211"

## ORIGIN

Query Match 0.9%; Score 23; DB 11; Length 147460;  
 Best Local Similarity 100.0%; Pred. No. 0.31;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 TTGTAACAAACAAAGAGTTGTTG 84  
 |||||  
 Db 118598 TTGTAACAAACAAAGAGTTGTTG 118620

RESULT 5  
 BX511002  
 LOCUS 152010 bp DNA linear VRT 23-FEB-2005

DEFINITION Zebrafish DNA sequence from clone DKEY-254G2 in linkage group 21, complete sequence.  
 ACCESSION BX511002  
 VERSION BX511002.14 GI:598990042  
 KEYWORDS HTG.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 152010)  
 Fosker, N.  
 Direct Submission  
 Submitted (22-FEB-2005) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
 On Feb 16, 2005 this sequence version replaced gi:58578314.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: zfish-help@sanger.ac.uk  
 -----

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see [http://www.sanger.ac.uk/Projects/D\\_rerio/fishmask.shtml](http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml) DKEY-254G2 is from a Zebrafish BAC library

VECTOR: pIndigoBAC-5

FEATURES  
 source  
 1. 152010  
 /location=Qualifiers  
 /organism="Danio rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="DKEY-254G2"  
 /clone\_lib="DantioKey"

## ORIGIN

Query Match 0.9%; Score 23; DB 11; Length 152010;  
 Best Local Similarity 100.0%; Pred. No. 0.31;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 TTGTAACAAACAAAGAGTTGTTG 84  
 |||||  
 Db 30354 TTGTAACAAACAAAGAGTTGTTG 30376

RESULT 6  
 CT025902

```

LOCUS          CT025902                211752 bp      DNA      linear      HTG 07-SEP-2005
DEFINITION     Danio rerio chromosome 21 clone CH211-78L3, *** SEQUENCING IN
PROGRESS ***, 6 unordered pieces.
ACCESSION      CT025902
VERSION        CT025902.2 GI:74271700
KEYWORDS       HTG; HTGS_PHASE1
SOURCE         Danio rerio (zebrafish)
ORGANISM       Danio rerio
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
               Cypriniformes; Cyprinidae; Danio.
REFERENCE      1 (bases 1 to 211752)
AUTHORS        Sims,S.
TITLE          Direct Submission
JOURNAL        Submitted (05-SEP-2005) Wellcome Trust Sanger Institute, Hinxton,
               Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
               zf1sh-help@sanger.ac.uk Clone requests:
               http://www.sanger.ac.uk/Projects/D_rerio/faq.shtmldataeight
               On Sep 7, 2005 this sequence version replaced gi:74197922.
COMMENT        ----- Genome Center
               Center: Wellcome Trust Sanger Institute
               Center code: SC
               Web site: http://www.sanger.ac.uk
               Contact: zf1sh-help@sanger.ac.uk
               ----- Project Information
               Center project name: zC78L3
               ----- Summary Statistics
               Assembly program: XGAP4; version 4.5
               Chemistry: Dye-terminator; 100% of reads
               Consensus quality: 210044 bases at least Q40
               Consensus quality: 210278 bases at least Q30
               Consensus quality: 210479 bases at least Q20
               Insert size: 211252; sum-of-contigs
               Insert size: 219668; 7.3% error; agarose-fp
               Quality coverage: 9.61x in Q20 bases; sum-of-contigs Quality
               coverage: 9.37x in Q20 bases; agarose-fp
               -----
               * NOTE: This is a 'working draft' sequence. It currently
               * consists of 6 contigs. The true order of the pieces
               * is not known and their order in this sequence record is
               * arbitrary. Gaps between the contigs are represented as
               * runs of N, but the exact sizes of the gaps are unknown.
               * This record will be updated with the finished sequence
               * as soon as it is available and the accession number will
               * be preserved.
               *
               * 1 16330: contig of 16330 bp in length
               * 16331 16430: gap of 100 bp
               * 16431 40188: contig of 23758 bp in length
               * 40189 40288: gap of 100 bp
               * 40289 139262: contig of 98974 bp in length
               * 139263 139362: gap of 100 bp
               * 139363 196540: contig of 57178 bp in length
               * 196541 196640: gap of 100 bp
               * 196641 204198: contig of 7558 bp in length
               * 204199 204298: gap of 100 bp
               * 204299 211752: contig of 7454 bp in length.
               Location/Qualifiers
               1..211752
                /organism="Danio rerio"
                /mol_type="genomic DNA"
                /db_xref="taxon:7955"
                /chromosomes="21"
                /clone="CH211-78L3"
                /clone_lib="CHORI-211"
                /clone .16330
               1..16330
                /note="assembly fragment:00231
                fragment chain:1
                clone end:SP6
                vector side:left"
                16431..40188
                /note="assembly fragment:00505
                fragment chain:1"
                40289..139262

```

```

                /note="assembly fragment:01733
                fragment chain:1"
                139363..196540
                /note="assembly fragment:00879
                fragment chain:1"
                196641..204198
                /note="assembly fragment:00117
                fragment chain:2"
                204299..211752
                /note="assembly fragment:00028
                fragment chain:2
                clone end:T7
                vector_side:right"
ORIGIN
Query Match          0.9%; Score 23; DB 12; Length 211752;
Best Local Similarity 100.0%; Pred. NO. 0.29;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      62 TTGTAACCAACCAACGAGTGTGTTG 84
Db      82162 TTGTAACCAACCAACGAGTGTGTTG 82184

RESULT 7
AC113793/c
LOCUS    AC113793                234428 bp      DNA      linear      HTG 15-NOV-2002
DEFINITION Rattus norvegicus clone CH230-252B6, WORKING DRAFT SEQUENCE, 3
           unordered pieces.
ACCESSION AC113793
VERSION   AC113793.5 GI:25006630
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 234428)
AUTHORS   Muzny,D,Marie., Metzker,M,Lee., Abranzon,S., Adams,C., Alder,J.,
           Allen,C., Allen,H., Alabrooks,S., Amin,A., Anguiano,D.,
           Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
           Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
           Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
           Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
           Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
           Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
           Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
           Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
           Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
           Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
           Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
           Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
           Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
           Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
           Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
           Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
           Hernandez,R., Hines,S., Hladun,S.B., Hodgson,A., Hogue,M.,
           Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
           Jackson,L., Jacob,S., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
           Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
           Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
           Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
           Lorenshewa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J.,
           Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
           Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
           Mawhinney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
           Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
           Morgan,M., Morris,K., Morris,S., Muidasa,M., Murphy,M., Nair,L.,
           Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
           Nwaokemeleh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
           Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
           Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
           Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,

```

Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, M., Savary, G., Scherer, S., Scott, G., Shattman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 234428)  
Worley, K.C.

Submitted (05-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 234428)

Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23195098.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GSHB  
Center clone name: CH230-252E6  
----- Summary Statistics

Assembly program: Phrap; version 0.990329  
Consensus quality: 162771 bases at least Q40  
Consensus quality: 164719 bases at least Q30  
Consensus quality: 166467 bases at least Q20  
Estimated insert size: 168120; sum-of-contigs estimation  
Quality coverage: 'x' in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 182487: contig of 182487 bp in length  
\* 182488 182587: gap of unknown length  
\* 182588 205254: contig of 22667 bp in length  
\* 205255 205354: gap of unknown length  
\* 205355 234428: contig of 29074 bp in length.  
Location/Qualifiers

## FEATURES

source 1. 234428  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clones="CH230-252E6"  
178049..179372  
/note="wgs contig"  
181022..182487  
/note="wgs contig"  
182488..182587  
/estimated\_length=unknown  
205255..205354  
/estimated\_length=unknown  
ORIGIN  
Query Match 0.9%; Score 23; DB 12; Length 234428;  
Best Local Similarity 100.0%; Pred. No. 0.29;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 366 AAAAGAAATTAATTAAGAA 388  
Db 205222 AAAAGAAATTAATTAAGAA 202500  
RESULT 8  
AK125056 4833 bp mRNA linear PRI 20-JAN-2006  
LOCUS Homo sapiens CDNA FLJ43066 fis, clone BRTHA3008608, highly similar to Homo sapiens partial TTN gene for titin.  
DEFINITION AK125056  
ACCESSION AK125056  
VERSION AK125056.1 GI:34531022  
KEYWORDS oligo capping; fis (full insert sequence).  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oyayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Iehii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamiyama, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoaka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T.O., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshihara, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, K., Tashiro, H., Tanigami, A., Fujisawa, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Omori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsunaga, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togaishi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.  
Complete sequencing and characterization of 21,243 full-length human cDNAs  
Nat. Genet. 36 (1), 40-45 (2004)  
14702039  
REFERENCE 2  
AUTHORS Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,

Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshina,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahara,K., Masuho,Y., Nagai,K. and Isogai,T.  
NEDO human cDNA sequencing project

# TITLE JOURNAL

## REFERENCE AUTHORS

## TITLE JOURNAL

## TITLE JOURNAL

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

Unpublished  
3 (bases 1 to 4833)  
Isogai,T. and Yamamoto,J.  
Direct Submission  
Submitted (15-JUL-2003) Takao Isogai, Helix Research Institute,  
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 252-0812, Japan  
(E-mail: flj-cdna@nifty.com, Tel:81-438-52-3975, Fax:81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology (RAB); cDNA library  
construction: Helix Research Institute (HRI) (supported by Japan  
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,  
HRI, and Biotechnology Center, National Institute of Technology and  
Evaluation; clone selection for full insert sequencing: HRI and  
RAB; annotation: Reverse Proteomics Research Institute, HRI and  
RAB.

# TITLE JOURNAL

## REFERENCE AUTHORS

## TITLE JOURNAL

## TITLE JOURNAL

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

Query Match 0.9%; Score 22; DB 5; Length 4833;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# TITLE JOURNAL

## REFERENCE AUTHORS

## TITLE JOURNAL

## TITLE JOURNAL

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

Query Match 0.9%; Score 22; DB 2; Length 5368;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# TITLE JOURNAL

## REFERENCE AUTHORS

## TITLE JOURNAL

## TITLE JOURNAL

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

Query Match 0.9%; Score 22; DB 2; Length 5368;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# TITLE JOURNAL

## REFERENCE AUTHORS

## TITLE JOURNAL

## TITLE JOURNAL

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

Query Match 0.9%; Score 22; DB 2; Length 5368;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# TITLE JOURNAL

## REFERENCE AUTHORS

## TITLE JOURNAL

## TITLE JOURNAL

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

Query Match 0.9%; Score 22; DB 2; Length 5368;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# TITLE JOURNAL

## REFERENCE AUTHORS

## TITLE JOURNAL

## TITLE JOURNAL

## COMMENT</



```

REFERENCE
AUTHORS Dahlin-Laborde,R.R., Yu,T.P. and Beetham,J.K.
TITLE GENETIC COMPLEMENTATION TO IDENTIFY DNA ELEMENTS THAT INFLUENCE
JOURNAL COMPLEMENT RESISTANCE IN LEISHMANIA CHAGASI
REFERENCE J. Parasitol. 91 (5), 1058-1063 (2005)
AUTHORS J. 2 (bases 1 to 31876)
TITLE Beetham,J.K. and Dahlin-Laborde,R.R.
JOURNAL Direct Submission
COMMENT Submitted (17-JUN-2004) Veterinary Pathology, Iowa State
University, 2754 Veterinary Medicine, Ames, IA 50011, USA
NCBI staff are still waiting for submitters to provide appropriate
feature information.
FEATURES
Source Location/Qualifiers
1..31876
/organism="Leishmania donovani chagasi"
/mol_type="genomic DNA"
/sub_species="chagasi"
/db_xref="taxon:44271"
ORIGIN
Query Match 0.9%; Score 22; DB 13; Length 31876;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 964 AAAAAACAAAGAAAAACGAATGA 985
|||||
Db 23015 AAAAAACAAAGAAAAACGAATGA 23036
|||||
RESULT 12
AX458481/c 37515 bp DNA linear PAT 08-JUL-2002
LOCUS
DEFINITION Sequence 27 from Patent WO0246454.
ACCESSION AX458481
VERSION AX458481.1 GI:21725145
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Schacht,O.
AUTHORS Diagnosis of diseases associated with angiogenesis
TITLE Patent: WO 0246454-A 27 13-JUN-2002;
JOURNAL Epigenomics AG (DE)
FEATURES
Source Location/Qualifiers
1..37515
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="chemically treated genomic DNA (Homo sapiens)"
ORIGIN
Query Match 0.9%; Score 22; DB 2; Length 37515;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 85 AAAAAACCAAACTAAAC 106
|||||
Db 24339 AAAAAACCAAACTAAAC 24318
|||||
RESULT 13
AC174086/c 44184 bp DNA linear HTG 10-DEC-2005
LOCUS
DEFINITION Strongylocentrotus purpuratus Clone R3-56D18, *** SEQUENCING IN
PROGRESS ***, 12 unordered pieces.
ACCESSION AC174086
VERSION AC174086.1 GI:83423536
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

```

# REFERENCE AUTHORS

Echinoidea; Euechinoidea; Echinacea; Echinoida;  
Strongylocentrotidae; Strongylocentrotus.  
1 (bases 1 to 4184)  
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,  
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,  
Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,  
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,  
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,  
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,  
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,  
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,  
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,  
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,  
Douchwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,  
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,  
Fallis,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,  
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,  
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,  
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,  
Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B.,  
Homsai,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,  
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,  
Karissom,B., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,  
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,  
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,  
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,  
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,  
Massey,B., Mawhney,B., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,  
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,  
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,  
Nguyen,N., Nickerson,E., Nwokenwo,S., Oguh,M., Okwuonu,G.,  
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,  
Peters,L., Pickens,R., Primus,S., Pu,L.L., Quiles,M., Renvy,G.,  
Rives,M., Rojas,A., Rojlobokan,I., Roife,M., Ruiz,S., Saveny,A.,  
Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,  
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,  
Sutton,A., Svatek,A., Tabot,P., Tamerisa,A., Tamerisa,K., Tang,H.,  
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,  
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,  
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Worley,K.,  
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,  
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
Weinstock,G. and Gibbs,R.

## Direct Submission

Unpublished  
2 (bases 1 to 4184)  
Worley,K.C.

## Direct Submission

Submitted (10-DEC-2005) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

## COMMENT

Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help.tmc.edu  
----- Project Information  
Center project name: SPZK  
Center clone name: R3-56D18  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye: 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 43098 bases at least Q40  
Consensus quality: 44501 bases at least Q30  
Consensus quality: 45343 bases at least Q20  
Estimated insert size: 78104; sum-of-contigs estimation  
Quality coverage: 1x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 12 contigs. The true order of the pieces

\* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```

1      6926: contig of 6926 bp in length
6927  7026: gap of unknown length
7027  9485: contig of 2459 bp in length
9486  9885: gap of unknown length
9886  11792: contig of 2207 bp in length
11793  11892: gap of unknown length
11893  14071: contig of 2179 bp in length
14072  14171: gap of unknown length
14172  17224: contig of 3053 bp in length
17225  17224: gap of unknown length
17225  19692: contig of 2368 bp in length
19693  19792: gap of unknown length
19793  22522: contig of 2730 bp in length
22523  22622: gap of unknown length
22623  25331: contig of 2709 bp in length
25332  25331: gap of unknown length
25332  27711: contig of 2280 bp in length
27712  27811: gap of unknown length
27812  34455: contig of 6644 bp in length
34456  34555: gap of unknown length
34556  41912: contig of 7357 bp in length
41913  42012: gap of unknown length
42013  44184: contig of 2172 bp in length.
42013  Location/Qualifiers
1. 44184
/organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
/db_xref="taxon:7668"
/clone="R3-56D18"
6927. 7026
/estimated_length=unknown
9486 9885
/estimated_length=unknown
11793. 11892
/estimated_length=unknown
14072. 14171
/estimated_length=unknown
17225. 17324
/estimated_length=unknown
19693. 19792
/estimated_length=unknown
22523. 22622
/estimated_length=unknown
25332. 25431
/estimated_length=unknown
27712. 27811
/estimated_length=unknown
34456. 34555
/estimated_length=unknown
41913. 42012
/estimated_length=unknown

```

## FEATURES

source

```

Query Match      0.9%; Score 22; DB 12; Length 44184;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1166 TGGTAGAGAAATATAATATA 1187
|||||
Db 40364 TGGTAGAGAAATATAATATA 40343
|||||

```

## RESULT 14

```

AC177789
LOCUS AC177789 96951 bp DNA linear HTG 27-JAN-2006
DEFINITION Strongylocentrotus purpuratus clone R3-1002C8, WORKING DRAFT
SEQUENCE, 9 unordered pieces.

```

## ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AC177789

AC177789.1 GI:85740534

HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_POOLED\_CLONE; HTGS\_ENRICHED.

Strongylocentrotus purpuratus

Strongylocentrotus purpuratus

Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

Echinoidea; Euechinoidea; Echinacea; Echinoida;

Strongylocentrotidae; Strongylocentrotus.

1 (bases 1 to 96951)

Shen, Y., Abraham, K.K., Abulimiti, A., Adams, C.Q., Aduba, G.,

Allen, C.C., Alsbrooks, S.L., Anosike, U.S., Archer, P.M.,

Arredondo, H.H., Attaway, T., Bandaranaike, D.P., Bangura, L.,

Barton, S.R., Bell, A.V., Bell, S.N., Beraducci, A.R., Bickham, C.,

Biswal, K., Blyth, P.R., Buhay, C.J., Canada, A., Cardenas, V.,

Carter, K., Chacko, J., Chandrabose, M.N., Chavez, A., Chavez, D.,

Chen, G., Chen, R., Chu, H., Clerc blankenburg, K.P., Cockrell, R.,

Cooper, J.A., Coyle, M.D., Cree, A., Cueto, C.B., Curry, S.M., Dai, W.,

Dao, M.D., Davila, M., Davis, C., Davy-Carroll, L., Del fierro, P.,

Demen, R., Denson, S., Ding, Y., Dinh, H.H., Donlin, J.E.,

Dugan-Rocha, S., Dunn, A.M., Durbin, K.J., Ebong, V.E., Egan, A.,

Espinoza, V.C., Fa, M., Fernandez, S., Fernando, P.R., Ferrer, A.R.,

Flagg, N., Forbes, L.D., Fowler, R.G., Fu, Q., Fuh, E., Gabisi, R.A.,

Ganardhanan, M., Garner, J., Garcia iii, R.M., Garcia, A.M.,

Garcia, S.M., Garner, T.T., Ghose, S., Gingras, M.,

Gonzalez-Garay, M.L., Guevara, W.V., Haaland, W.C., Haeblerlen, K.A.,

Hagans, B.J., Hall, O., Hamid, H., Hamilton, K.A., Hampton, O.A.,

Haynes, B.A., Harris, R.A., Havlak, P., Hawes, A.C., Hawkins, E.S.,

Hynes, S.J., Hemphill, L., Hernandez, J., Hines, S., Hixani, K.,

Hitchens, M.E., Hodgson, A.V., Hogue, M.E., Holder, M., Hollins, B.,

Howell, L.L., Hulyk, S.W., Hume, J., Jackson, A., Jackson, L.R.,

Jacob, S.K., Jhangiani, S.N., Jiang, H., Johnson, B., Johnson, R.,

Joshi, V., Joy, C., Kaikai, F.B., Kalafus, K.J., Kalu, J.B., Kang, Y.,

Keeler, J., Khan, Z.M., Kidwai, S., King, L.M., Kisano, H., Kovar, C.L.,

Kowis, A.N., Kowis, C.R., Lago, L.A., Lago, M.T., Lai, C., Lara, F.,

Le, T.T., Lee, S.L., Lee, T.W., Legall iii, F.H., Lemon, S.J.,

Lewis, L.R., Li, B., Li, Y., Li, Z., Linnell, M.A., Liu, J., Liu, W.,

Liu, Y., Liu, Y., Liyanage, D., London, P., Lopez, J., Lorensuwa, L.M.,

Luzado, R.J., Luc, T., Madu, R.C., Maheshwari, M., Maheshwari, R.,

Malloy, K., Mansouri, D.L., Martinez, E., Matejkova, P., Mathew, T.,

McCauley, S.K., McPherson, J.D., Mercado, C., Mercado, I.C.,

Metzker, M.L., Millin, A., Milosavljevic, A., Morgan, M.B., Morris, S.,

Munidasa, M., Murray, D.D., Muzny, D.M., Nazareth, L.V., Ngo, D.N.,

Nguyen, H.T., Nguyen, N.B., Nguyen, P.Q., Nwaokeme, O.O.,

Obregon, M., Odeh, E.A., Okonko, F., Okwuonu, G.O., Okwuonu, K.C.,

Onyeneke, J., Parish, B.J., Parker, D.N., Parra, A.A., Pasternak, S.,

Patel, B.M., Patel, R.R., Paul, H.A., Perez, A., Perez, L.M.,

Perez, Y.Y., Pham, T.L., Player, E.J., Primus, E.L., Pu, L., Puazo, M.,

Purkiss, C., Qin, X., Quiroz, J.B., Rabata, D., Rachin, E.K., Ren, Y.,

Richards, S., Rojas, A., Ruiz, S., Sabo, A., Santibanez, J.,

Savery, G.G., Scherer, S.E., Schneider, B.W., Sebasigari, R.,

Sexton, M.M., Shen, H., Sisson, I., Sneed, A.J., Sodergren, E., Song, X.,

Sorelle, R.P., Svatek, A.F., Taylor, E.W., Taylor, T.R., Thelus, R.,

Thomas, N., Thorn, R.D., Thornton, R.D., Tong, M.Y., Trejos, Z.Y.,

Usmani, K., Vargo, C.E., Vattathil, S., Vega, K.A., Villanar, D.,

Volkov, A., Walker, D.L., Wang, Q., Wang, S., Warren, J.T., Watt, J.E.,

Wei, X., Wheeler, D.A., White, C.S., Williams Jr, R.L., Williams, A.C.,

Williams, G.A., Williams, J.D., Wilson, K., Woodworth, J.R.,

Worley, K.C., Wright, R.A., Wu, J., Wu, W., Yakub, S., Yerrapragada, S.,

Yu, F., Yuan, D.T., Yuan, Y., Zhang, J., Zhang, L., Zhang, Z., Zhou, J.,

Zhu, Y., Weinstein, G. and Gibbs, R.A.

Direct Submission

Unpublished

2 (bases 1 to 96951)

Worley, K.C.

Direct Submission

Submitted (27-JAN-2006)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

## TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

## COMMENT

```

----- Project Information
Center clone name: R3-1002C8
Sequencing Vector: pUC18
Cloning Vector: pBACe3.6
Chemistry: Dye-terminator Big Dye
-----
Summary Statistics
Estimated insert size: ; sum-of-contigs estimation
Quality coverage: x in Q20 bases; sum-of-contigs estimation
-----
NOTE: The sequence in this assembly is a combination of BAC based
reads and whole genome shotgun sequencing reads assembled using
Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). The BAC reads
were identified through a deconvolution of an array containing
pools of BACs. Due to the incorporated WGS reads, there may be
contigs that consist entirely of whole genome shotgun sequence
reads and the sequence may extend beyond the ends of the clone.
Both end sequences and whole genome shotgun sequence only contigs
will be indicated in the features table.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 2076: contig of 2076 bp in length
*
2077 2086: gap of 10 bp
*
2087 15721: contig of 13635 bp in length
*
15722 15731: gap of 10 bp
*
15732 16899: contig of 1168 bp in length
*
16900 45975: gap of unknown length
*
45976 45985: contig of 28976 bp in length
*
45986 56247: gap of 10 bp
*
56248 56347: contig of 10262 bp in length
*
56348 76699: gap of unknown length
*
76700 94636: contig of 17937 bp in length
*
94637 94736: gap of unknown length
*
94737 95459: contig of 723 bp in length
*
95460 95559: gap of unknown length
*
95560 95951: contig of 1392 bp in length.
*
Location/Qualifiers
1. .96951
/organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
/db_xref="taxon:7668"
/clone="R3-1002C8"
1. .2076
/notes="assembly_name:Contig3"
2077. .2086
/notes="assembly_name:gap"
2077. .2086
/estimated_length=10
2087. .15721
/notes="assembly_name:Contig6"
15722. .15731
/notes="assembly_name:gap"
15722. .15731
/estimated_length=10
15732. .16899
/notes="assembly_name:Contig4"
16900. .16999
/estimated_length=unknown
17000. .45975
/notes="assembly_name:Contig9"
45976. .45985
/notes="assembly_name:gap"
45976. .45985
/estimated_length=10
45986. .56247
/notes="assembly_name:Contig5"

```

```

gap 56248..56347
/estimated_length=unknown
misc_feature 56348..76689
/notes="assembly_name:Contig8"
misc_feature 76690..76699
/notes="assembly_name:gap"
gap 76690..76699
/estimated_length=10
misc_feature 76700..94636
/notes="assembly_name:Contig7"
gap 94637..94736
/estimated_length=unknown
misc_feature 94737..95459
/notes="assembly_name:Contig1"
gap 95460..95559
/estimated_length=unknown
misc_feature 95560..96951
/notes="assembly_name:Contig2"
ORIGIN
Query Match 0.9%; Score 22; DB 12; Length 96951;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 362 TTGAAAAAGAAATTAATTAATAAAA 383
|||||
Db 7919 TTGAAAAAGAAATTAATTAATAAAA 7940
|||||
RESULT 15
CQ848088 103053 bp DNA linear PAT 19-AUG-2004
LOCUS
DEFINITION
Sequence 393 from Patent WO2004063362.
ACCESSION CQ848088
VERSION CQ848088.1 GI:51469598
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Glover,D., Bell,G., Frenz,L. and Midgley,C.
TITLE Cell cycle progression proteins
JOURNAL Patent: WO 2004063362-A 393 29-JUL-2004;
FEATURES
Location/Qualifiers
source 1. .103053
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="AJ277892"
ORIGIN
Query Match 0.9%; Score 22; DB 2; Length 103053;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2400 TCGAGAATATATCTGCAAGCT 2421
|||||
Db 26865 TGGAGAATATATCTGCAAGCT 26886
|||||
Search completed: January 16, 2007, 01:04:52
Job time : 14222 secs

```



GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2007, 20:59:53 ; Search time 1553 Seconds

(without alignments)  
11300.161 Million cell updates/sec

Title: US-10-528-631-1

Perfect score: 2517

Sequence: 1 gaatttagtgtagctga.....gaaacgacttgctccagta 2517

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 1

Total number of hits satisfying chosen parameters: 10489196

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq 8.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*
- 15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2517	100.0	2517	12	ADN11328 Aphis gos
2	22	0.9	1232	6	ABQ14818
3	22	0.9	1232	6	ABQ14819
4	22	0.9	5368	6	ABN80099 Human che
5	22	0.9	37515	6	ABQ66997 Human ang
6	22	0.9	103052	13	ADQ89963 Antagonis
7	21	0.8	21	12	ADN11332
8	21	0.8	558	10	ADB52255 Primary r
9	21	0.8	957	8	ACA37322 Prokaryot
10	21	0.8	57296	4	AAK78847 Human imm
11	21	0.8	57296	4	AAK78170 Human imm
12	21	0.8	57296	4	AAK79364 Human imm
13	21	0.8	57296	4	AAK86799 Human imm
14	21	0.8	101505	11	ACN44694 Human gen
15	21	0.8	110000	14	ABE42737 Continuation (14 o
16	21	0.8	160921	11	ACN44962 Human gen
17	21	0.8	200622	14	ABE39167 L. pneumo
18	20	0.8	20	12	ADN11333 Aphis gos

19	20	0.8	263	7	ADS69975	AdS69975	Corn seed
20	20	0.8	932	4	AAI24320	AAI24320	Human bre
21	20	0.8	1268	12	ADP80974	ADP80974	Human ova
22	20	0.8	1557	10	ACC61811	ACC61811	Gene sequ
23	20	0.8	1557	10	ADK63859	ADK63859	Disease t
24	20	0.8	1735	14	ADV97695	ADV97695	cDNA sequ
25	20	0.8	3257	2	AAx61632	AAx61632	B. burgdo
26	20	0.8	3354	2	AAx61631	AAx61631	B. burgdo
27	20	0.8	3385	8	ABV76204	ABV76204	Human imm
28	20	0.8	5379	6	ABL32330	ABL32330	Human imm
29	20	0.8	6133	6	ABK31165	ABK31165	Signal tr
30	20	0.8	6133	6	ABL70504	ABL70504	Chemical
31	20	0.8	6133	6	ABs61052	ABs61052	Human gen
32	20	0.8	6133	6	ABN79987	ABN79987	Human che
33	20	0.8	6403	6	ABL33987	ABL33987	Human imm
34	20	0.8	17784	4	AAI36793	AAI36793	Human mus
35	20	0.8	17784	8	ABX59781	ABX59781	cDNA enco
36	20	0.8	17784	12	ADJ30531	ADJ30531	Human mus
37	20	0.8	23545	13	ADQ89759	ADQ89759	Antagonis
38	20	0.8	23546	4	ABL02655	ABL02655	Drosophil
39	20	0.8	44014	4	ABL02654	ABL02654	Drosophil
40	20	0.8	85315	14	ABE05138	ABE05138	Continuation (7 of
41	20	0.8	110000	2	AAZ02480	AAZ02480	Continuation (7 of
42	20	0.8	110000	2	ABZ01425	ABZ01425	Continuation (8 of
43	20	0.8	110000	14	ABE39175	ABE39175	Continuation (29 o
44	20	0.8	110000	14	ABE42401	ABE42401	Continuation (27 o
45	20	0.8	111309	2	AAx20250	AAx20250	Borrelia

## ALIGNMENTS

## RESULT 1

ADN11328  
ID ADN11328 standard; cDNA; 2517 BP.

AC ADN11328;

DT 01-JUL-2004 (first entry)

DE Aphis gossypii myosin light chain kinase coding sequence.

KW Myosin light chain kinase; enzyme; pesticide; insecticide; cotton aphid;  
KW gene; ss.

OS Aphis gossypii.

FT Key Location/Qualifiers

FT CDS 1..2517

FT /\*tag= a

FT /product= "Myosin light chain kinase"

FT /partial

FT /note= "No start or stop codon"

XX WO2004029577-A2.

XX 08-APR-2004.

XX 18-SEP-2003; 2003WO-US029901.

XX 26-SEP-2002; 2002US-0413720P.

XX (FMCC ) FMC CORP.

XX Chen R, Chaguturu MK, Yuhua D, Allenza P, Halling BP;

XX WPI; 2004-340457/31.

XX P-PSDB; ADN11329.

XX New nucleic acid molecule encoding hemipteran myosin light chain kinase,  
XX useful in identifying or developing compounds with activity as pesticides  
XX or as pharmaceuticals.

PS Claim 3; SEQ ID NO 1; 21bp; English.  
XX  
CC The present is that of an isolated nucleic acid molecule encoding  
CC hemipteran (cotton aphid, *Aphis gossypii*) myosin light chain kinase. The  
CC nucleic acid molecule was obtained by PCR amplification using primers  
CC ADN11330-ADN1133 based on partial transcripts of the gene. The myosin  
CC light chain kinase polynucleotide and the encoded polypeptide can be used  
CC in the identification or development of compounds with activity as  
CC pesticides or as pharmaceuticals. Nucleic acid molecules consisting of a  
CC fragment of the present sequence, and having at least 10 nucleotides,  
CC especially 12-150 nucleotides and in particular 15-50 nucleotides, and a  
CC recombinant vector comprising the present sequence, are also claimed.

XX  
SQ Sequence 2517 BP; 897 A; 490 C; 514 G; 616 T; 0 U; 0 Other;

Query Match 100.0%; Score 2517; DB 12; Length 2517;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAATTTAGAGTACGCTGAAATGCTATGCTAGAGTAAGTAAACCTAGTGAAGTATCACCT	60
Db	1	GAATTTAGAGTACGCTGAAATGCTATGCTAGAGTAAGTAAACCTAGTGAAGTATCACCT	60
Qy	61	ATTGTAATAAACAAGAGTTGTTGMAAAACCCACCAAAACCTAAACCTTACGAAGTTGAT	120
Db	61	ATTGTAATAAACAAGAGTTGTTGMAAAACCCACCAAAACCTAAACCTTACGAAGTTGAT	120
Qy	121	GAAACTGGCAAAATAATACAGGAAGACAGATGGCAATATTAAGATTACGACCAATAT	180
Db	121	GAAACTGGCAAAATAATACAGGAAGACAGATGGCAATATTAAGATTACGACCAATAT	180
Qy	181	GTTTTGGACATTTATTCAAATAATACATACCAACCAAGTGGATATTAATAACACCAATCGTA	240
Db	181	GTTTTGGACATTTATTCAAATAATACATACCAACCAAGTGGATATTAATAACACCAATCGTA	240
Qy	241	TATGATTTATGACATATTAGAAAGAAATCGGAATCGGTGATTTGAGTAGTACACCGT	300
Db	241	TATGATTTATGACATATTAGAAAGAAATCGGAATCGGTGATTTGAGTAGTACACCGT	300
Qy	301	TGTAGGAACTGAACTGGAATATTTTGTGCGCAAAATTTATACAGTAGTACACATAAT	360
Db	301	TGTAGGAACTGAACTGGAATATTTTGTGCGCAAAATTTATACAGTAGTACACATAAT	360
Qy	361	GTTGAAAGAAATTAATTAATAAAGAAATTGACATATGAATGAACCAACTTCATCATCCGAA	420
Db	361	GTTGAAAGAAATTAATTAATAAAGAAATTGACATATGAATGAACCAACTTCATCATCCGAA	420
Qy	421	TTGATCAATTTGATGATGCTTTGCAAGATGAAGATGAATGCTTTAATATTTCGAATTT	480
Db	421	TTGATCAATTTGATGATGCTTTGCAAGATGAAGATGAATGCTTTAATATTTCGAATTT	480
Qy	481	TTGCTGGAGGAGCTATTTGAAAGGATCACTCAGNAGGATCTCAATGTCGGAGCA	540
Db	481	TTGCTGGAGGAGCTATTTGAAAGGATCACTCAGNAGGATCTCAATGTCGGAGCA	540
Qy	541	GAAGTGATCAATATATGCGACAGATATGTAAGCTATTAAAGCATATGCAATGAAGAAAT	600
Db	541	GAAGTGATCAATATATGCGACAGATATGTAAGCTATTAAAGCATATGCAATGAAGAAAT	600
Qy	601	ATCATTTAGATATCAAAACAGAAATATTAATGTGCCAGACAAAGAGAGTTCAAAAT	660
Db	601	ATCATTTAGATATCAAAACAGAAATATTAATGTGCCAGACAAAGAGAGTTCAAAAT	660
Qy	661	GTAAACTCATGATTTGGATTTGGCAACGAAGTGGATTCCTAACGAAATCGTTAAGATA	720
Db	661	GTAAACTCATGATTTGGATTTGGCAACGAAGTGGATTCCTAACGAAATCGTTAAGATA	720
Qy	721	TCGACGGGAACCTGCTGAGTTTGGGCTCCAGAAATAGTTGAAAGAGAACCCAGTTGGTTTC	780
Db	721	TCGACGGGAACCTGCTGAGTTTGGGCTCCAGAAATAGTTGAAAGAGAACCCAGTTGGTTTC	780
Qy	781	TATACAGATGTGGGCTGTGTGCTTGGCATATGTTCTTCTGATGGGCTGTACCA	840
Db	781	TATACAGATGTGGGCTGTGTGCTTGGCATATGTTCTTCTGATGGGCTGTACCA	840

Db	781	TATACAGATGTGGGCTGTGTGCTTGGCATATGTTCTTCTGATGGGCTGTACCA	840
Qy	841	TTTCGAGGAGAAACACGCTAGAGAGCTTAAACAGCTGAAGCTTGTGACTGGGACTTT	900
Db	841	TTTCGAGGAGAAACACGCTAGAGAGCTTAAACAGCTGAAGCTTGTGACTGGGACTTT	900
Qy	901	GATGAAGATACCTTTAAACATAGTTTTCAGACGAAGGAAAGATTTTATCAGACGACTTTTG	960
Db	901	GATGAAGATACCTTTAAACATAGTTTTCAGACGAAGGAAAGATTTTATCAGACGACTTTTG	960
Qy	961	ATTAAAAACAAGAAAAACGAATGACAGCTCAGAAATGTTTAAATACATCTTGGCTGATG	1020
Db	961	ATTAAAAACAAGAAAAACGAATGACAGCTCAGAAATGTTTAAATACATCTTGGCTGATG	1020
Qy	1021	GGAGACCACTCCGATCGTACAGCTGCACCTCAACTCGTCAATTTACAAAAATCAGAGAT	1080
Db	1021	GGAGACCACTCCGATCGTACAGCTGCACCTCAACTCGTCAATTTACAAAAATCAGAGAT	1080
Qy	1081	CAAAATTCGCAAAATAATACAGTGAATGGGATTCGTTTGTCTTACCACTTCGGAAGATATCA	1140
Db	1081	CAAAATTCGCAAAATAATACAGTGAATGGGATTCGTTTGTCTTACCACTTCGGAAGATATCA	1140
Qy	1141	GAATACAGTGTCTCAGAAAGCTTATGTPAGAAATATAAATAATACGAAAGCTCGTTT	1200
Db	1141	GAATACAGTGTCTCAGAAAGCTTATGTPAGAAATATAAATAATACGAAAGCTCGTTT	1200
Qy	1201	GATGGCGACAAGCACTCCAGGTTCTGTTTAAAGCTTCAAGTGCTTCTGCTACGAA	1260
Db	1201	GATGGCGACAAGCACTCCAGGTTCTGTTTAAAGCTTCAAGTGCTTCTGCTACGAA	1260
Qy	1261	GGCAAAAGTGTCAAGTTTCTACTGTCTGTGTTTGTGTAGCAACCGCATTGTGCTATGG	1320
Db	1261	GGCAAAAGTGTCAAGTTTCTACTGTCTGTGTTTGTGTAGCAACCGCATTGTGCTATGG	1320
Qy	1321	TTCCATAATAACGAAGAATTAAAGACAAAGTGTAAATTCATGAAGCGATATGCTGGTGAA	1380
Db	1321	TTCCATAATAACGAAGAATTAAAGACAAAGTGTAAATTCATGAAGCGATATGCTGGTGAA	1380
Qy	1381	GATTACAGCTTCATTTCAATAGAGCTTAAGCTTGTATGATAGAGGAGATATATAAAGA	1440
Db	1381	GATTACAGCTTCATTTCAATAGAGCTTAAGCTTGTATGATAGAGGAGATATATAAAGA	1440
Qy	1441	GCTGAAATAACCTATGGCTATAGGCAAGAGTCTGTTTCTCAACGTACAACTTTGGCCA	1500
Db	1441	GCTGAAATAACCTATGGCTATAGGCAAGAGTCTGTTTCTCAACGTACAACTTTGGCCA	1500
Qy	1501	AAAGCAGCACCGGTATACAGATGAAGTCCAAAGTCAGAAAGCAGAGAACCACTCGCT	1560
Db	1501	AAAGCAGCACCGGTATACAGATGAAGTCCAAAGTCAGAAAGCAGAGAACCACTCGCT	1560
Qy	1561	AATACATATTATTCGAGAGAGGAAAGTGCACCAAAATTTTCACTTCTTATTACGACCT	1620
Db	1561	AATACATATTATTCGAGAGAGGAAAGTGCACCAAAATTTTCACTTCTTATTACGACCT	1620
Qy	1621	CGTGTACATAAAATACATCAAACTTTGCAAGTTTACTGTGCTTTTAAAGTCGACGCCAATA	1680
Db	1621	CGTGTACATAAAATACATCAAACTTTGCAAGTTTACTGTGCTTTTAAAGTCGACGCCAATA	1680
Qy	1681	CCAACTTATACAAATGTTTCAGAGGAAACCAAGAGCTATCTAAGCGTGTATTACCACTTACC	1740
Db	1681	CCAACTTATACAAATGTTTCAGAGGAAACCAAGAGCTATCTAAGCGTGTATTACCACTTACC	1740
Qy	1741	CATACGATGGTGTGATTACATTGGAAATTTTGTGCTGCAAGCTCGAAGACTCAGGCAAA	1800
Db	1741	CATACGATGGTGTGATTACATTGGAAATTTTGTGCTGCAAGCTCGAAGACTCAGGCAAA	1800
Qy	1801	TATCGCTGTTGGCCACTTAATGTGCAAGGAGAAACAGCTTCGCTAGTATTGTA	1860
Db	1801	TATCGCTGTTGGCCACTTAATGTGCAAGGAGAAACAGCTTCGCTAGTATTGTA	1860
Qy	1861	GAAGGTACTGAACAAAGCCAGAGCAGGAGGATTTATCATAATATTTTACTTCACTCAGAT	1920
Db	1861	GAAGGTACTGAACAAAGCCAGAGCAGGAGGATTTATCATAATATTTTACTTCACTCAGAT	1920

QY 1921 GCAGGTACCGATCAGATCATTTTCAGACCGCGCCACCGTCAATACCAAGCGCACC 1980  
 DB 1921 GCAGGTACCGATCAGATCATTTTCAGACCGCGCCACCGTCAATACCAAGCGCACC 1980  
 QY 1981 GCCATCACTTCCAAACGTCACGGAAGCAGTTCCGTTCTTCAAAACCAATCCATCACCAACC 2040  
 DB 1981 GCCATCACTTCCAAACGTCACGGAAGCAGTTCCGTTCTTCAAAACCAATCCATCACCAACC 2040  
 QY 2041 AACTCATCAAGAAATCAGCGACACGACCGTTACTCAACCGCAGGAAGCGTCAAA 2100  
 DB 2041 AACTCATCAAGAAATCAGCGACACGACCGTTACTCAACCGCAGGAAGCGTCAAA 2100  
 QY 2101 AAATACGCGAATTAATCACTGACGCGATTCGAGTCCGTCAGATCCGTTAGTCTACAAA 2160  
 DB 2101 AAATACGCGAATTAATCACTGACGCGATTCGAGTCCGTCAGATCCGTTAGTCTACAAA 2160  
 QY 2161 GAATTAAGATTATCAACCGATGAAGCCATGTGCCCTCCGGACTTTTCTACTCGCTTAGTC 2220  
 DB 2161 GAATTAAGATTATCAACCGATGAAGCCATGTGCCCTCCGGACTTTTCTACTCGCTTAGTC 2220  
 QY 2221 GATACATCTGCAATGACGACAGTCGCTAGAACTTGTATGTAAGTCAACCGGCGATCCG 2280  
 DB 2221 GATACATCTGCAATGACGACAGTCGCTAGAACTTGTATGTAAGTCAACCGGCGATCCG 2280  
 QY 2281 GAGCCACAATCACAATGTTAAAGACGGAAGCTATCAGTTCATCTAAGCTCTTAGAT 2340  
 DB 2281 GAGCCACAATCACAATGTTAAAGACGGAAGCTATCAGTTCATCTAAGCTCTTAGAT 2340  
 QY 2341 CTGAATACAAACCCGATGACGAGCTTGAAGATCAATGAATTCCTCCGAGATGCT 2400  
 DB 2341 CTGAATACAAACCCGATGACGAGCTTGAAGATCAATGAATTCCTCCGAGATGCT 2400  
 QY 2401 GGAGAAATATCTGCAAGAGTACCAACTCGTTGGGAATGAAGAAACAAAGTTGCAAACTC 2460  
 DB 2401 GGAGAAATATCTGCAAGAGTACCAACTCGTTGGGAATGAAGAAACAAAGTTGCAAACTC 2460  
 QY 2461 ACAGTCAAGCTGTGGAGTATCCAAAACAAACCAAGCCGAAAGCTTCCTCCAGTA 2517  
 DB 2461 ACAGTCAAGCTGTGGAGTATCCAAAACAAACCAAGCCGAAAGCTTCCTCCAGTA 2517

## RESULT 2

ID ABQ14818 standard; DNA; 1232 BP.  
 AC ABQ14818;  
 XX  
 DT 12-JUL-2002 (first entry)  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1409.  
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
 KW drug; side effect; cancer; central nervous system; cardiovascular;  
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
 KW SNP; cell differentiation; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200218632-A2.  
 XX  
 PD 07-MAR-2002.  
 XX  
 PF 01-SEP-2001; 2001WO-EP010074.  
 XX  
 PR 01-SEP-2000; 2000DE-01043826.  
 PR 05-SEP-2000; 2000DE-01044543.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
 XX  
 DR WPI; 2002-371829/40.

XX  
 PT Determining the degree of cytosine methylation in genomic DNA, useful for  
 PT diagnosis and prognosis, comprises selective hybridization of amplicons  
 PT from chemically treated DNA.  
 XX  
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
 XX  
 CC This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridised to two classes, each with at least one member,  
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
 CC degree of hybridisation to both classes is determined from the label on  
 CC the amplicon. From the ratio of labels hybridised to the two classes of  
 CC oligomers, the degree of methylation is calculated. The method is used:  
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
 CC and of a wide range of diseases, e.g. cancer, disorders of the central  
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
 CC particularly by detecting mutations or single nucleotide polymorphisms  
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
 CC investigating cell differentiation. The method allows the methylation  
 CC status of many C residues to be determined simultaneously, ABQ13410-  
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
 CC for determining the degree of cytosine methylation described in the  
 CC disclosure of the invention  
 XX

Sequence 1232 BP; 137 A; 172 C; 455 G; 468 T; 0 U; 0 Other;

Query Match 0.9%; Score 22; DB 6; Length 1232;

Best Local Similarity 100.0%; Pred.No. 7.5;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AAAAAACCCACCAAACTTAAC 106

DB 1198 AAAAAACCCACCAAACTTAAC 1177

## RESULT 3

ID ABQ14819 standard; DNA; 1232 BP.  
 AC ABQ14819;  
 XX  
 DT 12-JUL-2002 (first entry)  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1410.  
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
 KW drug; side effect; cancer; central nervous system; cardiovascular;  
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
 KW SNP; cell differentiation; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200218632-A2.  
 XX  
 PD 07-MAR-2002.  
 XX  
 PF 01-SEP-2001; 2001WO-EP010074.  
 XX  
 PR 01-SEP-2000; 2000DE-01043826.  
 PR 05-SEP-2000; 2000DE-01044543.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
 XX  
 DR WPI; 2002-371829/40.

PT Determining the degree of cytosine methylation in genomic DNA, useful for  
 PT diagnosis and prognosis, comprises selective hybridization of amplicons

PT from chemically treated DNA.

XX Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridised to two classes, each with at least one member,  
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
 CC degree of hybridisation to both classes is determined from the label on  
 CC the amplicon. From the ratio of labels hybridised to the two classes of  
 CC oligomers, the degree of methylation is calculated. The method is used:  
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
 CC and of a wide range of diseases, e.g. cancer, disorders of the central  
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
 CC particularly by detecting mutations or single nucleotide polymorphisms  
 CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
 CC investigating cell differentiation. The method allows the methylation  
 CC status of many C residues to be determined simultaneously. AB013410-  
 CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
 CC for determining the degree of cytosine methylation described in the  
 CC disclosure of the invention

XX Sequence 1232 BP; 468 A; 455 C; 172 G; 137 T; 0 U; 0 Other;

Query Match 0.9%; Score 22; DB 6; Length 1232;

Best Local Similarity 100.0%; Pred. No. 7.5;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AAAAAACCCACCAAACTAAAC 106

|||||

DB 35 AAAAAACCCACCAAACTAAAC 56

RESULT 4

ABN80099/c

ID ABN80099 standard; DNA; 5368 BP.

AC ABN80099;

DT 15-JUL-2002 (first entry)

DE Human chemically modified disease associated gene SEQ ID NO 116.

KW Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;  
 KW heart disease; epilepsy; histone deacetylation; muscular dystrophy;  
 KW dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;  
 KW antidiabetic; cytostatic; anticonvulsant; ds.

OS Homo sapiens.

OS Synthetic.

PN WO200200927-A2.

XX 03-JAN-2002.

XX 02-JUL-2001; 2001WO-EP007536.

XX 30-JUN-2000; 2000DE-01032529.

XX 01-SEP-2000; 2000DE-01043826.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-130908/17.

XX Novel nucleic acid useful for diagnosis and therapy of diseases

PT associated with development genes such as diabetes, comprises a sequence  
 PT of a segment of chemically pretreated DNA of genes associated with  
 PT development.

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

XX

Query Match

Best Local Similarity

Matches 22;

QY

DB

RESULT 5

ABQ66997/c

ID ABQ66997 standard; DNA; 37515 BP.

XX

AC

XX

DT

DE

KW

KW

KW

KW

KW

OS

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

CC bases of chemically pretreated DNA of angiogenesis-associated genes (II)  
 CC having sequences (ABG66971-ABG67178) or their complements. (I), also  
 CC related oligomers, are used to evaluate the methylation status and/or  
 CC single-nucleotide polymorphisms, in angiogenesis-related genes, for  
 CC diagnosis and treatment of eye diseases, proliferative retinopathy,  
 CC neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis,  
 CC diabetic retinopathy, macular degeneration caused by neovascularisation,  
 CC psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and  
 CC Crohn's disease. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 37515 BP; 11137 A; 425 C; 7785 G; 18168 T; 0 U; 0 Other;

Query Match 0.9%; Score 22; DB 6; Length 37515;  
 Best Local Similarity 100.0%; Pred. No. 7;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AAAAAACCCACCAAACTAAAC 106  
 |||||  
 DB 24339 AAAAAACCCACCAAACTAAAC 24318

## RESULT 6

ID ADQ89963  
 XX ADQ89963 standard; DNA; 103052 BP.

AC ADQ89963;

DT 21-OCT-2004 (first entry)

DE Antagonist of cell cycle progression nucleotide sequence #197.

XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;

KW cell cycle progression; ds.

XX Homo sapiens.

OS WO2004063362-A2.

PN 29-JUL-2004.

PD 31-DEC-2003; 2003WO-GB005635.

PF 10-JAN-2003; 2003US-0439123P.

PR 06-MAY-2003; 2003US-0468402P.

XX (CYCL-) CYCLACEL LTD.

PI Glover D, Bell G, Frenz L, Midgley C;

XX WPI; 2004-544089/52.

DR P-PSDB; ADQ89964.

XX New cell cycle progression genes and proteins for modulating cell cycle  
 PT progression in cells, for preventing, treating or diagnosing cell  
 PT proliferative diseases (e.g. cancer) or for identifying modulators of  
 PT mitosis or meiosis.

XX Claim 1; SEQ ID NO 393; 461pp; English.

XX The present invention relates to a polynucleotide for preventing,  
 CC treating or diagnosing a disease in an individual. The composition or the  
 CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for  
 CC diagnosing, preventing or treating diseases (e.g. cell proliferative  
 CC diseases such as cancer) in an individual. These may also be used for  
 CC identifying substances capable of binding to or modulating the function  
 CC of the polypeptide, capable of affecting the function of the  
 CC corresponding gene, or capable of inhibiting the cell division cycle or  
 CC cell cycle progression, preferably mitosis and/or meiosis. The present  
 CC sequence represents an antagonist of cell cycle progression nucleotide  
 CC sequence.

SQ Sequence 103052 BP; 33344 A; 21528 C; 23840 G; 24340 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 22; DB 13; Length 103052;  
 Best Local Similarity 100.0%; Pred. No. 6.8;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2400 TGGAGAATATATCTGCAAGCT 2421  
 |||||  
 DB 26864 TGGAGAATATATCTGCAAGCT 26885

## RESULT 7

ID ADN11332  
 XX ADN11332 standard; DNA; 21 BP.

AC ADN11332;

DT 01-JUL-2004 (first entry)

DE Aphis gossypii myosin light chain kinase sense primer F2.

XX Myosin light chain kinase; enzyme; pesticide; insecticide; cotton aphid;  
 KW PCR; primer; ss.

OS Aphis gossypii.

XX WO2004029577-A2.

PN 08-APR-2004.

PD 18-SEP-2003; 2003WO-US029901.

PF 26-SEP-2002; 2002US-0413720P.

PR (FMCC) FMC CORP.

PI Chen R, Chaguturu MK, Yuhas D, Allenza P, Halling BP;

XX WPI; 2004-340457/31.

XX New nucleic acid molecule encoding hemipteran myosin light chain kinase,  
 PT useful in identifying or developing compounds with activity as pesticides  
 PT or as pharmaceuticals.

XX Example 1; SEQ ID NO 5; 21pp; English.

XX The present sequence is that of sense primer F2. The primer is based on a  
 CC partial transcript of the cotton aphid (Aphis gossypii) myosin light  
 CC chain kinase gene identified in an A. gossypii expressed sequence tag  
 CC library. The primer was used in the identification and RT-PCR  
 CC amplification of the A. gossypii myosin light chain kinase gene ADN11328.  
 CC Isolated myosin light chain kinase polynucleotides and polypeptides  
 CC ADN11329 can be used in the identification or development of compounds  
 CC with activity as pesticides or as pharmaceuticals.

XX Sequence 21 BP; 7 A; 2 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 21; DB 12; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTAGAGTGTACGCTGAA 21  
 |||||  
 DB 1 GAATTAGAGTGTACGCTGAA 21

## RESULT 8

ID ADB52255  
 XX ADB52255 standard; DNA; 558 BP.

AC ADB52255;

DT 04-DEC-2003 (first entry)

XX DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:2797.  
XX KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;  
XX KW toxicity marker; toxicity progression; drug screening;  
XX KW primary rat hepatocyte toxicity modelling; gene; ds.  
XX OS Rattus norvegicus.  
XX XX WO2003065993-A2.  
XX PN 14-AUG-2003.  
XX PD  
XX KW  
XX PF 04-FEB-2003; 2003WO-US003482.  
XX PR 04-FEB-2002; 2002US-0353171P.  
XX PR 13-MAR-2002; 2002US-0363534P.  
XX PR 08-APR-2002; 2002US-0370248P.  
XX PR 10-APR-2002; 2002US-0371134P.  
XX PR 10-APR-2002; 2002US-0371135P.  
XX PR 10-APR-2002; 2002US-0371150P.  
XX PR 11-APR-2002; 2002US-0371413P.  
XX PR 19-APR-2002; 2002US-0373601P.  
XX PR 19-APR-2002; 2002US-0373602P.  
XX PR 22-APR-2002; 2002US-0374139P.  
XX PR 08-MAY-2002; 2002US-0378370P.  
XX PR 09-MAY-2002; 2002US-0378652P.  
XX PR 09-MAY-2002; 2002US-0378653P.  
XX PR 09-MAY-2002; 2002US-0378655P.  
XX PR 09-JUL-2002; 2002US-0394230P.  
XX PR 09-JUL-2002; 2002US-0394253P.  
XX PR 04-SEP-2002; 2002US-0407688P.  
XX PR 28-JAN-2003; 2003US-0442900P.  
XX PA (GENE-) GENE LOGIC INC.  
XX XX  
XX PI Mendrick D, Porter M, Johnson K, Higgins B, Castle A, Orr M;  
XX PI Elashoff M;  
XX XX WPI; 2003-731472/69.  
XX XX  
XX PT Determining if a compound induces a toxic effect on a tissue or cell, for  
XX PT identifying hepatotoxic compounds, comprises comparing a gene expression  
XX PT profile of a tissue or cell sample to a database of Tox mean and non-Tox  
XX PT mean values.  
XX XX  
XX PS Claim 44; SEQ ID NO 2797; 874pp; English.  
XX XX  
XX CC The present invention describes a method for determining whether a  
XX CC compound induces a toxic effect on a tissue or cell. The method comprises  
XX CC preparing a gene expression profile of a tissue or cell sample exposed to  
XX CC the compound, and comparing the gene expression profile to a database  
XX CC comprising data or information on the Tox mean and non-Tox mean value.  
XX CC The method is useful for predicting or identifying at least one toxic  
XX CC effect, particularly hepatotoxicity, of a test or unknown compound. The  
XX CC genes listed in the specification are useful as diagnostic or toxicity  
XX CC markers for the prediction or identification of the physiological state  
XX CC of tissue or cell sample that has been exposed to a compound, or to  
XX CC identify or predict the toxic effects of a compound or an agent. These  
XX CC may also be used as markers for monitoring toxicity progression or for  
XX CC drug screening. The present sequence represents a primary rat hepatocyte  
XX CC toxicity modelling related gene sequence from the present invention.  
XX SQ Sequence 558 BP; 216 A; 94 C; 78 G; 170 T; 0 U; 0 Other;  
  
Query Match 0.8%; Score 21; DB 10; Length 558;  
Best Local Similarity 100.0%; Pred. NO. 24;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 71 CAAGAGAGTTGTTGAAAC 91  
Db 92 CAAGAGAGTTGTTGAAAC 112

RESULT 9  
ACA37322/C  
ID ACA37322 standard; DNA; 957 BP.  
XX AC ACA37322;  
XX DT 19-JUN-2003 (first entry)  
XX XX  
XX DE Prokaryotic essential gene #18979.  
XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;  
XX KW drug design; gene.  
XX OS Legionella pneumophila.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX XX  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX XX  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX XX WPI; 2003-029926/02.  
XX DR P-PSDB; ABU33452.  
XX XX  
XX PT New antisense nucleic acids, useful for identifying proteins or screening  
XX PT for homologous nucleic acids required for cellular proliferation to  
XX PT isolate candidate molecules for rational drug discovery programs.  
XX XX  
XX PS Claim 14; SEQ ID NO 25192; 1766pp; English.  
XX CC The invention relates to an isolated nucleic acid comprising any one of  
XX CC the 6213 antisense sequences given in the specification where expression  
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid  
XX CC encoding a polypeptide whose expression is inhibited by the antisense  
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX CC polypeptide or its fragment whose expression is inhibited by the  
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding  
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX CC proliferation or the activity of a gene in an operon required for  
XX CC proliferation; (7) identifying a compound that influences the activity of  
XX CC the gene product or that has an activity against a biological pathway;  
XX CC required for proliferation, or that inhibits cellular proliferation; (8)  
XX CC identifying a gene required for cellular proliferation or the biological  
XX CC pathway in which a proliferation-required gene or its gene product lies  
XX CC or a gene on which the test compound that inhibits proliferation of an  
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
XX CC compound's activity; (11) a culture comprising strains in which the gene  
XX CC product is overexpressed or underexpressed; (12) determining the extent  
XX CC to which each of the strains is present in a culture or collection of  
XX CC strains; or (13) identifying the target of a compound that inhibits the  
XX CC proliferation of an organism. The antisense nucleic acids are useful for  
XX CC identifying proteins or screening for homologous nucleic acids required  
XX CC for cellular proliferation to isolate candidate molecules for rational  
XX CC drug discovery programs, or for screening homologous nucleic acids  
XX CC required for proliferation in cells other than S. aureus, S. typhimurium,  
XX CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target  
XX CC prokaryotic essential genes. Note: The sequence data for this patent did  
XX CC not form part of the printed specification, but was obtained in  
XX CC electronic format directly from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 957 BP; 327 A; 172 C; 183 G; 275 T; 0 U; 0 Other;  
Query Match 0.8%; Score 21; DB 8; Length 957;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1796 GCAATATCGTGTGTGCCA 1816  
Db 670 GCAATATCGTGTGTGCCA 650  
RESULT 10  
AAK78847/c  
ID AAK78847 standard; DNA; 57296 BP.  
XX AC AAK78847;  
XX DT 07-NOV-2001 (first entry)  
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33659.  
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.  
XX OS Homo sapiens.  
XX PN WO200157182-A2.  
XX PD 09-AUG-2001.  
XX PF 17-JAN-2001; 2001WO-US001354.  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225577P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.

```

PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249219P.
PR 17-NOV-2000; 2000US-0249220P.
PR 17-NOV-2000; 2000US-0249221P.
PR 17-NOV-2000; 2000US-0249222P.
PR 17-NOV-2000; 2000US-0249223P.
PR 17-NOV-2000; 2000US-0249224P.
PR 17-NOV-2000; 2000US-0249225P.
PR 17-NOV-2000; 2000US-0249226P.
PR 17-NOV-2000; 2000US-0249227P.
PR 17-NOV-2000; 2000US-0249228P.
PR 17-NOV-2000; 2000US-0249229P.
PR 17-NOV-2000; 2000US-0249230P.
PR 17-NOV-2000; 2000US-0250150P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
PT
XX Disclosure; SEQ ID NO 33659; 3071pp + Sequence Listing; English.
XX
XX AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 57296 BP; 16827 A; 11528 C; 11876 G; 17065 T; 0 U; 0 Other;
Query Match 0.8%; Score 21; DB 4; Length 57296;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 356 ATAATGTTGAAAAGAAATTA 376
DB 53579 ATAATGTTGAAAAGAAATTA 53559
RESULT 11
AAK78170/c
ID AAK78170 standard; DNA; 57296 BP.
XX
AC AAK78170;
XX
XX 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32982.

```

```

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX WO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 14-AUG-2000; 2000US-0220964P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225271P.
PR 14-AUG-2000; 2000US-0225275P.
PR 14-AUG-2000; 2000US-0225278P.
PR 14-AUG-2000; 2000US-0225279P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226682P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.

```



```
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239933P.
PR 20-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241788P.
PR 20-OCT-2000; 2000US-0241789P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0241826P.
PR 08-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239933P.
PR 20-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241788P.
PR 20-OCT-2000; 2000US-0241789P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0241826P.
PR 08-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-483426/52.
Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Disclosure; SEQ ID NO 32982; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX SQ Sequence 57296 BP; 16827 A; 11528 C; 11876 G; 17065 T; 0 U; 0 Other;
Query Match 0.8%; Score 21; DB 4; Length 57296;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 356 ATAATGTTGAAAAGAAATTTAA 376
Db 53579 ATAATGTTGAAAAGAAATTTAA 53559
RESULT 12
AAK79364/C
ID AAK79364 standard; DNA; 57296 BP.
XX AC AAK79364;
XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34176.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX OS Homo sapiens.
XX FN WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US001354.
XX PR 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 24-FEB-2000; 2000US-0184684P.
XX PR 02-MAR-2000; 2000US-0186350P.
XX PR 16-MAR-2000; 2000US-0189874P.
XX PR 17-MAR-2000; 2000US-0190076P.
XX PR 18-APR-2000; 2000US-0198123P.
XX PR 19-MAY-2000; 2000US-0205515P.
XX PR 07-JUN-2000; 2000US-0209467P.
```

PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225113P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225477P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 18-AUG-2000; 2000US-0225759P.  
PR 22-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226581P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 23-AUG-2000; 2000US-0227182P.  
PR 30-AUG-2000; 2000US-0227009P.  
PR 01-SEP-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234597P.  
PR 25-SEP-2000; 2000US-0234598P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 13-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX  
XX WPI; 2001-483426/52.  
XX  
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating cancers and metastasis.  
XX  
PS Disclosure; SEQ ID NO 34176; 3071pp + Sequence Listing; English.  
XX  
XX AA54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome

CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patients own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting the  
CC nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/haematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/haematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention  
XX  
SQ Sequence 57296 BP; 16827 A; 11528 C; 11876 G; 17065 T; 0 U; 0 Other;

Query Match 0.8%; Score 21; DB 4; Length 57296;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 356 ATAATGTTGAAAAGAAATTA 376  
Db 53579 ATAATGTTGAAAAGAAATTA 53559

## RESULT 13

AAK86799/c

ID AAK86799 standard; DNA; 57296 BP.

XX AAK86799;

AC AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

XX AAK86799;

```
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 41611; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention
XX
XX Sequence 57296 BP; 16827 A; 11528 C; 11876 G; 17065 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 21; DB 4; Length 57296;
XX Best Local Similarity 100.0%; Pred. No. 22;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 356 ATAAATGTTGAAAAGAAATTAA 376
XX |||||||||||||||||||||||
XX
XX Db 53579 ATAAATGTTGAAAAGAAATTAA 53559
```

```
RESULT 14
ACN44694
ID ACN44694 standard; DNA; 101505 BP.
XX
XX ACN44694;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human genomic sequence hCG16728.
XX
XX Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
XX Homo sapiens.
XX
XX WO2003073826-A2.
XX
XX 12-SEP-2003.
XX
XX 28-FEB-2003; 2003WO-US006235.
XX
XX 01-MAR-2002; 2002US-00087192.
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW;
XX
XX WPI; 2003-328604/31.
XX
XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
XX comprises a nucleotide sequence.
XX
XX Claim 1; SEQ ID NO 1270; Opp; English.
XX
XX The present invention relates to novel DNA and protein sequences which
XX are associated with carcinomas. The sequences are useful for: (i) for
XX screening drug candidates; (ii) for screening of bioactive agent capable
XX of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
XX a bioactive agent capable of modulating the activity of CAP; (iv) for
XX evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
XX carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
XX carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
XX (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
XX determining Carcinoma Associated (CA) gene copy number. In addition, the
XX CA genes are useful as DNA vaccines and the CAP are useful as markers of
XX carcinoma including lymphoma. The present sequence is one such CA coding
XX sequence. Note: This patent is an equivalent to basic patent
XX US2002182586A1, for which no sequence data was published
XX
XX Sequence 101505 BP; 29533 A; 18497 C; 19380 G; 33584 T; 0 U; 511 Other;
XX
XX Query Match 0.8%; Score 21; DB 11; Length 101505;
XX Best Local Similarity 100.0%; Pred. No. 21;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 326 TTTTGTGCTGCCAAATTATAC 346
XX |||||||||||||||||||
XX
XX Db 56153 TTTTGTGCTGCCAAATTATAC 56173
XX
XX RESULT 15
AEB42737_13/c
Continuation (14 of 21) of AEB42737 from base 1300001 (L. pneumophila DNA SEQ ID NO 706.
XX WP Sequence split into 21 fragments LOCUS AEB42737 Accession Aeb42737
XX WP Fragment Name Begin End
XX WP AEB42737_00 1 110000
XX WP AEB42737_01 100001 210000
XX WP AEB42737_02 200001 310000
XX WP AEB42737_03 300001 410000
XX WP AEB42737_04 400001 510000
XX WP AEB42737_05 500001 610000
XX WP AEB42737_06 600001 710000
XX WP AEB42737_07 700001 810000
```

WP	ABB42737_08	800001	910000
WP	ABB42737_09	900001	1010000
WP	ABB42737_10	1000001	1110000
WP	ABB42737_11	1100001	1210000
WP	ABB42737_12	1200001	1310000
WP	ABB42737_13	1300001	1410000
WP	ABB42737_14	1400001	1510000
WP	ABB42737_15	1500001	1610000
WP	ABB42737_16	1600001	1710000
WP	ABB42737_17	1700001	1810000
WP	ABB42737_18	1800001	1910000
WP	ABB42737_19	1900001	2010000
WP	ABB42737_20	2000001	2017010

Query Match 0.8%; Score 21; DB 14; Length 110000;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1796 GCAATATCGCTGTGTGCCA 1816  
|||||  
Db 43802 GCAATATCGCTGTGTGCCA 43782

Search completed: January 15, 2007, 21:25:59  
Job time : 1558 secs

This Page Blank (uspio)

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2007, 21:04:00 ; Search time 468 Seconds

(without alignments)  
10063.207 Million cell updates/sec

Title: US-10-528-631-1

Perfect score: 2517

Sequence: 1 gaatttagtgtagctga.....gaaacgactgcctccagta 2517

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2806514

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /EMC Celleria\_SIDS3/ptodata/2/ina/1 COMB.seq.\*
- 2: /EMC Celleria\_SIDS3/ptodata/2/ina/5 COMB.seq.\*
- 3: /EMC Celleria\_SIDS3/ptodata/2/ina/6A COMB.seq.\*
- 4: /EMC Celleria\_SIDS3/ptodata/2/ina/6B COMB.seq.\*
- 5: /EMC Celleria\_SIDS3/ptodata/2/ina/7 COMB.seq.\*
- 6: /EMC Celleria\_SIDS3/ptodata/2/ina/H COMB.seq.\*
- 7: /EMC Celleria\_SIDS3/ptodata/2/ina/PCTUS COMB.seq.\*
- 8: /EMC Celleria\_SIDS3/ptodata/2/ina/PP COMB.seq.\*
- 9: /EMC Celleria\_SIDS3/ptodata/2/ina/RE COMB.seq.\*
- 10: /EMC Celleria\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
C 1	21	0.8	144922	3	US-09-949-016-15890, A
C 2	20	0.8	3258	3	US-09-830-230A-324
C 3	20	0.8	3354	3	US-09-830-230A-323
C 4	20	0.8	21723	3	US-09-949-016-16383
C 5	20	0.8	85368	3	US-09-949-016-12211
C 6	19	0.8	25	3	US-09-396-196G-76168
C 7	19	0.8	55	3	US-09-513-999C-34994
C 8	19	0.8	590	3	US-09-513-999C-843
C 9	19	0.8	601	3	US-09-949-016-35325
C 10	19	0.8	601	3	US-09-949-016-127711
C 11	19	0.8	601	3	US-09-949-016-127712
C 12	19	0.8	601	3	US-09-949-016-128048
C 13	19	0.8	601	3	US-09-949-016-128049
C 14	19	0.8	601	3	US-09-949-016-151827
C 15	19	0.8	601	3	US-09-949-016-151827
C 16	19	0.8	601	3	US-09-949-002-3301
C 17	19	0.8	3295	3	US-10-101-464A-463
C 18	19	0.8	4852	3	US-09-566-921-116
C 19	19	0.8	11428	3	US-09-949-016-12636
C 20	19	0.8	15073	3	US-09-949-016-15673
C 21	19	0.8	50000	3	US-09-662-254B-26
C 22	19	0.8	51773	3	US-09-949-016-16002
C 23	19	0.8	51905	3	US-09-949-002-667

24	19	0.8	51905	3	US-09-949-002-781	Sequence 781, App
25	19	0.8	79122	4	US-09-531-120-200	Sequence 200, App
26	19	0.8	96074	3	US-09-949-016-12760	Sequence 12760, A
27	19	0.8	96074	3	US-09-949-016-13611	Sequence 13611, A
28	19	0.8	110000	3	US-09-830-902-1	Sequence 1, Appli
29	19	0.8	271134	3	US-09-949-016-12705	Sequence 12705, A
30	19	0.8	304533	3	US-09-949-016-15371	Sequence 15371, A
31	19	0.8	304533	3	US-09-949-016-15372	Sequence 15372, A
32	19	0.8	305491	3	US-09-949-016-17550	Sequence 17550, A
33	19	0.8	343352	3	US-09-949-016-13498	Sequence 13498, A
34	19	0.8	640681	3	US-09-790-988-1	Sequence 1, Appli
35	18	0.7	50	3	US-10-131-827-2470	Sequence 2470, Ap
36	18	0.7	50	3	US-10-131-831-2470	Sequence 2470, Ap
37	18	0.7	242	3	US-09-397-787-286	Sequence 286, App
38	18	0.7	274	3	US-09-313-294A-1061	Sequence 1061, Ap
39	18	0.7	274	3	US-09-313-294A-1682	Sequence 1682, Ap
40	18	0.7	274	3	US-09-313-294A-1909	Sequence 1909, Ap
41	18	0.7	288	3	US-09-313-294A-4461	Sequence 4461, Ap
42	18	0.7	329	3	US-09-513-999C-9750	Sequence 9750, Ap
43	18	0.7	385	3	US-09-270-767-3920	Sequence 3920, Ap
44	18	0.7	385	3	US-09-270-767-19202	Sequence 19202, A
45	18	0.7	441	3	US-09-513-999C-12875	Sequence 12875, A

#### ALIGNMENTS

RESULT 1  
US-09-949-016-15890/c  
; Sequence 15890 Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15890  
; LENGTH: 144922  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15890

Query Match 0.8%; Score 21; DB 3; Length 144922;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 ATAATGTTGAAAAGAAATTA 376

Db 140048 ATAATGTTGAAAAGAAATTA 140028

#### RESULT 2

US-09-830-230A-324  
; Sequence 324, Application US/09830230A  
; Patent No. 6902893  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Lyme Disease Vaccines  
; FILE REFERENCE: PB481US  
; CURRENT APPLICATION NUMBER: US/09/830,230A  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: PCT/US98/12718  
; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: 60/057,483  
; PRIOR FILING DATE: 1997-09-03  
; PRIOR APPLICATION NUMBER: 60/053,344  
; PRIOR FILING DATE: 1997-07-22  
; PRIOR APPLICATION NUMBER: 60/053,377  
; PRIOR FILING DATE: 1997-07-22  
; PRIOR APPLICATION NUMBER: 60/050,359  
; PRIOR FILING DATE: 1997-06-20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 324  
; LENGTH: 3258  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-830-230A-324

Query Match 0.8%; Score 20; DB 3; Length 3258;  
Best Local Similarity 100.0%; Pred. No. 21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 AAAAGAATTAAATAAAAAG 385  
|||||  
Db 837 AAAAGAATTAAATAAAAAG 856

## RESULT 3

US-09-830-230A-323  
; Sequence 323, Application US/09830230A  
; Patent No. 6902893  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Lyme Disease Vaccines  
; FILE REFERENCE: PB481US  
; CURRENT APPLICATION NUMBER: US/09/830, 230A  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: PCT/US98/12718  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/057,483  
; PRIOR FILING DATE: 1997-09-03  
; PRIOR APPLICATION NUMBER: 60/053,344  
; PRIOR FILING DATE: 1997-07-22  
; PRIOR APPLICATION NUMBER: 60/053,377  
; PRIOR FILING DATE: 1997-07-22  
; PRIOR APPLICATION NUMBER: 60/050,359  
; PRIOR FILING DATE: 1997-06-20  
; NUMBER OF SEQ ID NOS: 756  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 323  
; LENGTH: 3354  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-830-230A-323

Query Match 0.8%; Score 20; DB 3; Length 3354;  
Best Local Similarity 100.0%; Pred. No. 21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 AAAAGAATTAAATAAAAAG 385  
|||||  
Db 933 AAAAGAATTAAATAAAAAG 952

## RESULT 4

US-09-949-016-16383/c  
; Sequence 16383, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949, 016  
; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16383  
; LENGTH: 21723  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-16383

Query Match 0.8%; Score 20; DB 3; Length 21723;  
Best Local Similarity 100.0%; Pred. No. 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 TTAATTAAAAAGAAATTGA 392  
|||||  
Db 3334 TTAATTAAAAAGAAATTGA 3315

## RESULT 5

US-09-949-016-12211  
; Sequence 12211, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949, 016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12211  
; LENGTH: 85368  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12211

Query Match 0.8%; Score 20; DB 3; Length 85368;  
Best Local Similarity 100.0%; Pred. No. 19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 AAGCAGATGGCAATATTAAA 165  
|||||  
Db 52460 AAGCAGATGGCAATATTAAA 52479

## RESULT 6

US-09-396-196G-76168  
; Sequence 76168, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806



```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76168
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-76168

Query Match          0.8%; Score 19; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 TCTGGAGGAGGACTATTG 502
      |||||
Db 7 TCTGGAGGAGGACTATTG 25

RESULT 7
US-09-513-999C-34994/C
; Sequence 34994, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 34994
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2
; OTHER INFORMATION: r=a or g
US-09-513-999C-34994

Query Match          0.8%; Score 19; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 593 AAAGAAATATCATTCATTT 611
      |||||
Db 50 AAAGAAATATCATTCATTT 32

RESULT 8
US-09-513-999C-843
; Sequence 843, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 843
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 294..590
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 519_
; OTHER INFORMATION: k=g or t
; NAME/KEY: UNSURE
; LOCATION: 76
; OTHER INFORMATION: Xaa=Asp or Tyr
US-09-513-999C-843

Query Match          0.8%; Score 19; DB 3; Length 590;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1866 TACTGAACAAAGCCCAAGAG 1884
      |||||
Db 329 TACTGAACAAAGCCCAAGAG 347

RESULT 9
US-09-949-016-35325/c
; Sequence 35325, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35325
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-35325

Query Match          0.8%; Score 19; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 576 TATTAAGCATATGCATGAA 594
      |||||
Db 310 TATTAAGCATATGCATGAA 292

RESULT 10
US-09-949-016-127711/c
; Sequence 127711, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
```

```
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127711
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-127711

Query Match          0.8%; Score 19; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 CAAAAAAATTAGAGGAAAA 147
Db 343 CAAAAAAATTAGAGGAAAA 325

RESULT 11
US-09-949-016-127712/c
; Sequence 127712, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127712
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-127712

Query Match          0.8%; Score 19; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 CAAAAAAATTAGAGGAAAA 147
Db 601 CAAAAAAATTAGAGGAAAA 583

RESULT 12
US-09-949-016-128048/c
; Sequence 128048, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128048
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-128048

Query Match          0.8%; Score 19; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 CAAAAAAATTAGAGGAAAA 147
Db 601 CAAAAAAATTAGAGGAAAA 583

RESULT 13
US-09-949-016-128049/c
; Sequence 128049, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128049
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-128049

Query Match          0.8%; Score 19; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 CAAAAAAATTAGAGGAAAA 147
Db 601 CAAAAAAATTAGAGGAAAA 583

RESULT 14
US-09-949-016-151827
; Sequence 151827, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151827
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-151827

Query Match          0.8%; Score 19; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 67;
```

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 AAAAATTAGAGGAAAG 148

459 AAAAAAATTAGACGAAAC

## RESULT 15

US-09-949-002-3301

Sequence 3301, Application US/09949002

; Patent No. 6900016

**GENERAL INFORMATION:**

;; APPLICANT: VENTER, J. Craig et al.

10 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

**\_\_\_\_; TITLE OF INVENTION: AND USES THEREOF**

; FILE REFERENCE: CL000790

US/09/949,002

; CURRENT FILING DATE: 2000-01-28

;; PRIOR APPLICATION NUMBER: 60/231,401

**PRIOR FILING DATE: 2000-09-08**

; NUMBER OF SEQ ID NOS: 10823

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3301

; LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-002-3301

### Query Match

Query Match 0.8%; Score 19; DB 3; Length 601;

Best Local Similarity 100.0%; Pred. No. 67;

Qy 1126 CTTGGAAGAAATATCAGAAT 1144

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525

Search completed: January 15, 2007, 21:51:40

Job time : 471 secs

This page blank (uspio)

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2007, 21:03:33 ; Search time 2673 Seconds  
(without alignments)  
11570.512 Million cell updates/sec

Title: US-10-528-631-1

Perfect score: 2517

Sequence: 1 gaatttagtgtagctga.....gaaacgactgcctccagta 2517

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

Word size : 1

Total number of hits satisfying chosen parameters: 37781012

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA Main.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	0.9	1232	9	US-10-363-345A-1409
C 2	22	0.9	1232	9	US-10-363-345A-1410
C 3	22	0.9	1232	10	US-10-363-483A-1409
C 4	22	0.9	1232	10	US-10-363-483A-1410
C 5	22	0.9	37515	8	US-10-433-793-27
C 6	22	0.9	103053	10	US-10-745-237-393
C 7	22	0.9	104299	15	US-11-000-688-1364
C 8	22	0.9	510510	9	US-10-741-600-17606
C 9	21	0.8	957	8	US-10-282-122A-25192
C 10	21	0.8	101505	6	US-10-087-192-1270
C 11	21	0.8	160921	6	US-10-087-192-1672
C 12	20	0.8	263	3	US-09-923-876-4991
C 13	20	0.8	263	3	US-09-923-876-4991
C 14	20	0.8	293	8	US-10-437-963-25464
C 15	20	0.8	327	4	US-09-925-065A-269841
C 16	20	0.8	327	5	US-09-925-065A-269841
C 17	20	0.8	370	8	US-10-424-599-7322

Sequence 48487, A  
Sequence 48488, A  
Sequence 50170, A  
Sequence 156300,  
Sequence 156300,  
Sequence 156300,  
Sequence 11532, A  
Sequence 77026, A  
Sequence 1175, Ap  
Sequence 156301,  
Sequence 156301,  
Sequence 15,  
Sequence 15, Appl  
Sequence 324, App  
Sequence 155091,  
Sequence 323, App  
Sequence 303, App  
Sequence 8, Appli  
Sequence 1960, Ap  
Sequence 3158, Ap  
Sequence 3158, Ap  
Sequence 189, App  
Sequence 1223, Ap  
Sequence 1222, Ap  
Sequence 185088,  
Sequence 76168, A  
Sequence 612911,  
Sequence 12361, A  
Sequence 32964, A  
Sequence 15600, A

US-10-972-079-48487  
US-10-972-079-48488  
US-10-972-079-50170  
US-10-027-632-156300  
US-10-027-632-156300  
US-10-767-701-11532  
US-10-932-182A-77026  
US-10-932-182A-1175  
US-10-027-632-156301  
US-10-027-632-156301  
US-10-840-512-15  
US-10-994-726-324  
US-10-425-115-155091  
US-10-994-726-323  
US-10-311-455-303  
US-10-221-613-8  
US-10-311-455-1960  
US-09-764-877-3158  
US-10-242-515-3158  
US-10-745-237-189  
US-11-097-143-1223  
US-11-097-143-1222  
US-10-719-956-185088  
US-10-809-189-76168  
US-11-121-849-612911  
US-09-783-590-12361  
US-09-918-995-32964  
US-10-021-323-15600

#### ALIGNMENTS

#### RESULT 1

US-10-363-345A-1409/c  
; Sequence 1409, Application US/10363345A  
; Publication No. US20040234960A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Method for determining the degree of methylation of defined  
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3  
; FILE REFERENCE: E01/1227  
; CURRENT APPLICATION NUMBER: US/10/363.345A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 1409  
; LENGTH: 1232  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; OTHER INFORMATION: CpG-island No: 1409  
US-10-363-345A-1409

Query Match 0.9%; Score 22; DB 9; Length 1232;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 85 AAAAAACCAAAAACTAAAC 106  
|||||  
Db 1198 AAAAAACCAAAAACTAAAC 1177

#### RESULT 2

US-10-363-345A-1410  
; Sequence 1410, Application US/10363345A  
; Publication No. US20040234960A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Kurt Berlin

```
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 1410
; LENGTH: 1232
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 1410
US-10-363-345A-1410
```

```
Query Match 0.9%; Score 22; DB 9; Length 1232;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 85 AAAAAACCCACCAAACTAAAC 106
| | | | | | | | | | | | | | | | | |
Db 35 AAAAAACCCACCAAACTAAAC 56
```

## RESULT 3

```
US-10-363-483A-1409/c
; Sequence 1409, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
```

```
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
```

```
; SEQ ID NO 1409
; LENGTH: 1232
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 1409
US-10-363-483A-1409
```

```
Query Match 0.9%; Score 22; DB 10; Length 1232;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 85 AAAAAACCCACCAAACTAAAC 106
| | | | | | | | | | | | | | | | | |
Db 1198 AAAAAACCCACCAAACTAAAC 1177
```

## RESULT 4

```
US-10-363-483A-1410
; Sequence 1410, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
```

```
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
```

```
; SEQ ID NO 1410
; LENGTH: 1232
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 1410
US-10-363-483A-1410
```

```
Query Match 0.9%; Score 22; DB 10; Length 1232;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 85 AAAAAACCCACCAAACTAAAC 106
| | | | | | | | | | | | | | | | | |
Db 35 AAAAAACCCACCAAACTAAAC 56
```

## RESULT 5

```
US-10-433-793-27/c
; Sequence 27, Application US/10433793
; Publication No. US20040142334A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/433,793
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 212
```

```
; SEQ ID NO 27
; LENGTH: 37515
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-433-793-27
```

```
Query Match 0.9%; Score 22; DB 8; Length 37515;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 85 AAAAAACCCACCAAACTAAAC 106
| | | | | | | | | | | | | | | | | |
Db 24339 AAAAAACCCACCAAACTAAAC 24318
```

## RESULT 6

```
US-10-745-237-393
; Sequence 393, Application US/10745237
; Publication No. US20050227301A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Cyclacel Limited
; APPLICANT: Glover, David
; APPLICANT: Bell, Graham
; APPLICANT: Frenz, Lisa
; APPLICANT: Midgley, Carol
```

```
; TITLE OF INVENTION: Cell Cycle Progression Proteins
; FILE REFERENCE: P015819WO CYK
; CURRENT APPLICATION NUMBER: US/10/745,237
; CURRENT FILING DATE: 2003-12-23
```

```
; PRIOR APPLICATION NUMBER: US 60/439,123
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/468,402
; PRIOR FILING DATE: 2003-05-06
```

```
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 393
; LENGTH: 103053
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: AJ277892
US-10-745-237-393
```

```
Query Match 0.9%; Score 22; DB 10; Length 103053;
Best Local Similarity 100.0%; Pred. No. 13;
```

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2400 TGGAGATATATCTGCAAGCT 2421  
|||||

DB 26865 TGGAGATATATCTGCAAGCT 26886  
|||||

RESULT 7  
US-11-000-688-1364  
; Sequence 1364, Application US/11000688  
; Publication No. US20050287544A1  
; GENERAL INFORMATION:  
; APPLICANT: BERTUCCI, Francois  
; APPLICANT: BOULGATTE, Remi  
; APPLICANT: BIRNBAUM, Daniel  
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS  
; FILE REFERENCE: 1423-R-03  
; CURRENT APPLICATION NUMBER: US/11/000,688  
; CURRENT FILING DATE: 2004-12-01  
; PRIOR APPLICATION NUMBER: US 60/525,987  
; PRIOR FILING DATE: 2003-12-01  
; NUMBER OF SEQ ID NOS: 1596  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1364  
; LENGTH: 104299  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial sequences: primer  
; NAME/KEY: misc feature  
; LOCATION: (1)-(104299)  
; OTHER INFORMATION: titin(TTN) gene.  
US-11-000-688-1364

Query Match 0.9%; Score 22; DB 15; Length 104299;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2400 TGGAGATATATCTGCAAGCT 2421  
|||||

DB 27088 TGGAGATATATCTGCAAGCT 27109  
|||||

RESULT 8  
US-10-741-600-17606/c  
; Sequence 17606, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17606  
; LENGTH: 510510  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-17606

Query Match 0.9%; Score 22; DB 9; Length 510510;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 589 CATGAAGAATATCATTCATT 610  
|||||

DB 177062 CATGAAGAATATCATTCATT 177041  
|||||

RESULT 9

US-10-282-122A-25192/c  
; Sequence 25192, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25192  
; LENGTH: 957  
; TYPE: DNA  
; ORGANISM: Legionella pneumophila  
US-10-282-122A-25192

Query Match 0.8%; Score 21; DB 8; Length 957;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1796 GCAATATCGTGTGTTGCCA 1816  
|||||

DB 670 GCAATATCGTGTGTTGCCA 650  
|||||

RESULT 10  
US-10-087-192-1270  
; Sequence 1270, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586

```
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1270
; LENGTH: 101505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(101505)
; OTHER INFORMATION: n = A, T, C or G
US-10-087-192-1270
```

```
Query Match          0.8%; Score 21; DB 6; Length 101505;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      326 TTTTGTGCTGCAAAATTATAC 346
          |||||||
Db      56153 TTTTGTGCTGCAAAATTATAC 56173
```

```
RESULT 11
US-10-087-192-1672/c
; Sequence 1672, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1672
; LENGTH: 160921
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-1672
```

```
Query Match          0.8%; Score 21; DB 6; Length 160921;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      356 ATAATGTTGAAAGAATTAA 376
          |||||||
Db      148048 ATAATGTTGAAAGAATTAA 148028
```

```
RESULT 12
US-09-923-876-4991
; Sequence 4991, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
```

```
; SEQ ID NO 4991
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700456138H1
; NAME/KEY: unsure
; LOCATION: 2, 66
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-4991
```

```
Query Match          0.8%; Score 20; DB 3; Length 263;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      904 GAAGATACCTTTAACAATAGT 923
          |||||||
Db      103 GAAGATACCTTTAACAATAGT 122
```

```
RESULT 13
US-09-923-876-4991
; Sequence 4991, Application US/09923876
; Publication No. US20030237110A9
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 4991
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030237110A9 700456138H1
; NAME/KEY: unsure
; LOCATION: 2, 66
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-4991
```

```
Query Match          0.8%; Score 20; DB 3; Length 263;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      904 GAAGATACCTTTAACAATAGT 923
          |||||||
Db      103 GAAGATACCTTTAACAATAGT 122
```

```
RESULT 14
US-10-437-963-25464/c
; Sequence 25464, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
```



;; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
;; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
;; FILE REFERENCE: 38-21(53221)B  
;; CURRENT APPLICATION NUMBER: US/10/437,963  
;; CURRENT FILING DATE: 2003-05-14  
;; NUMBER OF SEQ ID NOS: 204966  
;; SEQ ID NO 25464  
;; LENGTH: 293  
;; TYPE: DNA  
;; ORGANISM: Oryza sativa  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_30348C.1  
US-10-437-963-25464

Query Match 0.8%; Score 20; DB 8; Length 293;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1861 GAAGTACTGAACAAAGCCA 1880  
Db 138 GAAGTACTGAACAAAGCCA 119

## RESULT 15

US-09-925-065A-269841/c  
; Sequence 269841, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 269841  
; LENGTH: 327  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-269841

Query Match 0.8%; Score 20; DB 4; Length 327;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1892 AGTTATCACAATTAATTTACTT 1911  
Db 193 AGTTATCACAATTAATTTACTT 174

Search completed: January 15, 2007, 21:51:17  
Job time : 2676 secs

This Page Blank (uspto)

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2007, 21:06:44 ; Search time 684 Seconds

(without alignments)  
10028.174 Million cell updates/sec

Title: US-10-528-631-1

Perfect score: 2517

Sequence: 1 gaatttagagtgtagctga.....gaaacgactgcctccagta 2517

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3650718 seqs, 1362588608 residues

Word size : 1

Total number of hits satisfying chosen parameters: 7300626

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA New:

- 1: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*\*
- 2: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*\*
- 3: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*\*
- 4: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*\*
- 5: /EMC Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*\*
- 6: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*\*
- 7: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*\*
- 8: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*\*
- 9: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*\*
- 10: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq3:\*\*
- 11: /EMC Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2517	100.0	2517	6	US-10-528-631-1
2	22	0.9	294540	8	US-11-266-748A-23953
3	22	0.9	498224	7	US-11-033-056A-36988
4	21	0.8	21	6	US-10-528-631-5
5	20	0.8	20	6	US-10-528-631-6
6	20	0.8	543	7	US-11-204-780-29
7	20	0.8	849	8	US-11-266-748A-53097
8	20	0.8	849	8	US-11-266-748A-208131
9	20	0.8	849	8	US-11-266-748A-233471
10	20	0.8	1557	8	US-11-217-529-77026
11	20	0.8	1563	8	US-11-217-529-1175
12	20	0.8	2526	9	US-11-218-305-12198
13	20	0.8	71330	7	US-11-033-056A-38520
14	20	0.8	74025	7	US-11-033-056A-38206
15	20	0.8	89298	7	US-11-033-056A-36497
16	20	0.8	107996	9	US-11-021-837-42
17	20	0.8	219909	7	US-11-405-322-10
18	20	0.8	837141	7	US-11-033-056A-36860
19	20	0.8	837141	7	US-11-033-056A-37907
20	20	0.8	1038608	10	US-11-366-965-1
21	19	0.8	409	10	US-11-232-078-15600
22	19	0.8	411	10	US-11-292-078-17110

#### ALIGNMENTS

##### RESULT 1

US-10-528-631-1  
; Sequence 1, Application US/10528631  
; Publication No. US20060148031A1  
; GENERAL INFORMATION:  
; APPLICANT: FMC Corporation  
; APPLICANT: CHEN, Ruihua  
; APPLICANT: HALLING, Blaik P.  
; APPLICANT: CHAGUTURU Munirathan K.  
; APPLICANT: ALLENZA, Paul  
; APPLICANT: YUHAS, Debra A.  
; TITLE OF INVENTION: Hemipteran Myosin Light Chain Kinase  
; FILE REFERENCE: 60289-USA  
; CURRENT APPLICATION NUMBER: US/10528,631  
; CURRENT FILING DATE: 2005-03-22  
; PRIOR APPLICATION NUMBER: 60/413,720  
; PRIOR FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 2517  
; TYPE: DNA  
; ORGANISM: Aphis gossypii  
US-10-528-631-1

Query Match 100.0%; Score 2517; DB 6; Length 2517;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTTAGAGTGTACGCTGAAATATGTGTAGTAAAGTAAACCTAGTGAAGTATCACCT 60  
Db 1 GAATTTAGAGTGTACGCTGAAATATGTGTAGTAAAGTAAACCTAGTGAAGTATCACCT 60  
Qy 61 ATTGTAACCAAAAGAGTTGTTGAAAAAACCCACCAAACTAAACGTTACGAAGTTGAT 120  
Db 61 ATTGTAACCAAAAGAGTTGTTGAAAAAACCCACCAAACTAAACGTTACGAAGTTGAT 120  
Qy 121 GAACTGCGCAAAAATTAGAGGAAACGAGATGCGCAATATTAAGATTAGACCAATAT 180  
Db 121 GAACTGCGCAAAAATTAGAGGAAACGAGATGCGCAATATTAAGATTAGACCAATAT 180  
Qy 181 GTTTTTCACATTTTATTCAAAATACATACCAACACGAGTGGATATTTAAACACCAATCCGTA 240  
Db 181 GTTTTTCACATTTTATTCAAAATACATACCAACACGAGTGGATATTTAAACACCAATCCGTA 240

Sequence 235, App  
Sequence 52444, A  
Sequence 189523, A  
Sequence 64816, A  
Sequence 227681, A  
Sequence 203151, A  
Sequence 288485, A  
Sequence 339914, A  
Sequence 399368, A  
Sequence 470414, A  
Sequence 418080, A  
Sequence 78045, A  
Sequence 130856, A  
Sequence 3391, Ap  
Sequence 522, App  
Sequence 53228, A  
Sequence 1135, Ap  
Sequence 1136, Ap  
Sequence 156, App  
Sequence 15701, A  
Sequence 29594, A  
Sequence 3454, Ap  
Sequence 186312, A

23 19 0.8 470 10 US-11-290-215A-235  
24 19 0.8 668 8 US-11-266-748A-52444  
25 19 0.8 800 8 US-11-266-748A-189523  
26 19 0.8 918 7 US-11-371-354-64816  
27 19 0.8 942 8 US-11-266-748A-227681  
28 19 0.8 1000 8 US-11-266-748A-203151  
29 19 0.8 1000 8 US-11-266-748A-288485  
30 19 0.8 1000 8 US-11-266-748A-339914  
31 19 0.8 1000 8 US-11-266-748A-399368  
32 19 0.8 1000 8 US-11-266-748A-470414  
33 19 0.8 1059 8 US-11-266-748A-418080  
34 19 0.8 1320 8 US-11-266-748A-78045  
35 19 0.8 1320 8 US-11-266-748A-130856  
36 19 0.8 1331 9 US-11-056-355B-3291  
37 19 0.8 1527 9 US-11-348-413-522  
38 19 0.8 1533 9 US-11-056-355B-53228  
39 19 0.8 1550 8 US-11-216-545-1135  
40 19 0.8 1617 8 US-11-216-545-1136  
41 19 0.8 1642 6 US-10-574-398-156  
42 19 0.8 1671 9 US-11-056-355B-15701  
43 19 0.8 1679 8 US-11-266-748A-29594  
44 19 0.8 1818 9 US-11-218-305-3454  
45 19 0.8 2629 8 US-11-266-748A-186312

QY 241 TATGATTATTATGACATATTAGAGAAATCGGAATCGTGCATTTGGAGTAGTACACCGT 300  
DB 241 TATGATTATTATGACATATTAGAGAAATCGGAATCGTGCATTTGGAGTAGTACACCGT 300  
QY 301 TGTAGGGAACGTAAACTGGAATATTTTTGCTGCCAAATTTATACACGTAGGACATAAT 360  
DB 301 TGTAGGGAACGTAAACTGGAATATTTTTGCTGCCAAATTTATACACGTAGGACATAAT 360  
QY 361 GTTGAAGAAATTAATTAAGAAATTAATGACATATGAACCAACTTTCATCATCCGAAA 420  
DB 361 GTTGAAGAAATTAATTAAGAAATTAATGACATATGAACCAACTTTCATCATCCGAAA 420  
QY 421 TTGATCAATTTGATGATGCTTTTGAAGATGAAGATGAATGGTCTTTAATTTTGAATTT 480  
DB 421 TTGATCAATTTGATGATGCTTTTGAAGATGAAGATGAATGGTCTTTAATTTTGAATTT 480  
QY 481 TTCTCTGGAGGAGGCTTTTGAAGATGACCTCAGAGGATCTCAATGTCCGAAGCA 540  
DB 481 TTGTCTGGAGGAGGCTTTTGAAGATGACCTCAGAGGATCTCAATGTCCGAAGCA 540  
QY 541 GAAAGTATCAATATATGCGACAGATATGGAAGCTATTAAAGCATATGCATGAAGAAAT 600  
DB 541 GAAAGTATCAATATATGCGACAGATATGGAAGCTATTAAAGCATATGCATGAAGAAAT 600  
QY 601 ATCAATTCATTTAGATATCAAAACAGAAATATATATGTGCCAGACAAAGAGTTCAAAT 660  
DB 601 ATCAATTCATTTAGATATCAAAACAGAAATATATATGTGCCAGACAAAGAGTTCAAAT 660  
QY 661 GTAAACTCATGATTTTGGATTTGGCAACGAAGTTCGATCTCAAGAAATCGTTAAGATA 720  
DB 661 GTAAACTCATGATTTTGGATTTGGCAACGAAGTTCGATCTCAAGAAATCGTTAAGATA 720  
QY 721 TCGACGGAACTGCTGAGTTTGGGCTCCAGAAATAGTTGAAAGAGAACAGTTGGTTTC 780  
DB 721 TCGACGGAACTGCTGAGTTTGGGCTCCAGAAATAGTTGAAAGAGAACAGTTGGTTTC 780  
QY 781 TATACAGACATGTGGGCTGTGTGTCTTGGCATATGTTCTTCTGAGTGGGCTGTCAACA 840  
DB 781 TATACAGACATGTGGGCTGTGTGTCTTGGCATATGTTCTTCTGAGTGGGCTGTCAACA 840  
QY 841 TTGCGAGGAGAAACGACGTAGAGACGCTTAAACAGTGAAAGCTTGTGACGGACTTTT 900  
DB 841 TTGCGAGGAGAAACGACGTAGAGACGCTTAAACAGTGAAAGCTTGTGACGGACTTTT 900  
QY 901 GATGAAGATACCTTTTAAACATAGTTTTCAGACGAAGGAAAGATTTTATCAGACACTTTT 960  
DB 901 GATGAAGATACCTTTTAAACATAGTTTTCAGACGAAGGAAAGATTTTATCAGACACTTTT 960  
QY 961 ATTAAAAACAAGAAACGAATGACAGCTCACGAATGTTTAAATACATCCTTGGCTGATG 1020  
DB 961 ATTAAAAACAAGAAACGAATGACAGCTCACGAATGTTTAAATACATCCTTGGCTGATG 1020  
QY 1021 GGAGACACTCCGATCGTACAGCTGCACTCAACTCGTCCCAATTTACACAAATACAGAT 1080  
DB 1021 GGAGACACTCCGATCGTACAGCTGCACTCAACTCGTCCCAATTTACACAAATACAGAT 1080  
QY 1081 CAAATTCGCAAAAAATACAGTGTGGAATTCGTTTGGCTCTACCACTTGGAGAAATATCA 1140  
DB 1081 CAAATTCGCAAAAAATACAGTGTGGAATTCGTTTGGCTCTACCACTTGGAGAAATATCA 1140  
QY 1141 GAATACAGTCTCTCAGAAAGCTTTATGGTAGAATAATAAAATATACGAAAGCTCGTTT 1200  
DB 1141 GAATACAGTCTCTCAGAAAGCTTTATGGTAGAATAATAAAATATACGAAAGCTCGTTT 1200  
QY 1201 GATCGGGAACAGCAGCTCCAGGTTTGGTTTAAAGCTCAAGTGCATCTGCTACGAA 1260  
DB 1201 GATCGGGAACAGCAGCTCCAGGTTTGGTTTAAAGCTCAAGTGCATCTGCTACGAA 1260  
QY 1261 GGACAAAGTGTCAAGTTCTACTGTCGTGTTTATGCTGTAGCAACCGCATTTGTCATCG 1320  
DB 1261 GGACAAAGTGTCAAGTTCTACTGTCGTGTTTATGCTGTAGCAACCGCATTTGTCATCG 1320  
QY 1321 TTCCATAATAACGAAGAAATTAAGACAAAGTGTTPAAATTCATGAAGCGATATGCTGGTGA 1380

DB 1321 TTCCATAATAACGAAGAAATTAAGACAAAGTGTTPAAATTCATGAAGCGATATGCTGGTGA 1380  
QY 1381 GATTACACGCTTCATTTCAATAGAGCTTAAGCTTTGATGATAGGAGAAATATATAAAGA 1440  
DB 1381 GATTACACGCTTCATTTCAATAGAGCTTAAGCTTTGATGATAGGAGAAATATATAAAGA 1440  
QY 1441 GCTGAAAAATACCTATGCTGCTATAGGGAAGAGTCTGATTTCTCAACTGACAACTTTGGCCA 1500  
DB 1441 GCTGAAAAATACCTATGCTGCTATAGGGAAGAGTCTGATTTCTCAACTGACAACTTTGGCCA 1500  
QY 1501 AAAGCAGCACCGGTATACAGACATGAAGTCCAAACAGTCCAGAGACAGAAACCACTCGCT 1560  
DB 1501 AAAGCAGCACCGGTATACAGACATGAAGTCCAAACAGTCCAGAGACAGAAACCACTCGCT 1560  
QY 1561 AATACATATTTATTCGAAGAGAGAAAGTGCACCAAAATTTTCACTTTTATTTACGACCT 1620  
DB 1561 AATACATATTTATTCGAAGAGAGAAAGTGCACCAAAATTTTCACTTTTATTTACGACCT 1620  
QY 1621 CGTGTCAATAAATACATCAAACTTTGCAAGTTTACTGTGCTGTTTAAAGTCGCACGCCAATA 1680  
DB 1621 CGTGTCAATAAATACATCAAACTTTGCAAGTTTACTGTGCTGTTTAAAGTCGCACGCCAATA 1680  
QY 1681 CCAACTATACAAATGCTTCAGAGAACCAAGAGCTATCTAAGCGTGATTAACACATTAACC 1740  
DB 1681 CCAACTATACAAATGCTTCAGAGAACCAAGAGCTATCTAAGCGTGATTAACACATTAACC 1740  
QY 1741 CATACGGATGCTGATTTACATTTGGAATTTATGCTGCAAGCTTGAAGCTCAGGCAAA 1800  
DB 1741 CATACGGATGCTGATTTACATTTGGAATTTATGCTGCAAGCTTGAAGCTCAGGCAAA 1800  
QY 1801 TATCGCTGTGTTGCCACTTAATGTGCACGCGACAGAGAAACAGCTGCGTAGTGTGTA 1860  
DB 1801 TATCGCTGTGTTGCCACTTAATGTGCACGCGACAGAGAAACAGCTGCGTAGTGTGTA 1860  
QY 1861 GAAGGTACTGAAACAAAGCCAGAGCAGAGTATATCACATAATTTTACTTCACTCAGAT 1920  
DB 1861 GAAGGTACTGAAACAAAGCCAGAGCAGAGTATATCACATAATTTTACTTCACTCAGAT 1920  
QY 1921 CGCAGGTACACCGATCAGCATCATTTAGACCCGGCGCCAAACGGTCAATTAACGAAGCGCAC 1980  
DB 1921 CGCAGGTACACCGATCAGCATCATTTAGACCCGGCGCCAAACGGTCAATTAACGAAGCGCAC 1980  
QY 1981 GCCATCACTTCCAACTGCACGGAAGCAGTTCGCTGCTTCCAAACCAATTCATCACACC 2040  
DB 1981 GCCATCACTTCCAACTGCACGGAAGCAGTTCGCTGCTTCCAAACCAATTCATCACACC 2040  
QY 2041 AACTCATCAACGAAATCAGCGACACGACCGTTTACCTCAACCGACAGGAAGCGTCAAA 2100  
DB 2041 AACTCATCAACGAAATCAGCGACACGACCGTTTACCTCAACCGACAGGAAGCGTCAAA 2100  
QY 2101 AAATACGGCAATAAATCTGAAATGGAAGTTCGCTCAAGATCCGTTAGTTCACAAA 2160  
DB 2101 AAATACGGCAATAAATCTGAAATGGAAGTTCGCTCAAGATCCGTTAGTTCACAAA 2160  
QY 2161 GAAATTAAGATTAATCACCGGATGAAGCCTGCGCTCCGAGCTTTTCTACTCGTTAGTC 2220  
DB 2161 GAAATTAAGATTAATCACCGGATGAAGCCTGCGCTCCGAGCTTTTCTACTCGTTAGTC 2220  
QY 2221 GATACATCTGCAATGACGGACAGTTCGCTAGAACTTGTATGTAAGTGAACCGCGATCCG 2280  
DB 2221 GATACATCTGCAATGACGGACAGTTCGCTAGAACTTGTATGTAAGTGAACCGCGATCCG 2280  
QY 2281 GAGCCACAAATCAGATGTTTAAAGAACGGAAAGCTATCAGTTTCATCTTAACTGTTAGAT 2340  
DB 2281 GAGCCACAAATCAGATGTTTAAAGAACGGAAAGCTATCAGTTTCATCTTAACTGTTAGAT 2340  
QY 2341 CTGAAATACAAAAACCGATTAAGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400  
DB 2341 CTGAAATACAAAAACCGATTAAGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400  
QY 2401 GGAGAAATATATCGCAAAAGCTACCAACTCGTTGGGAATGAAGAAACAAAGTTGCAAACTC 2460

```
Db 2401 GGAGATATATCTGCAAGCTACCAACTGCTGGTGAATGAAGGAAACAAGTTGCAAACTC 2450
Qy 2461 ACAGTCAAGCTGGAGCTATCAAAACCAAAACCAAAACCAAGCTTCCTCCAGTA 2517
Db 2461 ACAGTCAAGCTGGAGCTATCAAAACCAAAACCAAAACCAAGCTTCCTCCAGTA 2517

RESULT 2
US-11-266-748A-23953
; Sequence 23953, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23953
; LENGTH: 294540
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23953

Query Match 0.9%; Score 22; DB 8; Length 294540;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2400 TGGAGATATATCTGCAAGCT 2421
Db 108445 TGGAGATATATCTGCAAGCT 108466

RESULT 3
US-11-033-056A-36988/c
; Sequence 36988, Application US/11033056A
; Publication No. US20060292572A1
; GENERAL INFORMATION:
; APPLICANT: STUART, ROBERT O.
; APPLICANT: STUART, ELIZABETH DUFF
; APPLICANT: WACHSMAN, WILLIAM
; APPLICANT: MERCOLA, DANIEL
; APPLICANT: MCCLELLAND, MICHAEL
; APPLICANT: WANG-RODRIGUEZ, JESSICA
; APPLICANT: TARRIN, DAVID
; APPLICANT: BERRY, CHARLES C.
; APPLICANT: ARDEN, KAREN
; APPLICANT: WASSERMAN, LINDA
; APPLICANT: GOODISON, STEVEN
; APPLICANT: KLACANSKY, IGOR
; TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
; FILE REFERENCE: 15670-073001
; CURRENT APPLICATION NUMBER: US/11/033,056A
```

```
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,382
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: 60/536,163
; NUMBER OF SEQ ID NOS: 38888
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36988
; LENGTH: 498224
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-033-056A-36988

Query Match 0.9%; Score 22; DB 7; Length 498224;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 589 CATGAAAGAAATATCATTCATT 610
Db 170820 CATGAAAGAAATATCATTCATT 170799

RESULT 4
US-10-528-631-5
; Sequence 5, Application US/10528631
; Publication No. US20060148031A1
; GENERAL INFORMATION:
; APPLICANT: FMC Corporation
; APPLICANT: CHEN, Ruihua
; APPLICANT: HALLING, Blaik P.
; APPLICANT: CHAGUTURU, Munirathan K.
; APPLICANT: ALLENZA, Paul
; APPLICANT: YUHAS, Debra A.
; TITLE OF INVENTION: Hemipteran Myosin Light Chain Kinase
; FILE REFERENCE: 60289-USA
; CURRENT APPLICATION NUMBER: US/10/528,631
; CURRENT FILING DATE: 2005-03-22
; PRIOR APPLICATION NUMBER: 60/413,720
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-528-631-5

Query Match 0.8%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTAGAGTGACGCTGAA 21
Db 1 GAATTAGAGTGACGCTGAA 21

RESULT 5
US-10-528-631-6/c
; Sequence 6, Application US/10528631
; Publication No. US20060148031A1
; GENERAL INFORMATION:
; APPLICANT: FMC Corporation
; APPLICANT: CHEN, Ruihua
; APPLICANT: HALLING, Blaik P.
; APPLICANT: CHAGUTURU, Munirathan K.
; APPLICANT: ALLENZA, Paul
; APPLICANT: YUHAS, Debra A.
; TITLE OF INVENTION: Hemipteran Myosin Light Chain Kinase
; FILE REFERENCE: 60289-USA
; CURRENT APPLICATION NUMBER: US/10/528,631
; CURRENT FILING DATE: 2005-03-22
```

; PRIOR APPLICATION NUMBER: 60/413,720  
; PRIOR FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-528-631-6

Query Match 0.8%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2498 GAAACGACTTGCCTCCAGTA 2517  
Db 20 GAAACGACTTGCCTCCAGTA 1

## RESULT 6

US-11-204-780-29  
; Sequence 29, Application US/11204780  
; Publication No. US20060288444A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto  
; APPLICANT: Monsanto  
; APPLICANT: Laurie, Cathy C  
; TITLE OF INVENTION: Soybean Polymorphisms and Methods of Genotyping  
; FILE REFERENCE: 38-21(53722)B  
; CURRENT APPLICATION NUMBER: US/11/204,780  
; CURRENT FILING DATE: 2005-08-15  
; PRIOR APPLICATION NUMBER: US 60/601,756  
; PRIOR FILING DATE: August 13, 2004  
; NUMBER OF SEQ ID NOS: 6578  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 29  
; LENGTH: 543  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-11-204-780-29

Query Match 0.8%; Score 20; DB 7; Length 543;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 484 TCTGGAGGAGAGCTATTGGA 503  
Db 414 TCTGGAGGAGAGCTATTGGA 433

## RESULT 7

US-11-266-748A-53097  
; Sequence 53097, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 53097  
; LENGTH: 849  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-53097

Query Match 0.8%; Score 20; DB 8; Length 849;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 AAAAAAGAAATTGACATAAT 398  
Db 118 AAAAAAGAAATTGACATAAT 137

## RESULT 8

US-11-266-748A-208131  
; Sequence 208131, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 208131  
; LENGTH: 849  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-208131

Query Match 0.8%; Score 20; DB 8; Length 849;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 AAAAAAGAAATTGACATAAT 398  
Db 118 AAAAAAGAAATTGACATAAT 137

## RESULT 9

US-11-266-748A-233471/c

; Sequence 233471, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 5815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; PRIOR FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 233471  
; LENGTH: 849  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-233471

Query Match 0.8%; Score 20; DB 8; Length 849;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 AAAAAAGAAATGTGACATAAT 398  
Db 732 AAAAAAGAAATGTGACATAAT 713

RESULT 10  
US-11-217-529-77026  
; Sequence 77026, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 77026  
; LENGTH: 1557  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-77026

Query Match 0.8%; Score 20; DB 8; Length 1557;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1336 GAATTAAGACAAAGTGTAA 1355  
Db 1372 GAATTAAGACAAAGTGTAA 1391

RESULT 11  
US-11-217-529-1175  
; Sequence 1175, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1175  
; LENGTH: 1563  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-1175

Query Match 0.8%; Score 20; DB 8; Length 1563;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1336 GAATTAAGACAAAGTGTAA 1355  
Db 1378 GAATTAAGACAAAGTGTAA 1397

RESULT 12  
US-11-218-305-12198  
; Sequence 12198, Application US/11218305  
; Publication No. US20060141495A1  
; GENERAL INFORMATION:  
; APPLICANT: MONSANTO TECHNOLOGY, LLC  
; APPLICANT: McLaird, Paul L.  
; APPLICANT: Tao, Mengbing  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
; FILE REFERENCE: 38-21 (53660)B  
; CURRENT APPLICATION NUMBER: US/11/218,305  
; CURRENT FILING DATE: 2005-09-01  
; PRIOR APPLICATION NUMBER: US 60/606,880  
; PRIOR FILING DATE: 2004-09-01  
; NUMBER OF SEQ ID NOS: 25043  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12198  
; LENGTH: 2526  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-11-218-305-12198

Query Match 0.8%; Score 20; DB 9; Length 2526;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 904 GAAGATACCTTTTAAACATAGT 923  
Db 552 GAAGATACCTTTTAAACATAGT 571

RESULT 13

```
US-11-033-056A-38520/c
; Sequence 38520, Application US/11033056A
; Publication No. US20060292572A1
; GENERAL INFORMATION:
; APPLICANT: STUART, ROBERT O.
; APPLICANT: STUART, ELIZABETH DUFF
; APPLICANT: WACHSMAN, WILLIAM
; APPLICANT: MERCOLA, DANIEL
; APPLICANT: MCCLELLAND, MICHAEL
; APPLICANT: WANG-RODRIGUEZ, JESSICA
; APPLICANT: TARIN, DAVID
; APPLICANT: BERRY, CHARLES C.
; APPLICANT: ARDEN, KAREN
; APPLICANT: WASSERMAN, LINDA
; APPLICANT: GOODISON, STEVEN
; APPLICANT: KLACANSKY, IGOR
; TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
; FILE REFERENCE: 15670-073001
; CURRENT APPLICATION NUMBER: US/11/033,056A
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,382
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: 60/536,163
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 3888
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38520
; LENGTH: 71330
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-033-056A-38520

Query Match          0.8%; Score 20; DB 7; Length 71330;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 AGCAGATGCAATATTAA 165
Db 64221 AGCAGATGCAATATTAA 64202

RESULT 14
US-11-033-056A-38206
; Sequence 38206, Application US/11033056A
; Publication No. US20060292572A1
; GENERAL INFORMATION:
; APPLICANT: STUART, ROBERT O.
; APPLICANT: STUART, ELIZABETH DUFF
; APPLICANT: WACHSMAN, WILLIAM
; APPLICANT: MERCOLA, DANIEL
; APPLICANT: MCCLELLAND, MICHAEL
; APPLICANT: WANG-RODRIGUEZ, JESSICA
; APPLICANT: TARIN, DAVID
; APPLICANT: BERRY, CHARLES C.
; APPLICANT: ARDEN, KAREN
; APPLICANT: WASSERMAN, LINDA
; APPLICANT: GOODISON, STEVEN
; APPLICANT: KLACANSKY, IGOR
; TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
; FILE REFERENCE: 15670-073001
; CURRENT APPLICATION NUMBER: US/11/033,056A
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,382
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: 60/536,163
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 3888
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38206
; LENGTH: 74025
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-033-056A-38206
```

```
Query Match          0.8%; Score 20; DB 7; Length 74025;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1234 AAGCCTCAAAGTGCATTCTG 1253
Db 37281 AAGCCTCAAAGTGCATTCTG 37300

RESULT 15
US-11-033-056A-36497/c
; Sequence 36497, Application US/11033056A
; Publication No. US20060292572A1
; GENERAL INFORMATION:
; APPLICANT: STUART, ROBERT O.
; APPLICANT: STUART, ELIZABETH DUFF
; APPLICANT: WACHSMAN, WILLIAM
; APPLICANT: MERCOLA, DANIEL
; APPLICANT: MCCLELLAND, MICHAEL
; APPLICANT: WANG-RODRIGUEZ, JESSICA
; APPLICANT: TARIN, DAVID
; APPLICANT: BERRY, CHARLES C.
; APPLICANT: ARDEN, KAREN
; APPLICANT: WASSERMAN, LINDA
; APPLICANT: GOODISON, STEVEN
; APPLICANT: KLACANSKY, IGOR
; TITLE OF INVENTION: CELL-TYPE-SPECIFIC PATTERNS OF GENE EXPRESSION
; FILE REFERENCE: 15670-073001
; CURRENT APPLICATION NUMBER: US/11/033,056A
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,382
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: 60/536,163
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 3888
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36497
; LENGTH: 89298
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-033-056A-36497

Query Match          0.8%; Score 20; DB 7; Length 89298;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 TTTATTCAAATACATACCA 210
Db 53445 TTTATTCAAATACATACCA 53426

Search completed: January 15, 2007, 22:02:54
Job time : 688 secs
```



GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2007, 21:00:27 ; Search time 11783 Seconds  
(without alignments)  
11945.087 Million cell updates/sec

Title: US-10-528-631-1  
Perfect score: 2517  
Sequence: 1 gaatttagtgtagctga.....gaaacgactgcctccagta 2517

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 2795965780 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96473154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est3:  
3: gb\_est4:  
4: gb\_est5:  
5: gb\_est6:  
6: gb\_hc:  
7: gb\_est2:  
8: gb\_est7:  
9: gb\_est8:  
10: gb\_est9:  
11: gb\_ges1:  
12: gb\_ges2:  
13: gb\_ges3:  
14: gb\_ges4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	101	4.0	436	8	CN7511344	CN7511344 APHL3SD-V
2	62	2.5	747	10	DY228274	DY228274 IDOAAK3YK
3	53	2.1	822	8	CV832566	CV832566 IDOACC20B
4	53	2.1	887	8	CV847515	CV847515 IDOAE3AC
5	47	1.9	657	10	DY226563	DY226563 IDOAAI8YL
6	41	1.6	299	8	CN749438	CN749438 APAL3SD-X
7	41	1.6	387	8	CN751444	CN751444 APHL3SD-V
8	39	1.5	289	8	CN749378	CN749378 APHL3SD-V
9	26	1.0	410	1	AJ799071	AJ799071 APHL3SD-V
10	26	1.0	706	1	AJ805860	AJ805860 AJ799071
11	25	1.0	161	8	CN751565	CN751565 APHL3SD-X
12	25	1.0	642	10	DR397255	DR397255 USDA-FP_1
13	23	0.9	769	4	BX879050	BX879050 BX879050
14	22	0.9	423	5	CJ151359	CJ151359 CJ151359
15	22	0.9	436	5	CD191334	CD191334 MS1-0070T
16	22	0.9	583	14	AG909847	AG909847 Drosophila
17	22	0.9	597	14	AG911670	AG911670 Drosophila
18	22	0.9	689	13	CL838572	CL838572 OR_CBA006
19	22	0.9	969	14	AL407683	AL407683 T7 end of

C 20	21	0.8	194	5	CK629189	CK629189 AM3-AA001
C 21	21	0.8	215	5	CK629223	CK629223 AM3-AA001
C 22	21	0.8	241	4	CB278874	CB278874 ru29f05.y
C 23	21	0.8	246	5	CK629255	CK629255 AM3-AA001
C 24	21	0.8	285	1	AV333214	AV333214 AV333214
C 25	21	0.8	327	5	CK629240	CK629240 AM3-AA001
C 26	21	0.8	329	5	CK629212	CK629212 AM3-AA001
C 27	21	0.8	348	5	CK629206	CK629206 AMO-AA001
C 28	21	0.8	352	5	CK629215	CK629215 AM3-AA001
C 29	21	0.8	376	7	AW531037	AW531037 UI-R-BT1-
C 30	21	0.8	378	5	CK629250	CK629250 AMO-AA001
C 31	21	0.8	394	10	DT906185	DT906185 S29-21647
C 32	21	0.8	396	10	DV714899	DV714899 RVL4367 W
C 33	21	0.8	403	1	AJ812573	AJ812573 13C1 Pine
C 34	21	0.8	438	14	AG188897	AG188897 Pan trogl
C 35	21	0.8	442	7	BE721960	BE721960 189824 MA
C 36	21	0.8	469	10	DV724468	DV724468 RVL16524
C 37	21	0.8	497	5	CK766922	CK766922 wmi01-3ms
C 38	21	0.8	497	13	DU345931	DU345931 109831310
C 39	21	0.8	506	3	BQ204921	BQ204921 UI-R-EP0-
C 40	21	0.8	514	1	AI175572	AI175572 EST219127
C 41	21	0.8	523	4	BW707581	BW707581 BW707581
C 42	21	0.8	526	11	BH056613	BH056613 RPCT-24-2
C 43	21	0.8	547	7	AW526365	AW526365 UI-R-B01-
C 44	21	0.8	549	2	BI396701	BI396701 ro60ell.y
C 45	21	0.8	558	1	AI638950	AI638950 rx02769s

#### ALIGNMENTS

CN7511344 436 bp mRNA linear EST 19-MAY-2004  
APHL3SD-V-G11 APHL3SD Acyrthosiphon pisum cDNA clone APHL3SDVG11  
5', mRNA sequence.

CN7511344  
CN751344.1 GI:47516341  
EST.

ACCESSION  
VERSION  
SOURCE  
ORGANISM

Acyrthosiphon pisum (pea aphid)  
Acyrthosiphon pisum  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE  
AUTHORS

1 (bases 1 to 436)  
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,  
Stern, D., Tagu, D. and Wincker, P.

TITLE

An expressed sequence tags database for the pea aphid Acyrthosiphon

JOURNAL

COMMENT

Unpublished (2004)  
Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory

(Buchner) or facultative endosymbionts.

PCR Primers

FORWARD: GCCGCAATCTCGTATAGCA

Plate: V row: G column: 11.

Location/Qualifiers

1. 436

/organism="Acyrthosiphon pisum"

/mol\_type="mRNA"

/cultivar="yr2"

/db\_xref="taxon:7029"

/clone="APHL3SDVG11"

/tissue\_type="head"

/dev\_stage="third instar nymph (L3)"

/lab\_host="TOP10"

/clone\_lib="APHL3SD"

/note="Vector: pDNR-LIB; Site\_1: SfiI; Site\_2: SfiI; Sample name: APHL3SD ; Plant growth place: INRA-Rennes."

UMR BIO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil conditions: peat ; Sowing date: 20/03/2003 ; Harvesting date: 10/04/2003 ; Stress date: no stress ; Description: aphids inoculated on one-week old Vicia faba germinations under non sterile conditions. ; experimental condition: short photoperiod (12-hr light/12-hr dark at 18 c)"

## ORIGIN

Query Match 4.0%; Score 101; DB 8; Length 436;  
Best Local Similarity 100.0%; Pred. No. 2.4e-42;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 TGGATTGCTTGTCTTACCACCTTGGGAAGATATCAGAATACAGTCTCTCAGAAAGCTT 1164  
|||||  
Db 217 TGGATTGCTTGTCTTACCACCTTGGGAAGATATCAGAATACAGTCTCTCAGAAAGCTT 276  
|||||

QY 1165 ATGGTAGAATAATATAATATACGAAGCTCTTTGATCG 1205  
|||||  
Db 277 ATGGTAGAATAATATAATATACGAAGCTCTTTGATCG 317  
|||||

RESULT 2  
DY228274  
LOCUS  
DEFINITION  
ID0AAK3YK02CM1 AphL3SD Acyrthosiphon pisum cDNA clone ID0AAK3YK02  
5', mRNA sequence.

ACCESSION  
VERSION  
DY228274.1 GI:86462402

KEYWORDS  
SOURCE  
ACyrthosiphon pisum (pea aphid)

ORGANISM  
ACyrthosiphon pisum  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE  
AUTHORS  
Stern,D.B., Wincker,P. and Tagu,D.

TITLE  
Large-scale gene discovery in the pea aphid Acyrthosiphon pisum  
(Hemiptera)

JOURNAL  
COMMENT  
Unpublished (2005)

INRA Rennes  
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France  
Tel: +33.2.23.48.51.65  
Fax: +33.2.23.48.51.50

PCR Primers  
FORWARD: GCCGATACTTCGTATAGCA  
Plate: 3Y row: K column: 2.

FEATURES  
Location/Qualifiers  
1..747

/organism="Acyrthosiphon pisum"  
/mol\_type="mRNA"  
/cultivar="yr2"  
/db\_xref="taxon:7029"  
/clone="ID0AAK3YK02"  
/tissue\_type="head"  
/dev\_stage="third instar nymph (L3)"  
/lab\_host="TOP10"  
/clone\_lib="AphL3SD"  
/note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;  
Sample name: AphL3SD ; Plant growth place: INRA-Rennes,  
UMR BIO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil  
conditions: peat ; Sowing date: 20/03/2003 ; Harvesting  
date: 10/04/2003 ; Stress date: no stress ; Description:  
aphids inoculated on one-week old Vicia faba germinations  
under non sterile conditions. ; experimental condition:  
short photoperiod (12-hr light/12-hr dark at 18 c)"

## ORIGIN

Query Match 2.5%; Score 62; DB 10; Length 747;  
Best Local Similarity 100.0%; Pred. No. 3.6e-21;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 613 GATATCAACCAAGAAATATAATGTGCCAGACAAAGAGTTTCAAAATGTAAACTCATC 672  
|||||

Db 624 GATATCAACCAAGAAATATAATGTGCCAGACAAAGAGTTTCAAAATGTAAACTCATC 683  
|||||  
QY 673 GA 674  
||  
Db 684 GA 685

RESULT 3  
CV832566/c  
LOCUS  
DEFINITION  
CV832566 822 bp mRNA linear EST 17-NOV-2004  
ID0ACC20BG06RM1 ID0ACC Acyrthosiphon pisum cDNA clone ID0ACC20BG06  
5', mRNA sequence.

ACCESSION  
VERSION  
CV832566.1 GI:55798249

KEYWORDS  
SOURCE  
ACyrthosiphon pisum (pea aphid)

ORGANISM  
ACyrthosiphon pisum  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE  
AUTHORS  
Sabater-Munoz,B., Legeai,F., Bonhomme,J., Dang,P., Dosat,C.,  
Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,  
Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,  
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.

TITLE  
JOURNAL  
COMMENT  
Annotated ESTs of the pea aphid  
Unpublished (2004)

INRA Rennes  
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France  
Tel: +33.2.23.48.51.65  
Fax: +33.2.23.48.51.50

PCR Primers  
FORWARD: CAGAAACAGCTATGACC  
Plate: 20B row: G column: 6.

FEATURES  
Location/Qualifiers  
1..822

/organism="Acyrthosiphon pisum"  
/mol\_type="mRNA"  
/cultivar="P123"  
/db\_xref="taxon:7029"  
/clone="ID0ACC20BG06"  
/tissue\_type="head"  
/dev\_stage="larvae L3 (parthenogenetic females)"  
/lab\_host="XL1-Blue"  
/clone\_lib="ID0ACC"  
/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;  
Sample name: ID0ACC ; Plant growth place: INRA Rennes, UMR  
BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil  
conditions: Soil ; Sowing date: 01/10/2003 ; Harvesting  
date: 17/10/2003 ; Description: aphids inoculated on  
one-week old Vicia faba germinations under non sterile  
conditions experimental condition: long photoperiod (16-hr  
light/8-hr dark at 18 degc)"

## ORIGIN

Query Match 2.1%; Score 53; DB 8; Length 822;  
Best Local Similarity 100.0%; Pred. No. 2.8e-16;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2362 GCGAGCTTGAAGATCAATCAACTATTTCCCGAAGATGCTGGAGATATATCTG 2414  
|||||

Db 803 GCGAGCTTGAAGATCAATCAAGTATTTCCCGAAGATGCTGGAGATATATCTG 751  
|||||

## RESULT 4

CV847515  
LOCUS  
DEFINITION  
CV847515 887 bp mRNA linear EST 17-NOV-2004  
ID0AEE3AC06RM1 ID0AEE Acyrthosiphon pisum cDNA clone ID0AEE3AC06  
5', mRNA sequence.

ACCESSION  
VERSION  
CV847515  
CV847515.1 GI:55813198

## KEYWORDS

## SOURCE

## ORGANISM

## EST.

Acyrtosiphon pisum (pea aphid)

Acyrtosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

## REFERENCE

## AUTHORS

1 (bases 1 to 887)  
Sabater-Munoz,B., Legeai,F., Bonhomme,J., Dang,P., Dessat,C.,  
Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,  
Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,  
Simon,J.C., Stern,D., Wincker,P. and Tagu,D.

## TITLE

Annotated ESTs of the pea aphid

## JOURNAL

Unpublished (2004)

## COMMENT

Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 3A row: C column: 6.

Location/Qualifiers

1. .887

/organism="Acyrtosiphon pisum"

/mol\_type="mRNA"

/cultivar="yr2"

/db\_xref="taxon:7029"

/clone="ID0AE3AC06"

/tissue\_type="antennae"

/dev\_stage="L3"

/lab\_host="XLI-Blue"

/clone\_lib="ID0AEE"

/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;  
Sample name: ID0AEE; Plant growth place: INRA Rennes, UMR  
BIO3P, 35327, 35653 Le Rheu Cedex France; Soil  
conditions: Soil; Sowing date: 15/04/2004; Harvesting  
date: 15/04/2004; Description: Aphids inoculated on  
one-week old Vicia faba under non-sterile conditions. A.  
pisum YR2 is holocyclic, i.e. able to change its  
reproductive mode under short photoperiods (sexual) versus  
long photoperiods (clonal). experimental condition: long  
photoperiod (16-hr light/8-hr dark at 18 degC)"

## ORIGIN

## Query Match

Best Local Similarity 2.1%; Score 53; DB 8; Length 887;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Qy

2362 GCGAGTTGAAGATCAATGAAGTATCCCGAAGATGCTGGAGATATATCTG 2414

|||||

86 GCGAGTTGAAGATCAATGAAGTATCCCGAAGATGCTGGAGATATATCTG 138

## RESULT 5

## LOCUS

DY226563 ID0AA18YL22RM1 ID0AEE Acyrthosiphon pisum cDNA clone ID0AA18YL22

5', mRNA sequence. 657 bp mRNA linear EST 03-FEB-2006

## ACCESSION

DY226563

DY226563

EST.

Acyrtosiphon pisum (pea aphid)

## ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

## REFERENCE

## AUTHORS

1 (bases 1 to 657)

Stern,D.L., Wincker,P. and Tagu,D.

## TITLE

Large-scale gene discovery in the pea aphid Acyrthosiphon pisum

## JOURNAL

(Hemiptera)

Unpublished (2005)

Contact: D. Tagu

INRA Rennes

## FEATURES

## source

1. .657

/organism="Acyrtosiphon pisum"

/mol\_type="mRNA"

/cultivar="yr2"

/db\_xref="taxon:7029"

/clone="ID0AA18YL22"

/tissue\_type="antennae"

/dev\_stage="L3"

/lab\_host="XLI-Blue"

/clone\_lib="ID0AEE"

/note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;

Sample name: ID0AEE; Plant growth place: INRA Rennes, UMR  
BIO3P, 35327, 35653 Le Rheu Cedex France; Soil  
conditions: Soil; Sowing date: 15/04/2004; Harvesting  
date: 15/04/2004; Description: Aphids inoculated on  
one-week old Vicia faba under non-sterile conditions. A.  
pisum YR2 is holocyclic, i.e. able to change its  
reproductive mode under short photoperiods (sexual) versus  
long photoperiods (clonal). experimental condition: long  
photoperiod (16-hr light/8-hr dark at 18 degC)"

## ORIGIN

## Query Match

Best Local Similarity 1.9%; Score 47; DB 10; Length 657;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Qy

1993 AACGTGCACGGAACAGTTCGGTCTTCAACCAATCCATCCAC 2039

|||||

551 AACGTGCACGGAACAGTTCGGTCTTCAACCAATCCATCCAC 597

## RESULT 6

## LOCUS

CN749438 299 bp mRNA linear EST 19-MAY-2004  
APAL3SD-XI-P2 APAL3SD Acyrthosiphon pisum cDNA clone APAL3SDXIF2  
5', mRNA sequence.

## ACCESSION

CN749438

CN749438.1 GI:47514435

EST.

Acyrtosiphon pisum (pea aphid)

## SOURCE

Acyrtosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 299)

Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,

Stern,D., Tagu,D. and Wincker,P.

An expressed sequence tags database for the pea aphid Acyrthosiphon

pisum

Unpublished (2004)

Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory

(Buchnera) or facultative endosymbionts.

PCR Primers

FORWARD: GCCGCATAACTTCGTATAGCA

Plate: XI row: F column: 2.

Location/Qualifiers

1. .299

/organism="Acyrtosiphon pisum"

/mol\_type="mRNA"

/cultivar="yr2"

/db\_xref="taxon:7029"

```

/clone="ApAL3SDXIF2"
/tissue_type="antennae"
/dev_stage="third instar nymph (L3)"
/lab_host="TOP10"
/clone_lib="ApAL3SD"
/note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB;
Sample name: ApAL3SD ; Plant growth place: INRA-Rennes,
UMR Bio3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
conditions: peat ; Sowing date: 25/03/2003 ; Harvesting
date: 10/04/2003 ; Stress date: no stress ; Description:
aphids inoculated on one-week old Vicia faba germinations
under non sterile conditions. ; experimental condition:
short photoperiod (12-hr light/12-hr dark at 18 c)"

```

## ORIGIN

```

Query Match      1.6%; Score 41; DB 8; Length 299;
Best Local Similarity 100.0%; Pred. No. 8.4e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 97 AAAACTAAACGTTACGAAGTTGATGAACCTGGCAAAAAAAT 137
|||||
Db 22 AAAACTAAACGTTACGAAGTTGATGAACCTGGCAAAAAAAT 62
|||||

```

## RESULT 7

```

CN751444
LOCUS ApHL3SD-VII-E6 ApHL3SD Acyrthosiphon pisum cDNA clone ApHL3SDVII186
5', mRNA sequence.
CN751444.1 GI:47516441
EST.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE

```

```

ORGANISM

```

```

Acyrthosiphon pisum (pea aphid)

```

```

Acyrthosiphon pisum

```

```

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 387)

```

## REFERENCE

```

AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.

```

```

TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum

```

```

Unpublished (2004)

```

```

COMMENT Contact: D. Tagu

```

```

INRA Rennes

```

```

UMR Bio3P, BP 35327, F-35653 Le Rheu Cedex France

```

```

Tel: +33.2.23.48.51.65

```

```

Fax: +33.2.23.48.51.50

```

```

Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts.

```

```

PCR Primers

```

```

FORWARD: GCCGCATAACTTCGTATAGCA

```

```

Plate: VII row: E column: 6.

```

```

Location/Qualifiers

```

```

1..387

```

## FEATURES

```

source

```

```

/organism="Acyrthosiphon pisum"

```

```

/mol_type="mRNA"

```

```

/cultivar="yr2"

```

```

/db_xref="taxon:7029"

```

```

/clone="ApHL3SDVII186"

```

```

/tissue_type="head"

```

```

/dev_stage="third instar nymph (L3)"

```

```

/lab_host="TOP10"

```

```

/clone_lib="ApHL3SD"

```

```

/note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB;
Sample name: ApHL3SD ; Plant growth place: INRA-Rennes,
UMR Bio3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
conditions: peat ; Sowing date: 20/03/2003 ; Harvesting
date: 10/04/2003 ; Stress date: no stress ; Description:
aphids inoculated on one-week old Vicia faba germinations
under non sterile conditions. ; experimental condition:
short photoperiod (12-hr light/12-hr dark at 18 c)"

```

## ORIGIN

```

Query Match      1.6%; Score 41; DB 8; Length 387;
Best Local Similarity 100.0%; Pred. No. 8.5e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 97 AAAACTAAACGTTACGAAGTTGATGAACCTGGCAAAAAAAT 137
|||||
Db 108 AAAACTAAACGTTACGAAGTTGATGAACCTGGCAAAAAAAT 148
|||||

```

## RESULT 8

```

CN749378
LOCUS ApAL3SD-VIII-H6 ApAL3SD Acyrthosiphon pisum cDNA clone
5', mRNA sequence.
CN749378.1 GI:47514375
EST.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE

```

```

ORGANISM

```

```

Acyrthosiphon pisum (pea aphid)

```

```

Acyrthosiphon pisum

```

```

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 289)

```

## REFERENCE

```

AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.

```

```

TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum

```

```

Unpublished (2004)

```

```

COMMENT Contact: D. Tagu

```

```

INRA Rennes

```

```

UMR Bio3P, BP 35327, F-35653 Le Rheu Cedex France

```

```

Tel: +33.2.23.48.51.65

```

```

Fax: +33.2.23.48.51.50

```

```

Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts.

```

```

PCR Primers

```

```

FORWARD: GCCGCATAACTTCGTATAGCA

```

```

Plate: VIII row: H column: 6.

```

```

Location/Qualifiers

```

```

1..289

```

## FEATURES

```

source

```

```

/organism="Acyrthosiphon pisum"

```

```

/mol_type="mRNA"

```

```

/cultivar="yr2"

```

```

/db_xref="taxon:7029"

```

```

/clone="ApAL3SDVII186"

```

```

/tissue_type="antennae"

```

```

/dev_stage="third instar nymph (L3)"

```

```

/lab_host="TOP10"

```

```

/clone_lib="ApAL3SD"

```

```

/note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB;
Sample name: ApAL3SD ; Plant growth place: INRA-Rennes,
UMR Bio3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
conditions: peat ; Sowing date: 25/03/2003 ; Harvesting
date: 10/04/2003 ; Stress date: no stress ; Description:
aphids inoculated on one-week old Vicia faba germinations
under non sterile conditions. ; experimental condition:
short photoperiod (12-hr light/12-hr dark at 18 c)"

```

## ORIGIN

```

Query Match      1.5%; Score 39; DB 8; Length 289;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 97 AAAACTAAACGTTACGAAGTTGATGAACCTGGCAAAAAA 135
|||||
Db 41 AAAACTAAACGTTACGAAGTTGATGAACCTGGCAAAAAA 79
|||||

```

## RESULT 9

```

AJ799071
LOCUS Antirrhinum majus whole plant Antirrhinum majus cDNA clone
DEFINITION AJ799071 Antirrhinum majus whole plant Antirrhinum majus cDNA clone

```

```

018_4_06_j19, mRNA sequence.
ACCESSION AJ799071
VERSION AJ799071.1 GI:511114399
KEYWORDS EST
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Plantaginaceae; Antirrhineae;
Antirrhinum.
REFERENCE 1 (bases 1 to 410)
AUTHORS Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
TITLE Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
DEFICIENS
JOURNAL Plant Cell 16 (12), 3197-3215 (2004)
PUBMED 15539471
COMMENT Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
source
Location/Qualifiers
1..410
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_4_06_j19"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

ORIGIN
Query Match 1.0%; Score 26; DB 1; Length 410;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 TCTGGAGGAGAGCTATTGGAAGGAT 509
|||||
Db 286 TCTGGAGGAGAGCTATTGGAAGGAT 311
|||||

RESULT 10
AJ805860
LOCUS AJ805860
DEFINITION Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018_6_02_e08, mRNA sequence.
ACCESSION AJ805860
VERSION AJ805860.1 GI:51121188
KEYWORDS EST.
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Plantaginaceae; Antirrhineae;
Antirrhinum.
REFERENCE 1 (bases 1 to 706)
AUTHORS Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
TITLE Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
DEFICIENS
JOURNAL Plant Cell 16 (12), 3197-3215 (2004)
PUBMED 15539471
COMMENT Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
source
Location/Qualifiers
1..706
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_6_02_e08"

/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

ORIGIN
Query Match 1.0%; Score 26; DB 1; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 TCTGGAGGAGAGCTATTGGAAGGAT 509
|||||
Db 286 TCTGGAGGAGAGCTATTGGAAGGAT 311
|||||

RESULT 11
CN751565
LOCUS CN751565
DEFINITION APhL3SD-XII-E11 APhL3SD Acyrthosiphon pisum cDNA clone
APhL3SDXIIIE11 5', mRNA sequence.
ACCESSION CN751565
VERSION CN751565.1 GI:47516562
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrospini; Acyrthosiphon.
REFERENCE 1 (bases 1 to 161)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33 2 23 48 51 65
Fax: +33 2 23 48 51 50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts.
PCR Primers
FORWARD: GCGCATAACTTCGTATAGCA
Plate: XII row: E column: 11.
FEATURES
source
Location/Qualifiers
1..161
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="yr2"
/db_xref="taxon:7029"
/clone="APhL3SDXIIIE11"
/tissue_type="head"
/dev_stage="third instar nymph (L3)"
/lab_host="TOP10"
/clone_lib="APhL3SD"
/notes="Vector: pDNR-LIB; Site 1: SfIIA; Site 2: SfiIB;
Sample Name: APhL3SD ; Plant growth place: INRA-Rennes,
UMR BIO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
conditions: peat ; Sowing date: 20/03/2003 ; Harvesting
date: 10/04/2003 ; Stress date: no stress ; Description:
aphids inoculated on one-week old Vicia faba germinations
under non sterile conditions. ; experimental condition:
short photoperiod (12-hr light/12-hr dark at 18 c)"

ORIGIN
Query Match 1.0%; Score 25; DB 8; Length 161;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1612 TTACGACCTCGTGTGCATACAAATAC 1636
|||||
Db 75 TTACGACCTCGTGTGCATACAAATAC 99
|||||

RESULT 12

```

DR397255 LOCUS  
 DEFINITION USDA-FP\_157194 Adult Alate Aphis gossypii (WHAGA) linear mRNA EST 19-AUG-2005  
 cDNA clone WHAGA108\_E01 5', mRNA sequence. Aphis gossypii  
 DR397255  
 ACCESSION DR397255.1 GI:73620686  
 VERSION  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Aphis gossypii (cotton aphid)  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Aphidini; Aphis.  
 1 (bases 1 to 642)  
 REFERENCE Hunter, W.B., Dang, P.M. and Lee, L.  
 AUTHORS Expressed Genes from Alate Aphis gossypii  
 TITLE Unpublished (2006)  
 JOURNAL  
 COMMENT Contact: Wayne B. Hunter  
 US Horticultural Research Laboratory  
 USDA - ARS  
 2001 South Rock Rd., Fort Pierce, FL 34945, USA  
 Tel: (772) 462-5898  
 Fax: (772) 462-5960  
 Email: whunter@uhr1.ars.usda.gov  
 Seq primer: T3 Primer.  
 Location/Qualifiers  
 1..642  
 /organism="Aphis gossypii"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:80765"  
 /clone="WHAGA108\_E01"  
 /sex="Mixed population"  
 /tissue\_type="Entire insect"  
 /dev\_stage="Adult Alate"  
 /lab\_host="X11-Blue"  
 /clone\_lib="Adult Alate Aphis gossypii (WHAGA)"  
 /note="Vector: pBluescript II SK+; Site 1: EORI; Site 2: XhoI; A high quality EST with at least 150 contiguous bases at Trace Tuner score of 20 or better. cDNA Library construction by Lawrence Lee."  
 ORIGIN  
 Query Match 1.0%; Score 25; DB 10; Length 642;  
 Best Local Similarity 100.0%; Pred. No. 0.43;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 112 GAAGTTGATGAACTGSCAAAAA 136  
 |||||||  
 Db 522 GAAGTTGATGAACTGSCAAAAA 546  
 |||||||  
 RESULT 13  
 BX879050 LOCUS  
 DEFINITION BX879050 tcbk Oncorhynchus mykiss cDNA clone tcbk0034c.d.07 5prim, mRNA sequence. EST.  
 ACCESSION BX879050  
 VERSION BX879050.2 GI:42793416  
 KEYWORDS EST.  
 SOURCE Oncorhynchus mykiss (rainbow trout)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 1 (bases 1 to 769)  
 REFERENCE Govoroun, M., Guiguen, Y. and Le Gac, F.  
 AUTHORS Construction and primary characterization of normalized cDNA  
 TITLE Libraries in rainbow trout, Oncorhynchus mykiss  
 JOURNAL Unpublished (2003)  
 COMMENT On Dec 18, 2003 this sequence version replaced gi:40120065.  
 Contact: Guiguen Y  
 INRA - SCRIBE  
 Campus de Beaulieu, RENNES cedex, 35042, France  
 Tel: 02.23.48.50.09

Fax: 02.23.48.50.20  
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr  
 Sequence cleaned of vector, adaptor and repetitions. Contact us  
 at sigenasupport@jouy.inra.fr to obtain the chromatogram of this  
 sequence.  
 Plate: 0034 row: d column: 7  
 Seq primer: M13R.  
 Location/Qualifiers  
 1..769  
 /organism="Oncorhynchus mykiss"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8022"  
 /clone="tcbk0034c.d.07"  
 /tissue\_type="multi-tissues"  
 /dev\_stage="from embryos to adults"  
 /lab\_host="DH10B"  
 /clone\_lib="tcbk"  
 /note="Vector: pT7T3D-PacI; AGENAE Rainbow trout  
 multi-tissues - normalized + 2 subtractions; Clone  
 distribution: AGENAE Resource centre, Francois PIUMI,  
 Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et  
 Etude du genome (LREG), Domaine de Vilvert, 78352,  
 Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33  
 (0) 1.34.65.22.73"  
 ORIGIN  
 Query Match 0.9%; Score 23; DB 4; Length 769;  
 Best Local Similarity 100.0%; Pred. No. 5.3;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 485 CTGGAGGAGAGCTATTGAAAGG 507  
 |||||||  
 Db 540 CTGGAGGAGAGCTATTGAAAGG 562  
 |||||||  
 RESULT 14  
 CJ151359 LOCUS  
 DEFINITION visual cortex Mus musculus cDNA clone K430026A05 5', mRNA sequence.  
 ACCESSION CJ151359  
 VERSION CJ151359.1 GI:76255498  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 423)  
 REFERENCE The PANTOM Consortium and RIKEN Genome Exploration Research Group  
 AUTHORS and Genome Science Group (Genome Network Project Core Group).  
 TITLE The transcriptional landscape of the mammalian genome  
 JOURNAL Science 309 (5740), 1559-1563 (2005)  
 PUBMED 16141072  
 COMMENT Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues. Tissues were provided by Michela Fagiolini  
 and Takao K. Hensch (Laboratory for Neuronal Circuit Development  
 Brain Science Institute RIKEN 2-1 Hirotsawa, Wako-shi, Saitama  
 351-0198 Japan) whose assistance we gratefully acknowledge.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/.  
 Location/Qualifiers

## source

1. 423  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="K430026A05"  
/tissue\_type="visual cortex"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library,  
C57BL/6J visual cortex"

## ORIGIN

Query Match 0.9%; Score 22; DB 5; Length 423;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1866 TACTGACCAAGCCCAAGAGCAG 1887

DB 143 TACTGACCAAGCCCAAGAGCAG 164

## RESULT 15

CD191334

LOCUS MS1-0070T-R331-F12-U.G MSI-0070 Schistosoma mansoni cDNA clone  
DEFINITION MS1-0070T-R331-F12.G, mRNA sequence.

ACCESSION CD191334

VERSION CD191334.1

KEYWORDS GI:34721277

SOURCE EST.

ORGANISM Schistosoma mansoni

Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 436)

Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,  
Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,  
Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,  
Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,  
Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,  
Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,  
Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,  
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,  
Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.

Transcriptome analysis of the acelomate human parasite Schistosoma

mansoni

Nat. Genet. 35 (2), 148-157 (2003)

12973350

COMMENT

Contact: Dr. Sergio Verjovski-Almeida

Departamento de Bioquímica

Instituto de Química - Universidade de São Paulo

Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP,

Brasil

Tel: +55-11-3091-2173

Fax: +55-11-3091-2186

Email: verjov@iq.usp.br

This sequence was derived from the FAPESP Schistosoma mansoni EST

Genome Project. All sequences in the project were assembled and

annotated. This entry and all the assembled sequences can be seen

in the following URL <http://bioinfo.iq.usp.br/schisto/>

Plate: MS1-0070T-R331 row: 12 column: F.

Location/Qualifiers

1. 436

/organism="Schistosoma mansoni"

/mol\_type="mRNA"

/db\_xref="taxon:6183"

/clone="MS1-0070T-R331-F12.G"

/sex="mixed pool"

/dev\_stage="schistosomulum"

/lab\_host="in vitro culture"

/clone\_lib="MS1-0070"

/note="Vector: pGEM T-easy"

## ORIGIN

Query Match 0.9%; Score 22; DB 5; Length 436;

Best Local Similarity 100.0%; Pred. No. 18;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 612 AGATATCAAAACCAGAAAATATA 633

DB 81 AGATATCAAAACCAGAAAATATA 102

Search completed: January 16, 2007, 00:42:28  
Job time : 11787 secs

*This page Blank (uspo)*



GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 17, 2007, 09:08:08 ; Search time 2 Seconds  
(without alignments)  
3.579 Million cell updates/sec

Title: US-10-528-631-1  
Perfect score: 2517  
Sequence: 1 gaatttagagtgcctga.....gaaacgactgcctccagta 2517

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 136 seqs, 1422 residues

Total number of hits satisfying chosen parameters: 272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 137 summaries

Database : gedb.\*

*Gran bank/E.MBC*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	14	0.6	14	1	CS173861	ACCESSION:CS173861
C 2	12	0.5	12	1	CQ766153	ACCESSION:CQ766153
C 3	12	0.5	12	1	CQ766321	ACCESSION:CQ766321
C 4	12	0.5	12	1	CQ766523	ACCESSION:CQ766523
C 5	12	0.5	12	1	CQ766549	ACCESSION:CQ766549
C 6	12	0.5	12	1	CQ828761	ACCESSION:CQ828761
C 7	12	0.5	12	1	AR637451	ACCESSION:AR637451
C 8	11	0.4	11	1	BD269252	ACCESSION:BD269252
C 9	11	0.4	11	1	CQ832956	ACCESSION:CQ832956
C 10	11	0.4	11	1	CQ833421	ACCESSION:CQ833421
C 11	11	0.4	11	1	CQ835093	ACCESSION:CQ835093
C 12	11	0.4	11	1	CQ835390	ACCESSION:CQ835390
C 13	11	0.4	11	1	CQ835793	ACCESSION:CQ835793
C 14	11	0.4	11	1	CQ836020	ACCESSION:CQ836020
C 15	11	0.4	11	1	CQ837255	ACCESSION:CQ837255
C 16	11	0.4	11	1	CQ837527	ACCESSION:CQ837527
C 17	11	0.4	11	1	CQ837558	ACCESSION:CQ837558
C 18	11	0.4	11	1	CQ837862	ACCESSION:CQ837862
C 19	11	0.4	11	1	CQ838131	ACCESSION:CQ838131
C 20	11	0.4	11	1	AR364706	ACCESSION:AR364706
C 21	11	0.4	11	1	AX393107	ACCESSION:AX393107
C 22	11	0.4	11	1	AX393218	ACCESSION:AX393218
C 23	11	0.4	11	1	AX394505	ACCESSION:AX394505
C 24	11	0.4	11	1	AX394512	ACCESSION:AX394512
C 25	11	0.4	11	1	AX421309	ACCESSION:AX421309
C 26	11	0.4	11	1	AX421314	ACCESSION:AX421314
C 27	11	0.4	11	1	AX471107	ACCESSION:AX471107
C 28	11	0.4	11	1	AX471484	ACCESSION:AX471484
C 29	11	0.4	11	1	AX623352	ACCESSION:AX623352
C 30	11	0.4	11	1	AX623626	ACCESSION:AX623626
C 31	11	0.4	11	1	AX625016	ACCESSION:AX625016
C 32	11	0.4	11	1	AX625604	ACCESSION:AX625604
C 33	11	0.4	11	1	AX625962	ACCESSION:AX625962

```

c 107      10 0.4 10 1 AR269009      ACCESSION:AR269009
c 108      10 0.4 10 1 AR303296      ACCESSION:AR303296
c 109      10 0.4 10 1 AR303312      ACCESSION:AR303312
c 110      10 0.4 10 1 AR303351      ACCESSION:AR303351
c 111      10 0.4 10 1 AR336845      ACCESSION:AR336845
c 112      10 0.4 10 1 AR336861      ACCESSION:AR336861
c 113      10 0.4 10 1 AR336881      ACCESSION:AR336881
c 114      10 0.4 10 1 AR371291      ACCESSION:AR371291
c 115      10 0.4 10 1 I50799       ACCESSION:I50799
c 116      10 0.4 10 1 AR487041      ACCESSION:AR487041
c 117      10 0.4 10 1 AR489512      ACCESSION:AR489512
c 118      10 0.4 10 1 AR491123      ACCESSION:AR491123
c 119      10 0.4 10 1 AR585246      ACCESSION:AR585246
c 120      10 0.4 10 1 AR647992      ACCESSION:AR647992
c 121      10 0.4 10 1 AR700611      ACCESSION:AR700611
c 122      10 0.4 10 1 AX112993      ACCESSION:AX112993
c 123      10 0.4 10 1 AX152148      ACCESSION:AX152148
c 124      10 0.4 10 1 AX152257      ACCESSION:AX152257
c 125      10 0.4 10 1 AX152398      ACCESSION:AX152398
c 126      10 0.4 10 1 AX152772      ACCESSION:AX152772
c 127      10 0.4 10 1 AX153073      ACCESSION:AX153073
c 128      10 0.4 10 1 AX153292      ACCESSION:AX153292
c 129      10 0.4 10 1 AX190773      ACCESSION:AX190773
c 130      10 0.4 10 1 AX190774      ACCESSION:AX190774
c 131      10 0.4 10 1 AX301608      ACCESSION:AX301608
c 132      10 0.4 10 1 AX301653      ACCESSION:AX301653
c 133      10 0.4 10 1 AX301685      ACCESSION:AX301685
c 134      10 0.4 10 1 AX301716      ACCESSION:AX301716
c 135      10 0.4 10 1 AX510717      ACCESSION:AX510717
c 136      10 0.4 10 1 AX685131      ACCESSION:AX685131
c 137      10 0.4 10 1 AX685134      ACCESSION:AX685134

```

## ALIGNMENTS

```

RESULT 1
CS173861/c
LOCUS      CS173861      14 bp      DNA      linear      PAT 12-OCT-2005
DEFINITION Sequence 310 from Patent EP1582530.
ACCESSION  CS173861
VERSION     CS173861.1  GI:77624741
KEYWORDS    synthetic construct
SOURCE      other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Hampe,J
TITLE       Diagnostic use of polymorphisms in the gene for BTNL2 associated
            with sarcoidosis
JOURNAL     Patent: EP 1582530-A 310 05-OCT-2005;
            Universitaetsklinikum Schleswig-Holstein (DK)
FEATURES    Location/Qualifiers
            source
            1..14
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

```

```

Query Match      0.6%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2230  GTCATGACGGACA 2243
Db      14  GTCATGACGGACA 1
|||||

```

```

RESULT 2
CS173861/c
LOCUS      CS173861      12 bp      DNA      linear      PAT 03-MAR-2004
DEFINITION Sequence 114 from Patent WO2004005547.
ACCESSION  CS173861
VERSION     CS173861.1  GI:44908413

```

```

KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Weinzierl,R.
TITLE        Method
JOURNAL      Patent: WO 2004005547-A 114 15 JAN 2004;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES     Location/Qualifiers
            source
            1..12
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="HS consensus sequence"

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      451  GAAGATGAATG 462
Db      12  GAAGATGAATG 1
|||||

```

RESULT 3

```

CS173861/c
LOCUS      CS173861      12 bp      DNA      linear      PAT 03-MAR-2004
DEFINITION Sequence 282 from Patent WO2004005547.
ACCESSION  CS173861
VERSION     CS173861.1  GI:44908581
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Weinzierl,R.
TITLE       Method
JOURNAL     Patent: WO 2004005547-A 282 15-JAN-2004;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES    Location/Qualifiers
            source
            1..12
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="HS motif"

```

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 AAAAAGAAATG 391
Db 12 AAAAAGAAATG 1
|||||

RESULT 4

```

CS173861/c
LOCUS      CS173861      12 bp      DNA      linear      PAT 03-MAR-2004
DEFINITION Sequence 484 from Patent WO2004005547.
ACCESSION  CS173861
VERSION     CS173861.1  GI:44908783
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Weinzierl,R.
TITLE       Method
JOURNAL     Patent: WO 2004005547-A 484 15-JAN-2004;
            IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES    Location/Qualifiers
            source
            1..12

```

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="HS motif"

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AAATACAAAAC 2355  
Db |||||

RESULT 5  
LOCUS CQ766549/c 12 bp DNA linear PAT 03-MAR-2004  
DEFINITION Sequence 510 from Patent WO2004005547.  
ACCESSION CQ766549  
VERSION CQ766549.1 GI:44908809  
KEYWORDS synthetic construct  
ORGANISM synthetic construct  
SOURCE other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Weinzierl, R.  
TITLE Patent: WO 2004005547-A 510 15-JAN-2004;  
JOURNAL IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)  
FEATURES  
source  
1. .12  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="HS motif"

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AAATACAAAAC 2355  
Db |||||

RESULT 6  
LOCUS CQ828761 12 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 479 from Patent WO2004053120.  
ACCESSION CQ828761  
VERSION CQ828761.1 GI:49732244  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Murioidea; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Weihe, E., Bieller, A. and Schaefer, M.K.  
TITLE Regulatory elements in the 5' region of the vrl gene  
JOURNAL Patent: WO 2004053120-A 479 24-JUN-2004;  
Gruenthal GmbH (DE)  
FEATURES  
source  
1. .12  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"  
/note="VSNFAT Q6"

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 TAGAGGAAAGC 149  
Db |||||

RESULT 7  
LOCUS AR637451/c 12 bp DNA linear PAT 20 APR-2005  
DEFINITION Sequence 36 from patent US 6855812.  
ACCESSION AR637451  
VERSION AR637451.1 GI:62771183  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Hanscom, S. and Crespi, C.  
TITLE p-glycoproteins and uses thereof  
JOURNAL Patent: US 6855812-A 36 15-FEB-2005;  
Becton, Dickinson and Company; Franklin Lakes, NJ  
FEATURES  
source  
1. .12  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1440 AGCTGAAATAC 1451  
Db |||||

RESULT 8  
LOCUS BD269252 11 bp DNA linear PAT 17-JUL-2003  
DEFINITION Expression and transport of antibiotic protein as FC-fused protein.  
ACCESSION BD269252  
VERSION BD269252.1 GI:33079020  
KEYWORDS JP 2002534962-A/13.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Lo, K.M., Zhang, J. and Gillies, S.D.  
TITLE Expression and transport of antibiotic protein as FC-fused protein  
JOURNAL Patent: JP 2002534962-A 13 22-OCT-2002;  
LEXIGEN PHARMACEUTICALS CORP  
COMMENT OS Artificial Sequence  
PN JP 2002534962-A/13  
PD 22-OCT-2002  
PF 07-JAN-2000 JP 2000592323  
PR 07-JAN-1999 US 60/115079  
PI KIN MING LO, JINYANG ZHANG, STEPHEN D GILLIES  
PC C12N15/09, A61K38/22, A61K48/00, A61P3/04, C07K14/47, PC C07K16/46,  
PC C07K19/00, C12N5/10, C12P21/00, C12N15/00, C12N5/00, A61K37/24 CC  
Description of Artificial Sequence: EcoRI/AflII linker-adaptor FH  
Key Location/Qualifiers  
FT source 1. .11  
/organism="Artificial Sequence".  
FEATURES  
source  
1. .11  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 851 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      620 AACAGAAAT 630
Db      1 AACAGAAAT 11

RESULT 14
CQ836020
LOCUS      CQ836020      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 1078 from Patent WO2004059001.
ACCESSION CQ836020
VERSION   CQ836020.1 GI:50835554
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 1078 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      968 ACAAGAAAAA 978
Db      1 ACAAGAAAAA 11

RESULT 15
CQ837255
LOCUS      CQ837255      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 2313 from Patent WO2004059001.
ACCESSION CQ837255
VERSION   CQ837255.1 GI:50836789
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin

```

```

JOURNAL      Patent: WO 2004059001-A 2313 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2109 CAATAAACTGA 2119
Db      1 CAATAAACTGA 11

RESULT 16
CQ837527/c
LOCUS      CQ837527      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 2585 from Patent WO2004059001.
ACCESSION CQ837527
VERSION   CQ837527.1 GI:50837061
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 2585 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2482 TCCAAAAACAA 2492
Db      1 TCCAAAAACAA 1

RESULT 17
CQ837558/c
LOCUS      CQ837558      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 2616 from Patent WO2004059001.
ACCESSION CQ837558
VERSION   CQ837558.1 GI:50837092
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 2616 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

```

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1230 TATTAGCCTC 1240  
 Db 11 TATTAGCCTC 1

RESULT 18  
 CQ837862/c  
 LOCUS CQ837862 11 bp DNA linear PAT 29-JUL-2004  
 DEFINITION Sequence 2920 from Patent WO2004059001.  
 ACCESSION CQ837862  
 VERSION CQ837862.1 GI:50837396  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.

REFERENCE 1  
 AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
 Conradt,M. and Hofmann,K.  
 TITLE Method for determining markers of human facial skin  
 JOURNAL Patent: WO 2004059001-A 2920 15-JUL-2004;  
 Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
 source Location/Qualifiers  
 1..11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1237 CCTCAAGTGC 1247  
 Db 11 CCTCAAGTGC 1

RESULT 19  
 CQ838131  
 LOCUS CQ838131 11 bp DNA linear PAT 29-JUL-2004  
 DEFINITION Sequence 3189 from Patent WO2004059001.  
 ACCESSION CQ838131  
 VERSION CQ838131.1 GI:50837665  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.

REFERENCE 1  
 AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
 Conradt,M. and Hofmann,K.  
 TITLE Method for determining markers of human facial skin  
 JOURNAL Patent: WO 2004059001-A 3189 15-JUL-2004;  
 Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
 source Location/Qualifiers  
 1..11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 AAAATACAGTG 1102  
 Db 11 AAAATACAGTG 1

Db 1 AAAATACAGTG 11

RESULT 20  
 AR364706  
 LOCUS AR364706 11 bp DNA linear PAT 03-SEP-2003  
 DEFINITION Sequence 1 from patent US 5422251.  
 ACCESSION AR364706  
 VERSION AR364706.1 GI:34427641  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 11)  
 AUTHORS Fresco,J.R.  
 TITLE Triple-stranded nucleic acids  
 JOURNAL Patent: US 5422251-A 1 06-JUN 1994,  
 Princeton University; Princeton, NJ,  
 EPX;

FEATURES  
 source Location/Qualifiers  
 1..11  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1576 GAAGAGAAGGA 1586  
 Db 1 GAAGAGAAGGA 11

RESULT 21  
 AX393107  
 LOCUS AX393107 11 bp DNA linear PAT 23-MAR-2002  
 DEFINITION Sequence 37 from Patent WO0210217.  
 ACCESSION AX393107  
 VERSION AX393107.1 GI:19701157  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.

REFERENCE 1  
 AUTHORS St Croix,B., Kinzler,K.W. and Vogelstein,B.  
 TITLE Endothelial cell expression patterns  
 JOURNAL Patent: WO 0210217-A 37 07-FEB-2002;  
 The Johns Hopkins University (US)

FEATURES  
 source Location/Qualifiers  
 1..11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 TGTTTAATACA 1007  
 Db 1 TGTTTAATACA 11

RESULT 22  
 AX393218  
 LOCUS AX393218 11 bp DNA linear PAT 23-MAR-2002  
 DEFINITION Sequence 148 from Patent WO0210217.  
 ACCESSION AX393218  
 VERSION AX393218.1 GI:19701268  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens (human)

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS St Croix,B., Kinzler,K.W. and Vogelstein,B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 148 07-FEB-2002;
The Johns Hopkins University (US)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 TGTGGAAGAA 90
Db 1 TGTGGAAGAA 11

RESULT 23
LOCUS AX394505
DEFINITION Sequence 50 from Patent WO0218638.
ACCESSION AX394505
VERSION AX394505.1 GI:21065643
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Ollisson,E.
TITLE Detection of cyp2d6 polymorphisms
JOURNAL Patent: WO 0218638-A 50 07-MAR-2002;
Gemini Genomics PLC (GB)
FEATURES
source
1. .11
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Query Match 0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1125 ACTTGAAGAA 1135
Db 1 ACTTGAAGAA 11

RESULT 24
LOCUS AX394512/c
DEFINITION Sequence 57 from Patent WO0218638.
ACCESSION AX394512
VERSION AX394512.1 GI:21065650
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Ollisson,E.
TITLE Detection of cyp2d6 polymorphisms
JOURNAL Patent: WO 0218638-A 57 07-MAR-2002;
Gemini Genomics PLC (GB)
FEATURES
source
1. .11
Location/Qualifiers
/organism="synthetic construct"

```

```

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Query Match 0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1125 ACTTGAAGAA 1135
Db 11 ACTTGAAGAA 1

RESULT 25
LOCUS AX421309
DEFINITION Sequence 57 from Patent WO0218641.
ACCESSION AX421309
VERSION AX421309.1 GI:21524717
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Ollisson,E.
TITLE Detection of cyp3a4 and cyp2c9 polymorphisms
JOURNAL Patent: WO 0218641-A 57 07-MAR-2002;
Gemini Genomics PLC (GB)
FEATURES
source
1. .11
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="5'-sequence to the polymorphic sites on the coding strand"

Query Match 0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 498 ATTTGAAGGA 508
Db 1 ATTTGAAGGA 11

RESULT 26
LOCUS AX421314/c
DEFINITION Sequence 62 from Patent WO0218641.
ACCESSION AX421314
VERSION AX421314.1 GI:21524722
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Ollisson,E.
TITLE Detection of cyp3a4 and cyp2c9 polymorphisms
JOURNAL Patent: WO 0218641-A 62 07-MAR-2002;
Gemini Genomics PLC (GB)
FEATURES
source
1. .11
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="5'-sequence to the polymorphic sites on the non-coding strand"

Query Match 0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 498 ATTTGAAGGA 508

```

```

Db      11 ATTTGAAGGA 1
|||||
RESULT 27
LOCUS   AX471107          11 bp  DNA      linear  PAT 12-AUG-2002
DEFINITION Sequence 684 from Patent WO02053773.
ACCESSION AX471107
VERSION   AX471107.1  GI:22206232
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominoidea; Homo.
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE    Method for determining skin stress or skin ageing in vitro
JOURNAL  Patent: WO 02053773-A 684 11-JUL-2002;
          HENKEL KGAA (DE)
FEATURES
source   Location/Qualifiers
          1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2109 CAATAAACTGA 2119
      11 bp  DNA      linear  PAT 09-AUG-2002
Db      1 CAATAAACTGA 11
|||||
RESULT 28
LOCUS   AX471484/c          11 bp  DNA      linear  PAT 09-AUG-2002
DEFINITION Sequence 1061 from Patent WO02053773.
ACCESSION AX471484
VERSION   AX471484.1  GI:22206609
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominoidea; Homo.
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE    Method for determining skin stress or skin ageing in vitro
JOURNAL  Patent: WO 02053773-A 1061 11-JUL-2002;
          HENKEL KGAA (DE)
FEATURES
source   Location/Qualifiers
          1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      660 TGTAAACTCA 670
      11 bp  DNA      linear  PAT 21-FEB-2003
Db      11 TGTAAACTCA 1
|||||
RESULT 29
LOCUS   AX623352          11 bp  DNA      linear  PAT 21-FEB-2003
DEFINITION Sequence 393 from Patent WO02053774.
ACCESSION AX623352

```

```

VERSION   AX623352.1  GI:28451293
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominoidea; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 393 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source   Location/Qualifiers
          1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1092 AAAATACAGTG 1102
      11 bp  DNA      linear  PAT 21-FEB-2003
Db      1 AAAATACAGTG 11
|||||
RESULT 30
LOCUS   AX623626/c          11 bp  DNA      linear  PAT 21-FEB-2003
DEFINITION Sequence 667 from Patent WO02053774.
ACCESSION AX623626
VERSION   AX623626.1  GI:28451567
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominoidea; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 667 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source   Location/Qualifiers
          1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      602 TCATTCATTTA 612
      11 bp  DNA      linear  PAT 21-FEB-2003
Db      11 TCATTCATTTA 1
|||||
RESULT 31
LOCUS   AX625016/c          11 bp  DNA      linear  PAT 21-FEB-2003
DEFINITION Sequence 2057 from Patent WO02053774.
ACCESSION AX625016
VERSION   AX625016.1  GI:28452957
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominoidea; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

```



TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 2057 11-JUL-2002; (DE)  
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)  
source Location/Qualifiers

1. .11

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 624 AGAAATATAA 634

Db 11 AGAAATATAA 1

RESULT 32  
AX625604/c  
LOCUS AX625604 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 2645 from Patent WO02053774.  
ACCESSION AX625604  
VERSION AX625604.1 GI:28453545  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1

Petersohn,D., Conradt,M. and Hofmann,K.  
Method for determining homeostasis of the skin  
Patent: WO 02053774-A 2645 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
Location/Qualifiers

1. .11

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 660 TGTAAACTCA 670

Db 11 TGTAAACTCA 1

RESULT 33  
AX625962  
LOCUS AX625962 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3003 from Patent WO02053774.  
ACCESSION AX625962  
VERSION AX625962.1 GI:28454000  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1

Petersohn,D., Conradt,M. and Hofmann,K.  
Method for determining homeostasis of the skin  
Patent: WO 02053774-A 3003 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
Location/Qualifiers

1. .11

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 TGGCAAAAAA 136

Db 1 TGGCAAAAAA 11

RESULT 34  
AX626328  
LOCUS AX626328 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3369 from Patent WO02053774.  
ACCESSION AX626328  
VERSION AX626328.1 GI:28454366  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1

Petersohn,D., Conradt,M. and Hofmann,K.  
Method for determining homeostasis of the skin  
Patent: WO 02053774-A 3369 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
Location/Qualifiers

1. .11

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 374 TAATTAATAA 384

Db 1 TAATTAATAA 11

RESULT 35  
AX626551  
LOCUS AX626551 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3592 from Patent WO02053774.  
ACCESSION AX626551  
VERSION AX626551.1 GI:28454589  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1

Petersohn,D., Conradt,M. and Hofmann,K.  
Method for determining homeostasis of the skin  
Patent: WO 02053774-A 3592 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
Location/Qualifiers

1. .11

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 371 AATTAATTA 381

Db 1 AATTAATTA 11

RESULT 36  
AX626551  
LOCUS AX626551 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3592 from Patent WO02053774.  
ACCESSION AX626551  
VERSION AX626551.1 GI:28454589  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1

Petersohn,D., Conradt,M. and Hofmann,K.  
Method for determining homeostasis of the skin  
Patent: WO 02053774-A 3592 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
Location/Qualifiers

1. .11

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 TGGCAAAAAA 136

Db 1 TGGCAAAAAA 11

RESULT 37  
AX626551  
LOCUS AX626551 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3592 from Patent WO02053774.  
ACCESSION AX626551  
VERSION AX626551.1 GI:28454589  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1

Petersohn,D., Conradt,M. and Hofmann,K.  
Method for determining homeostasis of the skin  
Patent: WO 02053774-A 3592 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
Location/Qualifiers

1. .11

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 36
AX626686/c
LOCUS      AX626686      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3727 from Patent WO02053774.
ACCESSION  AX626686
VERSION     AX626686.1 GI:28454724
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

REFERENCE
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3727 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      193 TATTCAAATA 203
Db      11 TATTCAAATA 1

RESULT 37
AX626781/c
LOCUS      AX626781      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3822 from Patent WO02053774.
ACCESSION  AX626781
VERSION     AX626781.1 GI:28454819
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

REFERENCE
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3822 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      758 TTGAAGAGAA 768
Db      11 TTGAAGAGAA 1

RESULT 38
AX627026
LOCUS      AX627026      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4067 from Patent WO02053774.
ACCESSION  AX627026
VERSION     AX627026.1 GI:28455064
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

REFERENCE
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4067 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1582 AAGGAAAGTGC 1592
Db      11 AAGGAAAGTGC 1

RESULT 39
AX627220/c
LOCUS      AX627220      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4261 from Patent WO02053774.
ACCESSION  AX627220
VERSION     AX627220.1 GI:28455258
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

REFERENCE
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4261 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2342 TGAAATACAAA 2352
Db      1 TGAAATACAAA 1

RESULT 40
AX627934/c
LOCUS      AX627934      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4975 from Patent WO02053774.
ACCESSION  AX627934
VERSION     AX627934.1 GI:28455972
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

REFERENCE
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4975 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1582 AAGGAAAGTGC 1592
Db      11 AAGGAAAGTGC 1

```

```

REFERENCE
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4067 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2342 TGAAATACAAA 2352
Db      1 TGAAATACAAA 1

RESULT 39
AX627220/c
LOCUS      AX627220      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4261 from Patent WO02053774.
ACCESSION  AX627220
VERSION     AX627220.1 GI:28455258
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

REFERENCE
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4261 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1582 AAGGAAAGTGC 1592
Db      11 AAGGAAAGTGC 1

RESULT 40
AX627934/c
LOCUS      AX627934      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4975 from Patent WO02053774.
ACCESSION  AX627934
VERSION     AX627934.1 GI:28455972
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

REFERENCE
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4975 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1582 AAGGAAAGTGC 1592
Db      11 AAGGAAAGTGC 1

```

```

source      1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 11; DB 1; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 GTCTTAATATT 473
Db 11 GTCTTAATATT 1

RESULT 41
AX628098/c
LOCUS AX628098 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5139 from Patent WO02053774.
ACCESSION AX628098
VERSION AX628098.1 GI:28456136
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5139 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1230 TATTAAGCCTC 1240
Db 11 TATTAAGCCTC 1

RESULT 42
AX628375/c
LOCUS AX628375 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5416 from Patent WO02053774.
ACCESSION AX628375
VERSION AX628375.1 GI:28456413
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5416 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1632 AATACATCAA 1642
Db 1 AATACATCAA 11

RESULT 45
AX628983/c
LOCUS AX628983 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6024 from Patent WO02053774.

```

---

```

QY 1237 CCTCAAGTGC 1247
Db 11 CCTCAAGTGC 1

RESULT 43
AX628695
LOCUS AX628695 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5736 from Patent WO02053774.
ACCESSION AX628695
VERSION AX628695.1 GI:28456733
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5736 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 TGTTTAATACA 1007
Db 1 TGTTTAATACA 11

RESULT 44
AX628920
LOCUS AX628920 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5961 from Patent WO02053774.
ACCESSION AX628920
VERSION AX628920.1 GI:28456958
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5961 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1632 AATACATCAA 1642
Db 1 AATACATCAA 11

RESULT 45
AX628983/c
LOCUS AX628983 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6024 from Patent WO02053774.

```

```

ACCESSION AX628983
VERSION AX628983.1 GI:28457021
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6024 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 667 CTCATCGATT 677
Db 11 CTCATCGATT 1

RESULT 46
LOCUS AX629085
DEFINITION Sequence 6126 from Patent WO02053774.
ACCESSION AX629085
VERSION AX629085.1 GI:28457123
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6126 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CAATAAACTGA 2119
Db 1 CAATAAACTGA 11

RESULT 47
LOCUS AX629850/c
DEFINITION Sequence 6891 from Patent WO02053774.
ACCESSION AX629850
VERSION AX629850.1 GI:28457888
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7318 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CAATAAACTGA 2119
Db 1 CAATAAACTGA 11

RESULT 48
LOCUS AX630086/c
DEFINITION Sequence 7127 from Patent WO02053774.
ACCESSION AX630086
VERSION AX630086.1 GI:28458124
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7127 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2484 CAAAAACAAAA 2494
Db 11 CAAAAACAAAA 1

RESULT 49
LOCUS AX630277
DEFINITION Sequence 7318 from Patent WO02053774.
ACCESSION AX630277
VERSION AX630277.1 GI:28458315
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7318 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

```

```

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6891 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2484 CAAAAACAAAA 2494
Db 11 CAAAAACAAAA 1

RESULT 48
LOCUS AX630086/c
DEFINITION Sequence 7127 from Patent WO02053774.
ACCESSION AX630086
VERSION AX630086.1 GI:28458124
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7127 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TACCAGTAGCA 354
Db 11 TACCAGTAGCA 1

RESULT 49
LOCUS AX630277
DEFINITION Sequence 7318 from Patent WO02053774.
ACCESSION AX630277
VERSION AX630277.1 GI:28458315
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7318 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

```

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 495 GCTATTGAAA 505  
 |||||  
 Db 1 GCTATTGAAA 11

RESULT 50  
 AX630773  
 LOCUS 11 bp DNA linear PAT 21-FEB-2003  
 DEFINITION Sequence 7814 from Patent WO02053774.  
 ACCESSION AX630773  
 VERSION AX630773.1 GI:28458813  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
 TITLE Method for determining homeostasis of the skin  
 JOURNAL Patent: WO 02053774-A 7814 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 FEATURES Location/Qualifiers  
 source 1..11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 AAAATACAGTG 1102  
 |||||  
 Db 1 AAAATACAGTG 11

RESULT 51  
 AX631047/C  
 LOCUS 11 bp DNA linear PAT 21-FEB-2003  
 DEFINITION Sequence 8088 from Patent WO02053774.  
 ACCESSION AX631047  
 VERSION AX631047.1 GI:28459089  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
 TITLE Method for determining homeostasis of the skin  
 JOURNAL Patent: WO 02053774-A 8088 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 FEATURES Location/Qualifiers  
 source 1..11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 602 TCATTCATTTA 612  
 |||||  
 Db 1 TCATTCATTTA 11

RESULT 52  
 AX632437/C  
 LOCUS 11 bp DNA linear PAT 21-FEB-2003  
 DEFINITION Sequence 9479 from Patent WO02053774.  
 ACCESSION AX632437  
 VERSION AX632437.1 GI:28468052  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
 TITLE Method for determining homeostasis of the skin  
 JOURNAL Patent: WO 02053774-A 9479 11-JUL-2002;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 FEATURES Location/Qualifiers  
 source 1..11  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 624 AGAAAATATAA 634  
 |||||  
 Db 11 AGAAAATATAA 1

RESULT 53  
 AX708109/C  
 LOCUS 11 bp DNA linear PAT 04-APR-2003  
 DEFINITION Sequence 45 from Patent WO03014387.  
 ACCESSION AX708109  
 VERSION AX708109.1 GI:29564060  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Wojnowski,L. and Presecan-Siedel,E.  
 TITLE Polymorphisms in the human gene for cypla2 and their use in  
 diagnostic and therapeutic applications  
 JOURNAL Patent: WO.03014387-A 45 20-FEB-2003;  
 Epidauros Biotechnologie AG (DE)  
 FEATURES Location/Qualifiers  
 source 1..11  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"

Query Match 0.4%; Score 11; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 TGTCGAAGCA 540  
 |||||  
 Db 11 TGTCGAAGCA 1

RESULT 54  
 AX1025/C  
 LOCUS 10 bp DNA linear PAT 25-NOV-1991  
 DEFINITION Nucleotide sequence 1 from patent number EP0245217.  
 ACCESSION AX1025  
 VERSION AX1025.1 GI:489244  
 KEYWORDS unidentified  
 SOURCE unidentified  
 ORGANISM unidentified

```

unclassified sequences.
1 (bases 1 to 10)
Grandi,G.
A nucleotide sequence capable of inducing high levels of
translation of a heterologous gene in Bacillus subtilis and
Escherichia coli
Patent: EP 0245217-A 1 11-NOV-1987;
ENIRICERCHE S.p.A
FEATURES
    source
        Location/Qualifiers
            1..10
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 AGAATTAATT 378
Db 10 AGAATTAATT 1

RESULT 55
AL1026
LOCUS 10 bp DNA linear PAT 25-NOV-1993
DEFINITION Nucleotide sequence 2 from patent number EP0245217.
ACCESSION AL1026
VERSION AL1026.1 GI:489245
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified sequences.
REFERENCE
1 (bases 1 to 10)
Grandi,G.
A nucleotide sequence capable of inducing high levels of
translation of a heterologous gene in Bacillus subtilis and
Escherichia coli
Patent: EP 0245217-A 2 11-NOV-1987;
ENIRICERCHE S.p.A
FEATURES
    source
        Location/Qualifiers
            1..10
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 AGAATTAATT 378
Db 1 AGAATTAATT 10

RESULT 56
AL17358/c
LOCUS 10 bp DNA linear PAT 14-APR-1994
DEFINITION terminator sequence.
ACCESSION AL17358
VERSION AL17358.1 GI:512197
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified sequences.
REFERENCE
1 (bases 1 to 10)
Eckes,P. and Schneider,R.
Virus resistant plants, method for their production
Patent: EP 0479180-A 19 08-APR-1992;
HOECHST AKTIENGESSELLSCHAFT
FEATURES
    source
        Location/Qualifiers
            1..10
                /organism="unidentified"

```

```

/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAACAAAA 75
Db 10 AAAAACAAAA 1

RESULT 57
AL17359
LOCUS 10 bp DNA linear PAT 14-APR-1994
DEFINITION terminator sequence.
ACCESSION AL17359
VERSION AL17359.1 GI:512198
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified sequences.
REFERENCE
1 (bases 1 to 10)
Eckes,P. and Schneider,R.
Virus resistant plants, method for their production
Patent: EP 0479180-A 20 08-APR-1992;
HOECHST AKTIENGESSELLSCHAFT
FEATURES
    source
        Location/Qualifiers
            1..10
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAACAAAA 75
Db 1 AAAAACAAAA 10

RESULT 58
AR053560/c
LOCUS 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 25 from patent US 5834248.
ACCESSION AR053560
VERSION AR053560.1 GI:5978422
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 10)
Faib,D.
Compositions and methods using rchd34, a gene upregulated by stress
stress
JOURNAL Patent: US 5834248-A 25 10-NOV-1998;
FEATURES
    source
        Location/Qualifiers
            1..10
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040
Db 10 CATCACCACC 1

RESULT 59
AR065887/c

```

```

LOCUS      AR065887      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 25 from patent US 5849578.
ACCESSION  AR065887
VERSION     AR065887.1 GI:5996103
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Falb,D.A.
TITLE       Compositions and methods for the treatment and diagnosis of
            cardiovascular disease using rchd528 as a target
JOURNAL     Patent: US 5849578-A 25 15-DEC-1998;
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2031 CATCACCACC 2040
Db      10 CATCACCACC 1

RESULT 60
LOCUS      AR080369/c      10 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION Sequence 25 from patent US 5968770.
ACCESSION  AR080369
VERSION     AR080369.1 GI:10007104
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Falb,D.A. and Gimbrone,M.A. Jr.
TITLE       Compositions and methods for the treatment and diagnosis of
            cardiovascular disease using rchd523 as a target
JOURNAL     Patent: US 5968770-A 25 19-OCT-1999;
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2031 CATCACCACC 2040
Db      10 CATCACCACC 1

RESULT 61
LOCUS      AR107804      10 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 50 from patent US 6110667.
ACCESSION  AR107804
VERSION     AR107804.1 GI:12823291
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE       Processes, apparatus and compositions for characterizing nucleotide
            sequences based on K-tuple analysis
JOURNAL     Patent: US 6110667-A 50 29-AUG-2000;
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2031 CATCACCACC 2040
Db      10 CATCACCACC 1

RESULT 62
LOCUS      AR148324/c      10 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 25 from patent US 6225084.
ACCESSION  AR148324
VERSION     AR148324.1 GI:15112414
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Falb,D.A. and Gimbrone,M.A. Jr.
TITLE       Compositions and methods for the treatment and diagnosis of
            cardiovascular disease using rchd534 as a target
JOURNAL     Patent: US 6225084-A 25 01-MAY-2001;
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      406 CTTTCATCATC 415
Db      1 CTTTCATCATC 10

RESULT 63
LOCUS      AR150611      10 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 30 from patent US 6228982.
ACCESSION  AR150611
VERSION     AR150611.1 GI:15115202
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Norden,B., Wittung,P., Buchardt,O., Egholm,M., Nielsen,P.E. and
            Berg,R.
TITLE       Double-stranded peptide nucleic acids
JOURNAL     Patent: US 6228982-A 30 08-MAY-2001;
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2031 CATCACCACC 2040
Db      10 CATCACCACC 1

RESULT 64
LOCUS      AX934711/c      10 bp      DNA      linear      PAT 05-JAN-2004
DEFINITION Sequence 25 from patent US 5849578.
ACCESSION  AX934711
VERSION     AX934711.1 GI:5996103
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE       Processes, apparatus and compositions for characterizing nucleotide
            sequences based on K-tuple analysis
JOURNAL     Patent: US 6110667-A 50 29-AUG-2000;
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      66 AAAAACAAAA 75
Db      1 AAAAACAAAA 10

RESULT 64
AX934711/c
LOCUS

```

```

/organism="unknown"
/mol_type="unassigned DNA"

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      406 CTTTCATCATC 415
Db      1 CTTTCATCATC 10

```

```

RESULT 62
LOCUS      AR148324/c      10 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 25 from patent US 6225084.
ACCESSION  AR148324
VERSION     AR148324.1 GI:15112414
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Falb,D.A. and Gimbrone,M.A. Jr.
TITLE       Compositions and methods for the treatment and diagnosis of
            cardiovascular disease using rchd534 as a target
JOURNAL     Patent: US 6225084-A 25 01-MAY-2001;
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2031 CATCACCACC 2040
Db      10 CATCACCACC 1

```

```

RESULT 63
LOCUS      AR150611      10 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 30 from patent US 6228982.
ACCESSION  AR150611
VERSION     AR150611.1 GI:15115202
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Norden,B., Wittung,P., Buchardt,O., Egholm,M., Nielsen,P.E. and
            Berg,R.
TITLE       Double-stranded peptide nucleic acids
JOURNAL     Patent: US 6228982-A 30 08-MAY-2001;
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      66 AAAAACAAAA 75
Db      1 AAAAACAAAA 10

RESULT 64
AX934711/c
LOCUS

```

```

DEFINITION Sequence 3 from Patent WO03089666.
ACCESSION AX934711
VERSION AX934711.1 GI:40641951
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Lee, J.S., Wettig, S.D. and Kraatz, H.B.
AUTHORS Methods and apparatus for molecular data storage, retrieval and
TITLE analysis
JOURNAL Patent: WO 03089666-A 3 30-OCT-2003;
UNIVERSITY OF SASKATCHEWAN TECHNOLOGIES INC. (CA)
FEATURES
source
1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Miss Match Sequence 1"

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 CATGAAGTCC 1531
Db 10 CATGAAGTCC 1

RESULT 65
BD016329
LOCUS 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Method of promoting plant transcription by using octopine T-DNA
promoter.
ACCESSION BD016329
VERSION BD016329.1 GI:22557467
KEYWORDS JP 2001190289-A/18.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE
1 (bases 1 to 10)
AUTHORS Barker, K.F. and Kemp, J.D.
TITLE Method of promoting plant transcription by using octopine T-DNA
JOURNAL Patent: JP 2001190289-A 18 17-JUL-2001;
MYCOGEN PLANT SCIENCE INC
COMMENT OS Agrobacterium tumefaciens
PN JP 2001190289-A/18
PD 17-JUL-2001
PF 22-NOV-2000 JP 2000356816
PR 18-NOV-1983 US 553786
PI RICHARD F BARKER, JOHN D KEMP
PC C12N15/09, A01H5/00, C12N5/10, C12N15/00, C12N5/00 CC Method of
promoting plant transcription by using octopine T- CC
DNA promoter
FH Key Location/Qualifiers
FT source 1. .10
/organism="Agrobacterium tumefaciens".
FEATURES
source
1. .10
/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/db_xref="taxon:358"

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 AATTAATAAAA 384
Db 1 AATTAATAAAA 10

```

```

RESULT 66
BD065093/c
LOCUS 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065093
VERSION BD065093.1 GI:22610696
KEYWORDS JP 2001509017-A/29.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE
1 (bases 1 to 10)
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Characterization of the yeast transcriptome
JOURNAL Patent: JP 2001509017-A 29 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/29
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU, BERT VOGELSTEIN, KENNETH W KINZLER PC
C12N15/10, C12N15/31, C07K14/395, C12Q1/68, C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source 1. .10
/organism="Saccharomyces cerevisiae (yeast)".
FEATURES
source
1. .10
/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db_xref="taxon:4932"

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 970 AAAGAAAAAC 979
Db 10 AAAGAAAAAC 1

```

```

RESULT 67
BD065167/c
LOCUS 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065167
VERSION BD065167.1 GI:22610770
KEYWORDS JP 2001509017-A/103.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE
1 (bases 1 to 10)
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Characterization of the yeast transcriptome
JOURNAL Patent: JP 2001509017-A 103 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/103
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU, BERT VOGELSTEIN, KENNETH W KINZLER PC
C12N15/10, C12N15/31, C07K14/395, C12Q1/68, C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source 1. .10
/organism="Saccharomyces cerevisiae (yeast)".
FEATURES
source
1. .10
/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"

```



```

/db_xref="taxon:4932"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1056 GTCAATATAC 1065
    |||||
Db 10 GTCAATATAC 1

RESULT 69
BD065321/c
LOCUS BD065321 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065321
VERSION BD065321.1 GI:22610924
KEYWORDS JP 2001509017-A/257.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 10)
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Characterization of the yeast transcriptome
JOURNAL Patent: JP 2001509017-A 257,10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/257
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source 1..10
/organism="Saccharomyces cerevisiae (yeast)"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 ATCAATAGAG 1405
    |||||
Db 10 ATCAATAGAG 1

RESULT 69
BD065358
LOCUS BD065358 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065358
VERSION BD065358.1 GI:22610961
KEYWORDS JP 2001509017-A/294.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 10)
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Characterization of the yeast transcriptome
JOURNAL Patent: JP 2001509017-A 294,10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/294
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source 1..10
/organism="Saccharomyces cerevisiae (yeast)"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 AAAAAAGAAA 388
    |||||
Db 1 AAAAAAGAAA 10

RESULT 70
BD073423/c
LOCUS BD073423 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Utilization of transcription factor Brn-3a.
ACCESSION BD073423
VERSION BD073423.1 GI:22619026
KEYWORDS JP 2001511344-A/5.
SOURCE Synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Damien,S.M. and Seymar,L.D.
TITLE Utilization of transcription factor Brn-3a
JOURNAL Patent: JP 2001511344-A 5,14-AUG-2001;
NEUROVEX LTD
COMMENT OS Artificial Sequence
PN JP 2001511344-A/5
PD 14-AUG-2001
PF 27-JUL-1998 JP 2000504246
PR 25-JUL-1997 GB 9715823,2,10-DEC-1997 US 08/988476 P1
SMITH MARTIN DAMIEN,LATCHMAN DAVID SEYMAR
PC C12N15/09,A61K38/17,A61K39/245,A61K48/00,A61P25/00,C07K14/47.
PC C12N7/00,
PC C12N15/00,A61K37/12
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..10
/organism="Artificial Sequence".

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 535 GAAGCAGAAG 544
    |||||
Db 10 GAAGCAGAAG 1

RESULT 71
BD161365
LOCUS BD161365 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161365
VERSION BD161365.1 GI:27867123
KEYWORDS JP 2002186482-A/187.
SOURCE Homo sapiens (human)

```

```

PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source 1..10
/organism="Saccharomyces cerevisiae (yeast)".

FEATURES
source
    Location/Qualifiers
    1..10
    /organism="Saccharomyces cerevisiae"
    /mol_type="genomic DNA"
    /db_xref="taxon:4932"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 AAAAAAGAAA 388
    |||||
Db 1 AAAAAAGAAA 10

RESULT 70
BD073423/c
LOCUS BD073423 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Utilization of transcription factor Brn-3a.
ACCESSION BD073423
VERSION BD073423.1 GI:22619026
KEYWORDS JP 2001511344-A/5.
SOURCE Synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Damien,S.M. and Seymar,L.D.
TITLE Utilization of transcription factor Brn-3a
JOURNAL Patent: JP 2001511344-A 5,14-AUG-2001;
NEUROVEX LTD
COMMENT OS Artificial Sequence
PN JP 2001511344-A/5
PD 14-AUG-2001
PF 27-JUL-1998 JP 2000504246
PR 25-JUL-1997 GB 9715823,2,10-DEC-1997 US 08/988476 P1
SMITH MARTIN DAMIEN,LATCHMAN DAVID SEYMAR
PC C12N15/09,A61K38/17,A61K39/245,A61K48/00,A61P25/00,C07K14/47.
PC C12N7/00,
PC C12N15/00,A61K37/12
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..10
/organism="Artificial Sequence".

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 535 GAAGCAGAAG 544
    |||||
Db 10 GAAGCAGAAG 1

RESULT 71
BD161365
LOCUS BD161365 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161365
VERSION BD161365.1 GI:27867123
KEYWORDS JP 2002186482-A/187.
SOURCE Homo sapiens (human)

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 187 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/187
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
Location/Qualifiers
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2295 ATGGTTAAAG 2304
|||||
DB 1 ATGGTTAAAG 10
RESULT 72
BD161384/c
LOCUS 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161384
VERSION BD161384.1 GI:27867142
KEYWORDS JP 2002186482-A/206.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 206 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/206
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
Location/Qualifiers
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2318 TCAGTTCATC 2327
|||||
DB 1 TCAGTTCATC 1
RESULT 73
BD166582/c
LOCUS 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166582
VERSION BD166582.1 GI:27872394
KEYWORDS JP 2002209591-A/127.
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 127 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/127
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50/C12P.1/02.
PC C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FEATURES
source
Location/Qualifiers
1..10
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1173 GAAATATAAA 1182
|||||
DB 10 GAAATATAAA 1
RESULT 74
BD166602/c
LOCUS 10 bp DNA linear PAT 17 JAN 2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166602
VERSION BD166602.1 GI:27872414
KEYWORDS JP 2002209591-A/147.
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 147 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/147
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50/C12P.1/02.
PC C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10

```

PR  
PR

```

19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'
FEATURES
source
Location/Qualifiers
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 819 TCTCTGAGT 828
|||||
DB 10 TCTCTGAGT 1

RESULT 78
BD238805/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Robert, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A/223.
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/223
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 819 TCTCTGAGT 828
|||||
DB 10 TCTCTGAGT 1

RESULT 79
BD238996/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Robert, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 414 15-OCT 2002.
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/414
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 ACCAGTAGCA 354
|||||
DB 10 ACCAGTAGCA 1

RESULT 79
BD238996/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Robert, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 414 15-OCT 2002.
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/414
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 ACCAGTAGCA 354
|||||
DB 10 ACCAGTAGCA 1

FEATURES
source
Location/Qualifiers
1..10
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

```

```

/db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1934 ATCAGCATCA 1943
Db 10 ATCAGCATCA 1

RESULT 80
BD239110
LOCUS      10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239110
VERSION     BD239110.1 GI:33048880
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 528 15-OCT-2002;
GENZYME    CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002534056-A/528
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089977,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
            C12N1/19,
            GOIN37/00,
            CC C12N15/00,C12N5/00,C12N15/00
            CC Preparation and use of superior vaccines
            FH Key Location/Qualifiers
            FT source 1..10
            FT /organism="Homo sapiens (human)"

FEATURES
    source
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 933 AGGAAAAGAT 942
Db 1 AGGAAAAGAT 10

RESULT 82
BD239343/c
LOCUS      10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239343
VERSION     BD239343.1 GI:33049113
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1132 AGAATATCAG 1141
Db 1 AGAATATCAG 10

RESULT 81

```

```

AUTHORS      Roberts,B.L. and Shankara,S.
TITLE        Preparation and use of superior vaccines
JOURNAL      Patent: JP 2002534056-A 761 15-OCT-2002;
COMMENT      GENZYME CORP
OS           Homo sapiens (human)
PN           JP 2002534056-A/761
PD           15-OCT-2002
PF           18-JUN-1999 JP 2000554749
PR           19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089597,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI          BRUCE L ROBERTS,SRINIVAS SHANKARA
PC          C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
          C12N1/19,
          C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
          G01N37/00,
          C12N15/00,C12N5/00,C12N15/00
CC          Preparation and use of superior vaccines
FH          Key Location/Qualifiers
FT          source 1..10
          Location/Qualifiers
          1..10
          /organism='Homo sapiens (human)'
          /organism='Homo sapiens'
          /organism="Homo sapiens"
          /mol_type="genomic DNA"
          /db_xref="taxon:9606"

FEATURES
source
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1837 GAAACCACT 1846
Db 10 GAAACCACT 1

LOCUS      BD239349 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239349
VERSION BD239349.1 GI:33049119
KEYWORDS JP 2002534056-A/767.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Roberts,B.L. and Shankara,S.
TITLE     Preparation and use of superior vaccines
JOURNAL   Patent: JP 2002534056-A 767 15-OCT-2002;
COMMENT   GENZYME CORP
OS        Homo sapiens (human)
PN        JP 2002534056-A/767
PD        15-OCT-2002
PF        18-JUN-1999 JP 2000554749
PR        19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089597,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI          BRUCE L ROBERTS,SRINIVAS SHANKARA
PC          C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
          C12N1/19,
          C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
          G01N37/00,
          C12N15/00,C12N5/00,C12N15/00
CC          Preparation and use of superior vaccines
FH          Key Location/Qualifiers
FT          source 1..10
          Location/Qualifiers
          1..10
          /organism="Homo sapiens"
          /mol_type="genomic DNA"
          /db_xref="taxon:9606"

FEATURES
source
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 803 GTGCTTGGC 812
Db 10 GTGCTTGGC 1

LOCUS      BD239511 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239511
VERSION BD239511.1 GI:33049281
KEYWORDS JP 2002534056-A/929.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Roberts,B.L. and Shankara,S.
TITLE     Preparation and use of superior vaccines
JOURNAL   Patent: JP 2002534056-A 929 15 OCT 2002;
COMMENT   GENZYME CORP
OS        Homo sapiens (human)
PN        JP 2002534056-A/929
PD        15-OCT-2002
PF        18-JUN-1999 JP 2000554749
PR        19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089597,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI          BRUCE L ROBERTS,SRINIVAS SHANKARA

```

```

PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
CC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
    source
    1..10
    Location/Qualifiers
    /organism='Homo sapiens'
    /mol_type='genomic DNA'
    /db_xref='taxon:9606'

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 ATTGATCAAT 429
    |||||
    1 ATTGATCAAT 10
Db

RESULT 85
BD239511/c
LOCUS
DEFINITION
ACCESSION BD239511
VERSION BD239511.1 GI:33049281
KEYWORDS JP 2002534056-A/929.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL PAT 17-JUL-2003
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/929
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
CC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
    source
    1..10
    Location/Qualifiers
    /organism='Homo sapiens'
    /mol_type='genomic DNA'
    /db_xref='taxon:9606'

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 ATTGATCAAT 429
    |||||
    1 ATTGATCAAT 10
Db

RESULT 86
BD239888
LOCUS
DEFINITION
ACCESSION BD239888
VERSION BD239888.1 GI:33049658
KEYWORDS JP 2002534056-A/1306.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL PAT 17-JUL-2003
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/1306
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
CC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
    source
    1..10
    Location/Qualifiers
    /organism='Homo sapiens'
    /mol_type='genomic DNA'
    /db_xref='taxon:9606'

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2295 ATGGTTAAAG 2304
    |||||
    1 ATGGTTAAAG 10
Db

```

```

/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 ATTGATCAAT 429
    |||||
    10 ATTGATCAAT 1
Db

RESULT 86
BD239888
LOCUS
DEFINITION
ACCESSION BD239888
VERSION BD239888.1 GI:33049658
KEYWORDS JP 2002534056-A/1306.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL PAT 17-JUL-2003
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/1306
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
CC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
    source
    1..10
    Location/Qualifiers
    /organism='Homo sapiens'
    /mol_type='genomic DNA'
    /db_xref='taxon:9606'

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2295 ATGGTTAAAG 2304
    |||||
    1 ATGGTTAAAG 10
Db

```

```

RESULT 87
BD239924/c
LOCUS      10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239924
VERSION     BD239924.1 GI:33049694
KEYWORDS   JP 2002534056-A/1342.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Roberts,B.L. and Shankara,S.
TITLE     Preparation and use of superior vaccines
JOURNAL   Patent: JP 2002534056-A 1342 15-OCT-2002;
GENZYME   CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002534056-A/1342
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090047 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N1/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
            C12N1/19,
            PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
            G01N37/00,
            CC Preparation and use of superior vaccines
            FH Key Location/Qualifiers
            FT source 1..10
            FT Location/Qualifiers
            FT /organism='Homo sapiens (human)'

FEATURES
            source
            1..10
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 TCAGAGAGAA 768
Db 10 TCAGAGAGAA 1

RESULT 88
BD239990
LOCUS      10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239990
VERSION     BD239990.1 GI:33049760
KEYWORDS   JP 2002534056-A/1408.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Roberts,B.L. and Shankara,S.
TITLE     Preparation and use of superior vaccines
JOURNAL   Patent: JP 2002534056-A 1552 15-OCT-2002;
GENZYME   CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002534056-A/1552
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090047 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N1/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
            C12N1/19,
            PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
            G01N37/00,
            CC Preparation and use of superior vaccines
            FH Key Location/Qualifiers
            FT source 1..10
            FT Location/Qualifiers
            FT /organism='Homo sapiens (human)'

FEATURES
            source
            1..10
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 TCAGAGAGAA 768
Db 10 TCAGAGAGAA 1

RESULT 89
BD240134/c
LOCUS      10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD240134
VERSION     BD240134.1 GI:33049904
KEYWORDS   JP 2002534056-A/1552.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Roberts,B.L. and Shankara,S.
TITLE     Preparation and use of superior vaccines
JOURNAL   Patent: JP 2002534056-A 1552 15-OCT-2002;
GENZYME   CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002534056-A/1552
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090079 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/089833 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090047 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N1/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
            C12N1/19,
            PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
            G01N37/00,
            CC Preparation and use of superior vaccines
            FH Key Location/Qualifiers
            FT source 1..10
            FT Location/Qualifiers
            FT /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1582 AAGGAAAGTG 1591
Db 1 AAGGAAAGTG 10

```





```

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 TTTAATACAT 1008
    |||||
Db 1 TTTAATACAT 10

RESULT 92
BD240412
LOCUS      10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240412
VERSION   BD240412.1 GI:33050182
KEYWORDS  JP 2002534056-A/1830.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominiidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Roberts,B.L. and Shankara,S.
TITLE     Preparation and use of superior vaccines
JOURNAL   Patent: JP 2002534056-A 1830 15-OCT-2002;
          GENZYME CORP
COMMENT    OS Homo sapiens (human)
          PN JP 2002534056-A/1830
          PD 15-OCT-2002
          PP 18-JUN-1999 JP 2000554749
          PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
          19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090043 PR
          19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090036 PR
          19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
          19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
          19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
          19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
          19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
          19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
          19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
          19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
          19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
          08-DEC-1998 US 60/111715
          PI BRUCE L ROBERTS,SRINIVAS SHANKARA
          PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
          C12N1/19
          PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
          G01N37/00,
          PC C12N15/00,C12N5/00,C12N15/00
          CC Preparation and use of superior vaccines
          FH Key Location/Qualifiers
          FT source 1..10
          FT /organism='Homo sapiens (human)'.
          FEATURES
            source
              1..10
                Location/Qualifiers
                  /organism="Homo sapiens"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 806 TCTTGGCATA 815
    |||||
Db 1 TCTTGGCATA 10

RESULT 94
BD240632/c
LOCUS      10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines
ACCESSION BD240632
VERSION   BD240632.1 GI:33050402
KEYWORDS  JP 2002534056-A/2050.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominiidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Roberts,B.L. and Shankara,S.
TITLE     Preparation and use of superior vaccines
JOURNAL   Patent: JP 2002534056-A 1866 15-OCT-2002;
          GENZYME CORP
COMMENT    OS Homo sapiens (human)
          PN JP 2002534056-A/1866
          PD 15-OCT-2002
          PP 18-JUN-1999 JP 2000554749
          PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
          19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090043 PR
          19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090036 PR
          19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
          19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
          19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
          19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
          19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
          19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
          19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
          19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
          19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
          08-DEC-1998 US 60/111715
          PI BRUCE L ROBERTS,SRINIVAS SHANKARA
          PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
          C12N1/19
          PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
          G01N37/00,
          PC C12N15/00,C12N5/00,C12N15/00
          CC Preparation and use of superior vaccines
          FH Key Location/Qualifiers
          FT source 1..10
          FT /organism='Homo sapiens (human)'.
          FEATURES
            source
              1..10
                Location/Qualifiers
                  /organism="Homo sapiens"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 831 GCTGTACCA 840
    |||||
Db 10 GCTGTACCA 1

RESULT 94
BD240632/c
LOCUS      10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines
ACCESSION BD240632
VERSION   BD240632.1 GI:33050402
KEYWORDS  JP 2002534056-A/2050.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominiidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Roberts,B.L. and Shankara,S.
TITLE     Preparation and use of superior vaccines
JOURNAL   Patent: JP 2002534056-A 1866 15-OCT-2002;
          GENZYME CORP
COMMENT    OS Homo sapiens (human)
          PN JP 2002534056-A/1866
          PD 15-OCT-2002
          PP 18-JUN-1999 JP 2000554749
          PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
          19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090043 PR
          19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090036 PR
          19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
          19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
          19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
          19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
          19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
          19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
          19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
          19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
          19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
          08-DEC-1998 US 60/111715
          PI BRUCE L ROBERTS,SRINIVAS SHANKARA
          PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
          C12N1/19
          PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
          G01N37/00,
          PC C12N15/00,C12N5/00,C12N15/00
          CC Preparation and use of superior vaccines
          FH Key Location/Qualifiers
          FT source 1..10
          FT /organism='Homo sapiens (human)'.
          FEATURES
            source
              1..10
                Location/Qualifiers
                  /organism="Homo sapiens"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 831 GCTGTACCA 840
    |||||
Db 10 GCTGTACCA 1

```



```

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 GAAGATGAAA 460
Db 10 GAAGATGAAA 1
|||||
10 bp DNA PAT 19-APR-2004

RESULT 98
LOCUS CQ793729/c
DEFINITION Sequence 25 from Patent EP1403372.
ACCESSION CQ793729
VERSION CQ793729.1 GI:46406676
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1
AUTHORS Falb,D.A. and Gimbrone,M.A.
TITLE Composition and methods for the treatment and diagnosis of
cardiovascular disease
JOURNAL Patent: EP 1403372-A 25 31-MAR-2004;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
1. .10
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040
Db 10 CATCACCACC 1
|||||
10 bp DNA PAT 05-JUL-2004

RESULT 99
LOCUS CQ828459
DEFINITION Sequence 177 from Patent WO2004053120.
ACCESSION CQ828459
VERSION CQ828459.1 GI:49731942
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.
TITLE Regulatory elements in the 5' region of the vrl gene
JOURNAL Patent: WO 2004053120-A 177 24-JUN-2004;
Gruenthal GmbH (DE)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="VSAP4 Q5"

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1212 AGCAGCTCCA 1221

```

---

```

Db 1 AGCAGCTCCA 10
|||||
10 bp DNA PAT 01-DEC-2004

RESULT 100
LOCUS CQ857812/c
DEFINITION Sequence 71 from Patent WO2004099445.
ACCESSION CQ857812
VERSION CQ857812.1 GI:51851937
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Figtree,G.A., Farral,M., Channon,K. and Watkins,H.
TITLE Diagnosis of an estrogen-sensitive disorder
JOURNAL Patent: WO 2004070059-A 71 19-AUG-2004;
ISIS INNOVATION LIMITED (GB)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2087 CGAAGACGCT 2096
Db 10 CGAAGACGCT 1
|||||
10 bp DNA PAT 01-DEC-2004

RESULT 101
LOCUS CQ944928
DEFINITION Sequence 75 from Patent WO2004099445.
ACCESSION CQ944928
VERSION CQ944928.1 GI:56294269
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kahl,G., Winter,P., Krueger,D., Reich,S., Matsumura,H. and
Terauchi,R.
TITLE Use of a type iii restriction enzyme to isolate identification tags
comprising more than 25 nucleotides
JOURNAL Patent: WO 2004099445-A 75 18-NOV-2004;
Iwate Prefectural Government (JP)
FEATURES
source
1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence:Synthetic DNA
(Tag Sequence)"

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2308 GGAAGAGCTA 2317
Db 1 GGAAGAGCTA 10
|||||
10 bp DNA PAT 01-DEC-2004

RESULT 102
LOCUS CQ983525/c

```

```

DEFINITION Sequence 20 from Patent WO2005003384.
ACCESSION C0983525
VERSION C0983525.1 GI:58191886
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bender, M. and Jacobsen, C. S.
TITLE Method for selective detection of a target nucleic acid
JOURNAL Patent: WO 2005003384-A 20 13-JAN-2005;
Danmarks og Gronlands Geologiske Undersogelse (DK)
FEATURES
source
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="probe based on primer BSRI541/20 (ribosomal
database project)"
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 506 GGATCACCTC 515
|||||
Db 10 GGATCACCTC 1
RESULT 103
CS073999/c
LOCUS 10 bp RNA linear PAT 05-MAY-2005
DEFINITION Sequence 13 from Patent WO2005033310.
ACCESSION CS073999
VERSION CS073999.1 GI:63090678
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Erdmann, V., Grueneweller, A., Kurreck, J., Christoph, T. and Gillen, C.
TITLE Pim-1 specific dsRNA compounds
JOURNAL Patent: WO 2005033310-A 13 14-APR-2005;
Gruenenthal GmbH (DE)
FEATURES
source
1..10
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1601 TCACCTTCTT 1610
|||||
Db 10 TCACCTTCTT 1
RESULT 104
E39644/c
LOCUS 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39644
VERSION E39644.1 GI:18621735
KEYWORDS JP 2000279181-A/177.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
Hashimoto, S., Matsushima, K. and Suzuki, T.
Genes with human dendritic cell expression
Patent: JP 2000279181-A 177 10-OCT-2000;
SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN JP 2000279181-A/177
PD 10-OCT-2000
PP 01-APR-1999 JP 1999095481
PR SHINICHI HASHIMOTO, KOJI MATSUSHIMA, TAKUJI SUZUKI
PC C12N15/09, C07K14/475, C07K16/18, C12N15/00
CC
FH Key 1..10 Location/Qualifiers
FT source /organism="Homo sapiens (human)"
FT
FEATURES
source
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 624 AGAAATATA 633
|||||
Db 10 AGAAATATA 1
RESULT 105
125490/c
LOCUS 10 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 10 from patent US 5552270.
ACCESSION 125490
VERSION 125490.1 GI:1605360
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Khrapko, K. R., Khorlin, A. A., Ivanov, I. B., Ershov, G. M., Lysov, J. P.,
Florentiev, V. L. and Mirzabekov, A. D.
TITLE Methods of DNA sequencing by hybridization based on optimizing
concentration of matrix-bound oligonucleotide and device for
carrying out same
JOURNAL Patent: US 5552270-A 10 03-SEP-1996;
FEATURES
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 327 TTTTGCTGCC 336
|||||
Db 10 TTTTGCTGCC 1
RESULT 106
AR200463
LOCUS 10 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6 from patent US 6357163.
ACCESSION AR200463
VERSION AR200463.1 GI:20251351
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)

```

AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.  
 TITLE Use of nucleic acid analogues in diagnostics and analytical procedures  
 JOURNAL Patent: US 6357163-A 6 19-MAR-2002;  
 FEATURES Location/Qualifiers  
 source 1..10  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAAACAAA 75  
 Db 1 AAAAAACAAA 10

RESULT 107  
 AR269009/c  
 LOCUS AR269009 10 bp DNA linear PAT 10-APR-2003  
 DEFINITION Sequence 57 from patent US 6500646.  
 ACCESSION AR269009  
 VERSION AR269009.1 GI:29699825  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Kuriyama,S. and Hasegawa,T.  
 TITLE Cell membrane-directed drugs  
 JOURNAL Patent: US 6500646-A 57 31-DEC-2002;  
 Mochida Pharmaceutical Co., Ltd.; Tokyo;  
 JPX;

FEATURES Location/Qualifiers  
 source 1..10  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 989 CTCACGAATG 998  
 Db 10 CTCACGAATG 1

RESULT 108  
 AR303296/c  
 LOCUS AR303296 10 bp DNA linear PAT 12-JUN-2003  
 DEFINITION Sequence 21 from patent US 6544736.  
 ACCESSION AR303296  
 VERSION AR303296.1 GI:31692072  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.  
 TITLE Method for synthesizing cDNA from mRNA sample  
 JOURNAL Patent: US 6544736-A 21 08-APR-2003;  
 Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo;  
 JPX;

FEATURES Location/Qualifiers  
 source 1..10  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 61;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 844 GCAGGAGAAA 853  
 Db 10 GCAGGAGAAA 1

RESULT 109  
 AR303312  
 LOCUS AR303312 10 bp DNA linear PAT 12-JUN-2003  
 DEFINITION Sequence 37 from patent US 6544736.  
 ACCESSION AR303312  
 VERSION AR303312.1 GI:31692088  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.  
 TITLE Method for synthesizing cDNA from mRNA sample  
 JOURNAL Patent: US 6544736-A 37 08-APR 2003;  
 Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo;  
 JPX;

FEATURES Location/Qualifiers  
 source 1..10  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 GGAAGAGCAG 151  
 Db 1 GGAAGAGCAG 10

RESULT 110  
 AR303351/c  
 LOCUS AR303351 10 bp DNA linear PAT 12-JUN-2003  
 DEFINITION Sequence 76 from patent US 6544736.  
 ACCESSION AR303351  
 VERSION AR303351.1 GI:31692127  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.  
 TITLE Method for synthesizing cDNA from mRNA sample  
 JOURNAL Patent: US 6544736-A 76 08-APR-2003;  
 Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo;  
 JPX;

FEATURES Location/Qualifiers  
 source 1..10  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 GGAAGAGCAG 151  
 Db 10 GGAAGAGCAG 1

RESULT 111  
 AR336845/c

LOCUS AR336845 10 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 20 from patent US 6566130.  
ACCESSION AR336845  
VERSION AR336845.1 GI:33722695  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.  
TITLE Androgen-regulated gene expressed in prostate tissue  
JOURNAL Patent: US 6566130-A 20 20-MAY-2003;  
Henry M. Jackson Foundation for the Advancement of Military  
Medicine; Rockville, MD  
FEATURES  
source  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 828 TGGGCTGTCA 837  
|||||  
Db 10 TGGGCTGTCA 1  
RESULT 112  
AR336861/c  
LOCUS AR336861 10 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 36 from patent US 6566130.  
ACCESSION AR336861  
VERSION AR336861.1 GI:33722711  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.  
TITLE Androgen-regulated gene expressed in prostate tissue  
JOURNAL Patent: US 6566130-A 36 20-MAY-2003;  
Henry M. Jackson Foundation for the Advancement of Military  
Medicine; Rockville, MD  
FEATURES  
source  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1837 GAAACCACT 1846  
|||||  
Db 10 GAAACCACT 1  
RESULT 113  
AR336881  
LOCUS AR336881 10 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 56 from patent US 6566130.  
ACCESSION AR336881  
VERSION AR336881.1 GI:33722731  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.  
TITLE Androgen-regulated gene expressed in prostate tissue  
JOURNAL Patent: US 6566130-A 56 20-MAY-2003;  
Henry M. Jackson Foundation for the Advancement of Military  
Medicine; Rockville, MD  
FEATURES  
source  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 150799/c  
LOCUS AR336881 10 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 30 from patent US 5643727.  
ACCESSION AR336881  
VERSION AR336881.1 GI:2472502  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Reed,J.C. and Harigai,M.  
TITLE BCL-2 gene inhibitory element binding factor  
JOURNAL Patent: US 5643727-A 30 01-JUL-1997;  
Henry M. Jackson Foundation for the Advancement of Military  
Medicine; Rockville, MD  
FEATURES  
source  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1404 AGCTAAGCTT 1413  
|||||  
Db 10 AGCTAAGCTT 1  
RESULT 115  
AR487041

Medicine; Rockville, MD  
Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1874 AAAGCCCAAGA 1883  
|||||  
Db 1 AAAGCCCAAGA 10  
RESULT 114  
AR371291  
LOCUS AR371291 10 bp DNA linear PAT 12 SEP 2003  
DEFINITION Sequence 28 from patent US 6395474.  
ACCESSION AR371291  
VERSION AR371291.1 GI:34608223  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.  
TITLE Peptide nucleic acids  
JOURNAL Patent: US 6395474-A 28 28-MAY-2002;  
Henry M. Jackson Foundation for the Advancement of Military  
Medicine; Rockville, MD  
FEATURES  
source  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 66 AAAAAACAAA 75  
|||||  
Db 1 AAAAAACAAA 10  
RESULT 115  
150799/c  
LOCUS AR371291 10 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 30 from patent US 5643727.  
ACCESSION AR371291  
VERSION AR371291.1 GI:2472502  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Reed,J.C. and Harigai,M.  
TITLE BCL-2 gene inhibitory element binding factor  
JOURNAL Patent: US 5643727-A 30 01-JUL-1997;  
Henry M. Jackson Foundation for the Advancement of Military  
Medicine; Rockville, MD  
FEATURES  
source  
1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1404 AGCTAAGCTT 1413  
|||||  
Db 10 AGCTAAGCTT 1  
RESULT 116  
AR487041

```

LOCUS       AR487041               10 bp      DNA          linear          PAT 14-MAY-2004
DEFINITION   Sequence 15 from patent US 6706477.
ACCESSION    AR487041
VERSION      AR487041.1 GI:47251988
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Zauderer,M.
TITLE        Methods for producing polynucleotide libraries in vaccinia virus
JOURNAL      Patent: US 6706477-A 15 16-MAR-2004;
              University of Rochester; Rochester, NY
FEATURES     source
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1449 TACCTATGGC 1458
Db      1 TACCTATGGC 10

RESULT 117
AR489512
LOCUS       AR489512               10 bp      DNA          linear          PAT 15-MAY-2004
DEFINITION   Sequence 28 from patent US 6710163.
ACCESSION    AR489512
VERSION      AR489512.1 GI:47256537
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE        Peptide nucleic acid synthons
JOURNAL      Patent: US 6710163-A 28 23-MAR-2004;
              Location/Qualifiers
FEATURES     source
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1449 TACCTATGGC 1458
Db      1 TACCTATGGC 10

RESULT 118
AR491123
LOCUS       AR491123               10 bp      DNA          linear          PAT 15-MAY-2004
DEFINITION   Sequence 28 from patent US 6713602.
ACCESSION    AR491123
VERSION      AR491123.1 GI:47258983
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Buchardt,O., Buchardt,D., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE        Synthetic procedures for peptide nucleic acids
JOURNAL      Patent: US 6713602-A 28 30-MAR-2004;
              Location/Qualifiers
FEATURES     source
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      66 AAAAAACAAAA 75
Db      1 AAAAAACAAAA 10

RESULT 119
AR585246
LOCUS       AR585246               10 bp      DNA          linear          PAT 15 DEC 2004
DEFINITION   Sequence 15 from patent US 6800442.
ACCESSION    AR585246
VERSION      AR585246.1 GI:56629045
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Zauderer,M.
TITLE        Methods of selecting polynucleotides encoding antigens
JOURNAL      Patent: US 6800442-A 15 05-OCT-2004;
              University of Rochester; Rochester, NY
FEATURES     source
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1449 TACCTATGGC 1458
Db      1 TACCTATGGC 10

RESULT 120
AR647992
LOCUS       AR647992               10 bp      mRNA          linear          PAT 20 APR 2004
DEFINITION   Sequence 15 from patent US 6872518.
ACCESSION    AR647992
VERSION      AR647992.1 GI:62787232
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Zauderer,M.
TITLE        Methods for selecting polynucleotides encoding T cell epitopes
JOURNAL      Patent: US 6872518-A 15 29-MAR-2005;
              University of Rochester; Rochester, NY
FEATURES     source
              1..10
              /organism="unknown"
              /mol_type="mRNA"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1449 TACCTATGGC 1458
Db      1 TACCTATGGC 10

RESULT 121
AR700611/c
LOCUS       AR700611/c             10 bp      DNA          linear          PAT 20 SEP 2004
DEFINITION   Sequence 83 from patent US 6921814.
ACCESSION    AR700611

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      66 AAAAAACAAAA 75
Db      1 AAAAAACAAAA 10

```

```

RESULT 119
AR585246
LOCUS       AR585246               10 bp      DNA          linear          PAT 15 DEC 2004
DEFINITION   Sequence 15 from patent US 6800442.
ACCESSION    AR585246
VERSION      AR585246.1 GI:56629045
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Zauderer,M.
TITLE        Methods of selecting polynucleotides encoding antigens
JOURNAL      Patent: US 6800442-A 15 05-OCT-2004;
              University of Rochester; Rochester, NY
FEATURES     source
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1449 TACCTATGGC 1458
Db      1 TACCTATGGC 10

```

```

RESULT 120
AR647992
LOCUS       AR647992               10 bp      mRNA          linear          PAT 20 APR 2004
DEFINITION   Sequence 15 from patent US 6872518.
ACCESSION    AR647992
VERSION      AR647992.1 GI:62787232
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Zauderer,M.
TITLE        Methods for selecting polynucleotides encoding T cell epitopes
JOURNAL      Patent: US 6872518-A 15 29-MAR-2005;
              University of Rochester; Rochester, NY
FEATURES     source
              1..10
              /organism="unknown"
              /mol_type="mRNA"

```

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1449 TACCTATGGC 1458
Db      1 TACCTATGGC 10

```

```

RESULT 121
AR700611/c
LOCUS       AR700611/c             10 bp      DNA          linear          PAT 20 SEP 2004
DEFINITION   Sequence 83 from patent US 6921814.
ACCESSION    AR700611

```



Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 ACCAGTAGCA 354  
|||||  
Db 10 ACCAGTAGCA 1

## RESULT 126

AX152772  
LOCUS AX152772 10 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 687 from Patent WO0138577.  
ACCESSION AX152772  
VERSION AX152772.1 GI:14534423  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
TITLE Human transcriptomes  
JOURNAL Patent: WO 0138577-A 687 31-MAY-2001;  
The Johns Hopkins University (US)

FEATURES  
source  
1..10  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 AAAGCCAAGA 1883  
|||||  
Db 1 AAAGCCAAGA 10

## RESULT 127

AX153073  
LOCUS AX153073 10 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 988 from Patent WO0138577.  
ACCESSION AX153073  
VERSION AX153073.1 GI:14534724  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
TITLE Human transcriptomes  
JOURNAL Patent: WO 0138577-A 988 31-MAY-2001;  
The Johns Hopkins University (US)

FEATURES  
source  
1..10  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 CAATAAAGTG 2118  
|||||  
Db 1 CAATAAAGTG 10

## RESULT 128

## AX153292/c

LOCUS AX153292 10 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 1207 from Patent WO0138577.  
ACCESSION AX153292  
VERSION AX153292.1 GI:14534943  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

## REFERENCE

AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
TITLE Human transcriptomes  
JOURNAL Patent: WO 0138577-A 1207 31-MAY-2001;  
The Johns Hopkins University (US)

FEATURES  
source  
1..10  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 819 TCTTCTGAGT 828  
|||||  
Db 10 TCTTCTGAGT 1

## RESULT 129

AX190773  
LOCUS AX190773 10 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 124 from Patent WO0142493.  
ACCESSION AX190773  
VERSION AX190773.1 GI:15144057  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM

REFERENCE  
AUTHORS Olek,A. and Piepenbrock,C.  
TITLE Method for the parallel detection of the degree of methylation of genomic dna  
JOURNAL Patent: WO 0142493-A 124 14-JUN-2001;  
Epigenomics AG (DE)

FEATURES  
source  
1..10  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32610"  
/note="Chemisch vorbehandelte Genom DNA"

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 AATTAATTAA 380  
|||||  
Db 1 AATTAATTAA 10

## RESULT 130

AX190774/c  
LOCUS AX190774 10 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 125 from Patent WO0142493.  
ACCESSION AX190774  
VERSION AX190774.1 GI:15144058  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM

REFERENCE  
AUTHORS Olek,A. and Piepenbrock,C.  
TITLE Method for the parallel detection of the degree of methylation of genomic dna  
JOURNAL Patent: WO 0142493-A 125 14-JUN-2001;  
Epigenomics AG (DE)

FEATURES  
source  
1..10  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32610"  
/note="Chemisch vorbehandelte Genom DNA"

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 AATTAATTAA 380  
|||||  
Db 1 AATTAATTAA 10

```

REFERENCE
AUTHORS      Olek, A. and Piepenbrock, C.
TITLE        Method for the parallel detection of the degree of methylation of
              genomic dna
JOURNAL      Epigenomics AG (DE)
FEATURES     source
              1. .10
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="chemisch vorbehandelte Genom-DNA"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      371 AATTAATTA 380
Db      10 AATTAATTA 1

RESULT 131
LOCUS      AX301608      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 322 from Patent WO0185941.
ACCESSION  AX301608
VERSION     AX301608.1 GI:17382691
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Versteeg, R. and Caron, H.N.
TITLE       Myc targets
JOURNAL     Patent: WO 0185941-A 322 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES    source
            1. .10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      188 ACATTATTC 197
Db      10 ACATTATTC 1

RESULT 132
LOCUS      AX301653      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 367 from Patent WO0185941.
ACCESSION  AX301653
VERSION     AX301653.1 GI:17382736
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Versteeg, R. and Caron, H.N.
TITLE       Myc targets
JOURNAL     Patent: WO 0185941-A 367 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES    source
            1. .10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      188 ACATTATTC 197
Db      10 ACATTATTC 1

RESULT 133
LOCUS      AX301653      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 399 from Patent WO0185941.
ACCESSION  AX301653
VERSION     AX301653.1 GI:17382768
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Versteeg, R. and Caron, H.N.
TITLE       Myc targets
JOURNAL     Patent: WO 0185941-A 399 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES    source
            1. .10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      487 GGAGGAGAGC 496
Db      1 GGAGGAGAGC 10

RESULT 134
LOCUS      AX301716      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 430 from Patent WO0185941.
ACCESSION  AX301716
VERSION     AX301716.1 GI:17382799
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Versteeg, R. and Caron, H.N.
TITLE       Myc targets
JOURNAL     Patent: WO 0185941-A 430 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES    source
            1. .10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      65 TAAAAACAAA 74

```

```

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2344 AAATACAAA 2353
Db      10 AAATACAAA 1

RESULT 133
LOCUS      AX301685      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 399 from Patent WO0185941.
ACCESSION  AX301685
VERSION     AX301685.1 GI:17382768
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Versteeg, R. and Caron, H.N.
TITLE       Myc targets
JOURNAL     Patent: WO 0185941-A 399 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES    source
            1. .10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      487 GGAGGAGAGC 496
Db      1 GGAGGAGAGC 10

RESULT 134
LOCUS      AX301716      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 430 from Patent WO0185941.
ACCESSION  AX301716
VERSION     AX301716.1 GI:17382799
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Versteeg, R. and Caron, H.N.
TITLE       Myc targets
JOURNAL     Patent: WO 0185941-A 430 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES    source
            1. .10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      65 TAAAAACAAA 74

```

Db 1 TAAAAACAAA 10  
|||||

## RESULT 135

AX510717  
LOCUS AX510717 10 bp DNA linear PAT 27-SEP-2002  
DEFINITION Sequence 5 from Patent WO0227027.  
ACCESSION AX510717  
VERSION AX510717.1 GI:23391954

## KEYWORDS

synthetic construct  
synthetic construct  
other sequences; artificial sequences.

## SOURCE

## ORGANISM

## REFERENCE

1 Zauderer, M.  
Method of screening for therapeutics for infectious diseases

TITLE Patent: WO 0227027-A 5 04-APR-2002;

JOURNAL THE UNIVERSITY OF ROCHESTER (US)

## FEATURES

source  
1..10  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer"

## Query Match

Best Local Similarity 100.0%; Score 10; DB 1; Length 10;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 TACCTATGGC 1458  
|||||

Db 1 TACCTATGGC 10

## RESULT 136

AX685131  
LOCUS AX685131 10 bp DNA linear PAT 29-MAR-2003  
DEFINITION Sequence 8 from Patent WO022889.  
ACCESSION AX685131  
VERSION AX685131.1 GI:29371482

## KEYWORDS

synthetic construct  
synthetic construct  
other sequences; artificial sequences.

## SOURCE

## ORGANISM

## REFERENCE

1 Lieber C.M., Woolley A.T., Hahn, J.I. and Housman, D.

AUTHORS Direct haplotyping using carbon nanotube probes

TITLE Patent: WO 022889-A 8 21-MAR-2002;

JOURNAL PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US) ; Massachusetts

## FEATURES

source  
1..10  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic PNA label"

## Query Match

Best Local Similarity 100.0%; Score 10; DB 1; Length 10;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2505 CTTGCCTCCA 2514  
|||||

Db 1 CTTGCCTCCA 10

## RESULT 137

AX685134/c  
LOCUS AX685134 10 bp DNA linear PAT 29-MAR-2003  
DEFINITION Sequence 11 from Patent WO022889.  
ACCESSION AX685134  
VERSION AX685134.1 GI:29371485

## KEYWORDS

synthetic construct  
synthetic construct  
other sequences; artificial sequences.

## SOURCE

## ORGANISM

## REFERENCE

1 Lieber, C.M., Woolley, A.T., Hahn, J.I. and Housman, D.

AUTHORS Direct haplotyping using carbon nanotube probes

TITLE Patent: WO 022889-A 11 21-MAR-2002;

JOURNAL PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US) ; Massachusetts

## FEATURES

source  
1..10  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic PNA label"

## Query Match

Best Local Similarity 100.0%; Score 10; DB 1; Length 10;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2505 CTTGCCTCCA 2514  
|||||

Db 10 CTTGCCTCCA 1

Search completed: January 17, 2007, 09:08:11

Job time : 3 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 17, 2007, 09:09:27 ; Search time 1 Seconds  
(without alignments)  
2.180 Million cell updates/sec

Title: US-10-528-631-1  
Perfect score: 2517  
Sequence: 1 gaattagagtgacgtga.....gaacgacttgcctccagta 2517

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 43 seqs, 433 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 43 summaries

Database : issdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12	0.5	12	1	US-10-101-433A-36
C 2	11	0.4	11	1	5422251-1
C 3	10	0.4	10	1	US-07-949-541A-10
C 4	10	0.4	10	1	US-08-235-503B-24
C 5	10	0.4	10	1	US-08-390-858B-30
C 6	10	0.4	10	1	US-08-440-787A-95
C 7	10	0.4	10	1	US-08-480-994-25
C 8	10	0.4	10	1	US-08-616-844-25
C 9	10	0.4	10	1	US-08-599-554-25
C 10	10	0.4	10	1	US-08-485-573-25
C 11	10	0.4	10	1	US-08-388-353-403
C 12	10	0.4	10	1	US-08-388-353-613
C 13	10	0.4	10	1	US-08-388-353-732
C 14	10	0.4	10	1	US-08-388-353-733
C 15	10	0.4	10	1	US-08-488-551B-403
C 16	10	0.4	10	1	US-08-488-551B-613
C 17	10	0.4	10	1	US-08-488-551B-732
C 18	10	0.4	10	1	US-08-488-551B-733
C 19	10	0.4	10	1	US-08-944-868A-25
C 20	10	0.4	10	1	US-08-944-868A-25
C 21	10	0.4	10	1	US-08-508-761B-30
C 22	10	0.4	10	1	US-08-925-743-25
C 23	10	0.4	10	1	US-08-522-384-50
C 24	10	0.4	10	1	US-08-944-496-25
C 25	10	0.4	10	1	US-08-925-767-25
C 26	10	0.4	10	1	US-08-088-661F-30
C 27	10	0.4	10	1	US-08-150-156A-6
C 28	10	0.4	10	1	US-08-108-591B-28
C 29	10	0.4	10	1	US-09-331-793-57
C 30	10	0.4	10	1	US-09-508-753B-21
C 31	10	0.4	10	1	US-09-508-753B-37
C 32	10	0.4	10	1	US-09-508-753B-76
C 33	10	0.4	10	1	US-09-769-482-20

C 34 10 0.4 10 1 US-09-769-482-36 Sequence 16, Appl  
35 10 0.4 10 1 US-09-769-482-56 Sequence 56, Appl  
36 10 0.4 10 1 US-09-822-250A-15 Sequence 15, Appl  
37 10 0.4 10 1 US-08-468-719A-28 Sequence 28, Appl  
38 10 0.4 10 1 US-08-462-977B-28 Sequence 15, Appl  
39 10 0.4 10 1 US-10-034-350A-15 Sequence 15, Appl  
40 10 0.4 10 1 US-08-935-177-15 Sequence 83, Appl  
41 10 0.4 10 1 US-09-772-105-83 Sequence 35, Appl  
42 10 0.4 10 1 US-09-030-832-35 Sequence 24, Appl  
43 10 0.4 10 1 PCT-US95-05265-24

## ALIGNMENTS

RESULT 1  
US-10-101-433A-36/c  
; Sequence 36, Application US/10101433A  
; Patent No. 6855812  
; GENERAL INFORMATION:  
; APPLICANT: Hanscom, Sara  
; APPLICANT: Crespi, Charles  
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF  
; FILE REFERENCE: G00307/70019  
; CURRENT APPLICATION NUMBER: US/10/101,433A  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: US 60/277,095  
; PRIOR FILING DATE: 2001-03-19  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Macaca mulatta  
US-10-101-433A-36

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1440 AGCTGAAATAC 1451  
Db 12 AGCTGAAATAC 1

RESULT 2  
5422251-1  
; Patent No. 5422251  
; APPLICANT: FRESCO, JACQUES R.  
; TITLE OF INVENTION: TRIPLE-STRANDED NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 4  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/187,890  
; FILING DATE: 28-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 841,218  
; FILING DATE: 27-FEB-1992  
; APPLICATION NUMBER: 622,330  
; FILING DATE: 27-NOV-1990  
; APPLICATION NUMBER: 366,244  
; FILING DATE: 09-JUN-1989  
; APPLICATION NUMBER: 935,047  
; FILING DATE: 26-NOV-1986  
; SEQ ID NO:1:  
; LENGTH: 11  
5422251-1

Query Match 0.4%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1576 GAAGAGAAGGA 1586  
|||||||

Db 1 GAAGAGAGGA 11

RESULT 3  
US-07-949-541A-10/c  
; Sequence 10, Application US/07949541A  
; Patent No. 5552270  
; GENERAL INFORMATION:  
; APPLICANT: Khrapko, Konstantin R.  
; APPLICANT: Khorlin, Alexandr A.  
; APPLICANT: Ivanov, Igor B.  
; APPLICANT: Ershov, Gennady M.  
; APPLICANT: Lysov, Yuri P.  
; APPLICANT: Florentiev, Vladimir L.  
; APPLICANT: Mirzabekov, Andrei D.  
; TITLE OF INVENTION: Method for Determining a DNA Nucleotide  
; TITLE OF INVENTION: Sequence and a Device for Carrying Out Same  
; Patent No. 5552270  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ladag & Parity  
; STREET: 26 West 61st Street  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10023  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage  
; COMPUTER: IBM PC/XT/AT or compatibles  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/949,541A  
; FILING DATE: 09-No. 5552270-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/RU92/00052  
; FILING DATE: 18-Mar-1992  
; APPLICATION NUMBER: Russian Federation 4919321  
; FILING DATE: 18-Mar-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janet I. Cord  
; REGISTRATION NUMBER: 33,778  
; REFERENCE/DOCKET NUMBER: U-8999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 708-1800  
; TELEFAX: (212) 246-8959  
; TELEX: 233288  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: chemically synthesized  
; MOLECULE TYPE: deoxyribonucleotide  
; FEATURE: oligonucleotide was synthesized by phosphoramidite  
; FEATURE: method.  
; OTHER INFORMATION: The sequence is listed from 3' to 5' left  
; OTHER INFORMATION: to right and this is a part of SEQ ID NO:1.  
US-07-949-541A-10

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 327 TTTTGTGCGC 336  
Db 10 TTTTGTGCGC 1

RESULT 4  
US-08-235-503B-24/c  
; Sequence 24, Application US/08235503B

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 AGCAGATGCC 156  
Db 10 AGCAGATGCC 1

RESULT 5  
US-08-390-858B-30/c  
; Sequence 30, Application US/08390858B  
; Patent No. 5643727  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Harigai, Masayoshi  
; TITLE OF INVENTION: Bcl-2 Gene Inhibitory Element Binding  
; TITLE OF INVENTION: Factor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/390,858B

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 AGCAGATGCC 156  
Db 10 AGCAGATGCC 1

Patent No. 5563036  
; GENERAL INFORMATION:  
; APPLICANT: Peterson, Michael G  
; APPLICANT: Baichwal, Vijay R  
; APPLICANT: Strulovici, Berta  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,503B  
; FILING DATE: 29-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: A-59332/RAO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-235-503B-24

;; FILING DATE: 16-FEB-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Campbell, Cathryn A.  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-LJ 1366  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;; INFORMATION FOR SEQ ID NO: 30:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cdna  
;; US-08-390-858B-30

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1404 AGCTAAGCTT 1413  
Db 10 AGCTAAGCTT 1

RESULT 6  
US-08-440-787A-95/c  
; Sequence 95, Application US/08440787A  
; Patent No. 5770434  
; GENERAL INFORMATION:  
; APPLICANT: Huse, William D.  
; TITLE OF INVENTION: Soluble Peptides Having Constrained,  
; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making  
; NUMBER OF SEQUENCES: 174  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,787A  
; FILING DATE: 15-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/978,893  
; FILING DATE: 10-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-IX 1586  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 95:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-440-787A-95

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 470 TATTCGAATT 479  
Db 10 TATTCGAATT 1

RESULT 7  
US-08-480-994-25/c  
; Sequence 25, Application US/08480994  
; Patent No. 5834248  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,994  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/386,844  
; FILING DATE: 10-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; US-08-480-994-25

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2031 CATCACCACC 2040  
Db 10 CATCACCACC 1

RESULT 8  
US-08-616-844-25/c  
; Sequence 25, Application US/08616844  
; Patent No. 5849578  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

```

; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/616,844
; FILING DATE: 15-MAR-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/599,654
; FILING DATE: 09-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-053
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; US-08-616-844-25

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040
Db 10 CATCACCACC 1

RESULT 9
US-08-599-654-25/c
; Sequence 25, Application US/08599654
; Patent No. 5882925
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,654
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-041
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; US-08-599-654-25

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040
Db 10 CATCACCACC 1

RESULT 10
US-08-485-573-25/c
; Sequence 25, Application US/08485573
; Patent No. 5968770
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,573
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:

```



; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 25:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; HYPOTHETICAL: NO  
 ; US-08-485-573-25

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040  
 |||||  
 Db 10 CATCACCACC 1

RESULT 11  
 US-08-388-353-403/c  
 ; Sequence 403, Application US/08388353  
 ; Patent No. 6010895  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Deacon, Nicholas J.  
 ; APPLICANT: Learmont, Jennifer C.  
 ; APPLICANT: McPhee, Dale A.  
 ; APPLICANT: Crowe, Suzanne  
 ; APPLICANT: Cooper, David  
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
 ; NUMBER OF SEQUENCES: 800  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Scully, Scott, Murphy & Presser  
 ; STREET: 400 Garden City Plaza  
 ; CITY: Garden City  
 ; STATE: New York  
 ; COUNTRY: United States  
 ; ZIP: 11530  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/388,353  
 ; FILING DATE: 14-FEB-1995  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Digiglio, Frank S.  
 ; REGISTRATION NUMBER: 31,346  
 ; REFERENCE/DOCKET NUMBER: 9606  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (516) 742-4343  
 ; TELEFAX: (516) 742-4366  
 ; TELEX: 230 901 SANS UR  
 ; INFORMATION FOR SEQ ID NO: 403:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-388-353-403

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 CAGTGGATAT 224  
 |||||

Db 10 CAGTGGATAT 1

RESULT 12  
 US-08-388-353-613  
 ; Sequence 613, Application US/08388353  
 ; Patent No. 6010895  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Deacon, Nicholas J.  
 ; APPLICANT: Learmont, Jennifer C.  
 ; APPLICANT: McPhee, Dale A.  
 ; APPLICANT: Crowe, Suzanne  
 ; APPLICANT: Cooper, David  
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
 ; NUMBER OF SEQUENCES: 800  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Scully, Scott, Murphy & Presser  
 ; STREET: 400 Garden City Plaza  
 ; CITY: Garden City  
 ; STATE: New York  
 ; COUNTRY: United States  
 ; ZIP: 11530  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/388,353  
 ; FILING DATE: 14-FEB-1995  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Digiglio, Frank S.  
 ; REGISTRATION NUMBER: 31,346  
 ; REFERENCE/DOCKET NUMBER: 9606  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (516) 742-4343  
 ; TELEFAX: (516) 742-4366  
 ; TELEX: 230 901 SANS UR  
 ; INFORMATION FOR SEQ ID NO: 613:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-388-353-613

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GAACGTCTGA 737  
 |||||  
 Db 1 GAACGTCTGA 10

RESULT 13  
 US-08-388-353-732  
 ; Sequence 732, Application US/08388353  
 ; Patent No. 6010895  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Deacon, Nicholas J.  
 ; APPLICANT: Learmont, Jennifer C.  
 ; APPLICANT: McPhee, Dale A.  
 ; APPLICANT: Crowe, Suzanne  
 ; APPLICANT: Cooper, David  
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
 ; NUMBER OF SEQUENCES: 800  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Scully, Scott, Murphy & Presser  
 ; STREET: 400 Garden City Plaza  
 ; CITY: Garden City

```
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 11530
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/388,353
/ FILING DATE: 14-FEB-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Digiglio, Frank S.
/ REGISTRATION NUMBER: 31,346
/ REFERENCE/DOCKET NUMBER: 9606
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 742-4343
/ TELEFAX: (516) 742-4366
/ INFORMATION FOR SEQ ID NO: 732:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-388-353-732

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1232 TTAAGCCTCA 1241
Db 1 TTAAGCCTCA 10

RESULT 14
US-08-388-353-733
/ Sequence 733, Application US/08388353
/ Patent No. 6010895
/ GENERAL INFORMATION:
/ APPLICANT: Deacon, Nicholas J.
/ APPLICANT: Learmont, Jennifer C.
/ APPLICANT: McPhee, Dale A.
/ APPLICANT: Crowe, Suzanne
/ APPLICANT: Cooper, David
/ TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
/ NUMBER OF SEQUENCES: 800
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Scully, Scott, Murphy & Presser
/ STREET: 400 Garden City Plaza
/ CITY: Garden City
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 11530
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/388,353
/ FILING DATE: 14-FEB-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Digiglio, Frank S.
/ REGISTRATION NUMBER: 31,346
/ REFERENCE/DOCKET NUMBER: 9606
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 742-4343
/ TELEFAX: (516) 742-4366
```

```
/ TELEX: 230 901 SANS UR
/ INFORMATION FOR SEQ ID NO: 733:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-388-353-733
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1233 TAAGCCTCAA 1242
Db 1 TAAGCCTCAA 10
```

```
RESULT 15
US-08-488-551B-403/C
/ Sequence 403, Application US/08488551B
/ Patent No. 6015861
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas J. Deacon
/ APPLICANT: Dale A. McPhee
/ APPLICANT: David Cooper
/ TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV 1
/ NUMBER OF SEQUENCES: 841
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
/ STREET: 400 GARDEN CITY PLAZA
/ CITY: GARDEN CITY
/ STATE: NEW YORK
/ COUNTRY: U.S.A.
/ ZIP: 11530-0299
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,551B
/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PM3864 (AU)
/ FILING DATE: 14-FEB-1994
/ APPLICATION NUMBER: PM4002 (AU)
/ FILING DATE: 21-FEB-1994
/ APPLICATION NUMBER: PN0284 (AU)
/ FILING DATE: 23-DEC-1994
/ APPLICATION NUMBER: US 08/388,353
/ FILING DATE: 14-FEB-1995
/ APPLICATION NUMBER: PN3021/95
/ FILING DATE: 17-MAY-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: FRANK S. DIGIGLIO
/ REFERENCE/DOCKET NUMBER: 9606Z
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 742-4343
/ TELEFAX: (516) 742-4366
/ INFORMATION FOR SEQ ID NO: 403:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ US-08-488-551B-403
```

```
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 215 CAGTGGATAT 224  
 Db 10 CAGTGGATAT 1

## RESULT 16

US-08-488-551B-613  
 ; Sequence 613, Application US/08488551B  
 ; Patent No. 6015661  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nicholas J. Deacon  
 ; APPLICANT: Dale A. McPhee  
 ; APPLICANT: David Cooper  
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
 ; NUMBER OF SEQUENCES: 841  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
 ; STREET: 400 GARDEN CITY PLAZA  
 ; CITY: GARDEN CITY  
 ; STATE: NEW YORK  
 ; COUNTRY: U.S.A.  
 ; ZIP: 11530-0299  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/488,551B  
 ; FILING DATE: 07-JUN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PM3864 (AU)  
 ; FILING DATE: 14-FEB-1994  
 ; APPLICATION NUMBER: PM4002 (AU)  
 ; FILING DATE: 21-FEB-1994  
 ; APPLICATION NUMBER: PM0284 (AU)  
 ; FILING DATE: 23-DEC-1994  
 ; APPLICATION NUMBER: US 08/388,353  
 ; FILING DATE: 14-FEB-1995  
 ; APPLICATION NUMBER: PM3021/95  
 ; FILING DATE: 17-MAY-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: FRANK S. DIGIGLIO  
 ; REFERENCE/DOCKET NUMBER: 9606Z  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (516) 742-4343  
 ; TELEFAX: (516) 742-4366  
 ; INFORMATION FOR SEQ ID NO: 613:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; US-08-488-551B-613

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GAAGTGTGA 737  
 Db 1 GAAGTGTGA 10

## RESULT 17

US-08-488-551B-732  
 ; Sequence 732, Application US/08488551B  
 ; Patent No. 6015661  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nicholas J. Deacon  
 ; APPLICANT: Dale A. McPhee

; APPLICANT: David Cooper  
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
 ; NUMBER OF SEQUENCES: 841  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
 ; STREET: 400 GARDEN CITY PLAZA  
 ; CITY: GARDEN CITY  
 ; STATE: NEW YORK  
 ; COUNTRY: U.S.A.  
 ; ZIP: 11530-0299  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/488,551B  
 ; FILING DATE: 07-JUN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PM3864 (AU)  
 ; FILING DATE: 14-FEB-1994  
 ; APPLICATION NUMBER: PM4002 (AU)  
 ; FILING DATE: 21-FEB-1994  
 ; APPLICATION NUMBER: PM0284 (AU)  
 ; FILING DATE: 23-DEC-1994  
 ; APPLICATION NUMBER: US 08/388,353  
 ; FILING DATE: 14-FEB-1995  
 ; APPLICATION NUMBER: PM3021/95  
 ; FILING DATE: 17-MAY-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: FRANK S. DIGIGLIO  
 ; REFERENCE/DOCKET NUMBER: 9606Z  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (516) 742-4343  
 ; TELEFAX: (516) 742-4366  
 ; INFORMATION FOR SEQ ID NO: 732:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; US-08-488-551B-732

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1232 TTAAGCCTCA 1241  
 Db 1 TTAAGCCTCA 10

## RESULT 18

US-08-488-551B-733  
 ; Sequence 733, Application US/08488551B  
 ; Patent No. 6015661  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nicholas J. Deacon  
 ; APPLICANT: Dale A. McPhee  
 ; APPLICANT: David Cooper  
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
 ; NUMBER OF SEQUENCES: 841  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
 ; STREET: 400 GARDEN CITY PLAZA  
 ; CITY: GARDEN CITY  
 ; STATE: NEW YORK  
 ; COUNTRY: U.S.A.  
 ; ZIP: 11530-0299  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,551B  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PM3864 (AU)  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: PM4002 (AU)  
FILING DATE: 21-FEB-1994  
APPLICATION NUMBER: PM0284 (AU)  
FILING DATE: 23-DEC-1994  
APPLICATION NUMBER: US 08/386,353  
FILING DATE: 14-FEB-1995  
APPLICATION NUMBER: PM3021/95  
FILING DATE: 17-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: FRANK S. DIGIGLIO  
REFERENCE/DOCKET NUMBER: 9606Z  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
INFORMATION FOR SEQ ID NO: 733:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-488-551B-733

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1233 TAAGCCTCAA 1242  
DB 1 TAAGCCTCAA 10

RESULT 19  
US-08-944-868A-25/c  
Sequence 25, Application US/08944868A  
Patent No. 6018025  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,868A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,654  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A

REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-041  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic oligonucleotide"  
HYPOTHETICAL: NO  
US-08-944-868A-25

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040  
DB 10 CATCACCACC 1

RESULT 20  
US-08-944-423A-25/c  
Sequence 25, Application US/08944423A  
Patent No. 6020463  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,423A  
FILING DATE: 06-OCT-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: JUN-07-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

; TOPOLOGY: linear  
 ; MOLECULE TYPE: other nucleic acid  
 ; DESCRIPTION: /desc = "synthetic oligonucleotide"  
 ; HYPOTHETICAL: NO  
 ; US-08-944-423A-25

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040  
 Db 10 CATCACCACC 1

RESULT 21  
 US-08-508-761B-30  
 ; Sequence 30, Application US/08508761B  
 ; Patent No. 6027920  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Joliff, Gwennael  
 ; APPLICANT: Guyonvarch, Arnel  
 ; APPLICANT: Purification, Relano  
 ; APPLICANT: Duchiron, Francis  
 ; APPLICANT: Renaud, Michel  
 ; TITLE OF INVENTION: System for Protein Expression and  
 ; TITLE OF INVENTION: Secretion Especially in Corynebacteria  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC  
 ; STREET: 400 Seventh St. N.W.  
 ; CITY: Washington D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20004

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/508,761B  
 ; FILING DATE: 31-JUL-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 91/09652  
 ; FILING DATE: 29-JUL-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 91/09870  
 ; FILING DATE: 02-AUG-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Player, William E.  
 ; REGISTRATION NUMBER: 31,409  
 ; REFERENCE/DOCKET NUMBER: P58525NA  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 638-6666  
 ; TELEFAX: (202) 393-5350

; INFORMATION FOR SEQ ID NO: 30:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORGANISM: synthetic  
 ; US-08-508-761B-30

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1579 GAGNAGGAAA 1588

Db 1 GAGAAGGAAA 10  
 |||||

RESULT 22  
 US-08-925-743-25/c  
 ; Sequence 25, Application US/08925743  
 ; Patent No. 6054558  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FALB, DEAN A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
 ; NUMBER OF SEQUENCES: 38  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036-2711

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/925,743  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/485,573  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7853-032  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864  
 ; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 25:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; HYPOTHETICAL: NO  
 ; US-08-925-743-25

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040  
 Db 10 CATCACCACC 1

RESULT 23  
 US-08-522-384-50  
 ; Sequence 50, Application US/08522384  
 ; Patent No. 6110667  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LOPEZ-NIETO, CARLOS E  
 ; APPLICANT: NIGAM, SANJAY KUMAR  
 ; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR  
 ; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES  
 ; FILE REFERENCE: 2458-4029  
 ; CURRENT APPLICATION NUMBER: US/08/522,384  
 ; CURRENT FILING DATE: 1996-11-15  
 ; NUMBER OF SEQ ID NOS: 122  
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 50  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Primer  
US-08-522-384-50

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 CTTTCATC 415  
Db 1 CTTTCATC 10

RESULT 24  
US-08-944-496-25/c  
; Sequence 25, Application US/08944496  
; Patent No. 6124433  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/944,496  
; FILING DATE: 06-OCT-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/599,654  
; FILING DATE: 09-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/386,844  
; FILING DATE: 10-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CORUZZI, LAURA A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-104  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic oligonucleotide"  
; HYPOTHETICAL: NO  
US-08-944-496-25

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040  
Db 10 CATCACCACC 1

RESULT 25  
US-08-925-767-25/c  
; Sequence 25, Application US/08925767  
; Patent No. 6225084  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/925,767  
; FILING DATE: 09-SEPT-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/386,844  
; FILING DATE: 10-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-097  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
US-08-925-767-25

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040  
Db 10 CATCACCACC 1

RESULT 26  
US-08-088-661F-30  
; Sequence 30, Application US/08088661F  
; Patent No. 6228982  
; GENERAL INFORMATION:  
; APPLICANT: No. 6228982den, Bengel  
; APPLICANT: Wittung, Pernilla  
; APPLICANT: Buchardt, Ole  
; APPLICANT: Egholm, Michael

; APPLICANT: Nielsen, Peter B.  
; APPLICANT: Berg, Rolf  
; TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids  
; FILE REFERENCE: IS11108  
; CURRENT APPLICATION NUMBER: US/08/088,661P  
; CURRENT FILING DATE: 1993-07-02  
; PRIOR APPLICATION NUMBER: 08/054,363  
; PRIOR FILING DATE: 1993-04-26  
; PRIOR APPLICATION NUMBER: PCT/EP92/01219  
; PRIOR FILING DATE: 1992-05-19  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence  
US-08-088-661P-30

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAACAAAA 75  
Db 1 AAAAACAAAA 10

RESULT 27  
US-08-150-156A-6  
; Sequence 6, Application US/08150156A  
; Patent No. 6357163  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN  
; TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES  
; NUMBER OF SEQUENCES: 40  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA: US/08/150,156A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 0986/91  
; FILING DATE: 24-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 0987/91  
; FILING DATE: 24-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 0510/92  
; FILING DATE: 15-APR-1992  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; PUBLICATION INFORMATION:  
; DOCUMENT NUMBER: WO PCT/EP92/01220  
; FILING DATE: 22-MAY-1992  
US-08-150-156A-6

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAACAAAA 75  
Db 1 AAAAACAAAA 10

RESULT 28  
US-08-108-591B-28  
; Sequence 28, Application US/08108591B  
; Patent No. 6395474  
; GENERAL INFORMATION:  
; APPLICANT: Buchardt, Ole  
; APPLICANT: Egholm, Michael  
; APPLICANT: Nielsen, Peter Eigil  
; APPLICANT: Berg, Rolf Henrik  
; TITLE OF INVENTION: Peptide Nucleic Acids  
; FILE REFERENCE: IS10540  
; CURRENT APPLICATION NUMBER: US/08/108,591B  
; CURRENT FILING DATE: 2001-08-13  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: No. 6395474el Sequence  
US-08-108-591B-28

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAACAAAA 75  
Db 1 AAAAACAAAA 10

RESULT 29  
US-09-331-793-57/c  
; Sequence 57, Application US/09331793  
; Patent No. 6500646  
; GENERAL INFORMATION:  
; APPLICANT: KURIYAMA, Shinichi  
; APPLICANT: HASEGAWA, Takaishi  
; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS  
; FILE REFERENCE: 1110-253P  
; CURRENT APPLICATION NUMBER: US/09/331,793  
; CURRENT FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 57  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Synthetic DNA Primers  
US-09-331-793-57

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 989 CTCACGAATG 998  
Db 10 CTCACGAATG 1

RESULT 30  
US-09-508-753B-21/c  
; Sequence 21, Application US/09508753B  
; Patent No. 6544736  
; GENERAL INFORMATION:  
; APPLICANT: Akira SHIMAMOTO  
; APPLICANT: Yasuhiro FURUICHI  
; APPLICANT: Yuko SHIBATA

```

; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-21

```

```

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      844 GCAGGAGAAA 853
Db      10 GCAGGAGAAA 1

```

```

RESULT 31
US-09-508-753B-37
; Sequence 37, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 37
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-37

```

```

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      142 GGAAGAAGCAG 151
Db      1 GGAAGAAGCAG 10

```

```

RESULT 32
US-09-508-753B-76/c
; Sequence 76, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI

```

```

; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 76
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-76

```

```

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      142 GGAAGAAGCAG 151
Db      10 GGAAGAAGCAG 1

```

```

RESULT 33
US-09-769-482-20/c
; Sequence 20, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: POYNUCLEOTIDE ARRAY
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-20

```

```

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      828 TGGGCTGTCTCA 837
Db      10 TGGGCTGTCTCA 1

```

```

RESULT 34
US-09-769-482-36/c
; Sequence 36, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY

```



```
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-36

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1837 GAAACCAAGCT 1846
Db      |||||
        10 GAAACCAAGCT 1

RESULT 35
US-09-769-482-56
; Sequence 56, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POLYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-56

Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 AAAGCCAAGA 1883
Db      |||||
        1 AAAGCCAAGA 10

RESULT 36
US-09-822-250A-15
; Sequence 15, Application US/09822250A
; Patent No. 6708477
; GENERAL INFORMATION:
; APPLICANT: Zaudeter, Maurice
; TITLE OF INVENTION: Methods for Producing Polynucleotide Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
```

```
; CURRENT APPLICATION NUMBER: US/09/822,250A
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MR_8 primer
US-09-822-250A-15
```

```
Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1449 TACCTATGGC 1458
Db      |||||
        1 TACCTATGGC 10
```

```
RESULT 37
US-08-468-719A-28
; Sequence 28, Application US/08468719A
; Patent No. 6710163
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS SYNTHONS
; FILE REFERENCE: ISPS-1999
; CURRENT APPLICATION NUMBER: US/08/468,719A
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/108,591
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-08-468-719A-28
```

```
Query Match          0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 66 AAAACACAAA 75
Db      |||||
        1 AAAACACAAA 10
```

```
RESULT 38
US-08-462-977B-28
; Sequence 28, Application US/08462977B
; Patent No. 6713602
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS-1993
; CURRENT APPLICATION NUMBER: US/08/462,977B
; CURRENT FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 43
```

SOFTWARE: PatentIn version 3.0  
SEQ ID NO 28  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: No. 6713602el Sequence  
US-08-462-977B-28

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAAACAAA 75  
DB 1 AAAAAACAAA 10

RESULT 39  
US-10-034-350A-15  
Sequence 15, Application US/10034350A  
Patent No. 6800442  
GENERAL INFORMATION:  
APPLICANT: Zauderer, Maurice  
TITLE OF INVENTION: Methods of Selecting Polynucleotides Encoding Antigens  
FILE REFERENCE: 1821.0010002  
CURRENT APPLICATION NUMBER: US/10/034,350A  
CURRENT FILING DATE: 2002-01-03  
PRIOR APPLICATION NUMBER: US 08/935,377  
PRIOR FILING DATE: 1997-09-22  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 15  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-10-034-350A-15

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 TACCTATGCC 1458  
DB 1 TACCTATGCC 10

RESULT 40  
US-08-935-377-15  
Sequence 15, Application US/08935377  
Patent No. 6872518  
GENERAL INFORMATION:  
APPLICANT: Zauderer, Maurice  
TITLE OF INVENTION: T Cells Specific for Target Antigens and  
TITLE OF INVENTION: Vaccines Based Thereon  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: D. C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/935,377

FILING DATE: 22-SEP-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-935-377-15

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 TACCTATGCC 1458  
DB 1 TACCTATGCC 10

RESULT 41  
US-09-772-105-83/c  
Sequence 83, Application US/09772105  
Patent No. 6921814  
GENERAL INFORMATION:  
APPLICANT: Ozelius, Laurie J.  
APPLICANT: Breakefield, Xandra O.  
TITLE OF INVENTION: TORSIN, TORSIN-RELATED GENES, AND  
TITLE OF INVENTION: METHODS OF DETECTING NEURONAL DISEASES  
FILE REFERENCE: 0838.1001009  
CURRENT APPLICATION NUMBER: US/09/772,105  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: US 09/218,363  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: US 09/099,454  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: US 60/050,244  
PRIOR FILING DATE: 1997-06-19  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 83  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Exon/intron of TORB  
US-09-772-105-83

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 CTGAGTTTGC 743  
DB 10 CTGAGTTTGC 1

RESULT 42  
US-09-030-832-35  
Sequence 35, Application US/09030812  
Patent No. 7029870  
GENERAL INFORMATION:  
APPLICANT: Hanna, Michael C.  
APPLICANT: Kirkness, Ewen F.  
TITLE OF INVENTION: GABA<sub>A</sub> Receptor Epsilon Subunit  
NUMBER OF SEQUENCES: 46

;;  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
;; STREET: 1100 New York Avenue, NW, Suite 600  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005-3934  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/030,832  
;; FILING DATE: Herewith  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/888,012  
;; FILING DATE: 03-JUL-1997  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Steffe, Eric K.  
;; REGISTRATION NUMBER: 36,688  
;; REFERENCE/DOCKET NUMBER: 1488.0950001/EKS/SGW  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEFAX: (202) 371-2540  
;; INFORMATION FOR SEQ ID NO: 35:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cdna  
;; US-09-030-832-35

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 506 GGATCACCTC 515  
|||  
Db 1 GGATCACCTC 10

RESULT 43  
PCT-US95-05265-24/c  
;; Sequence 24. Application PC/TUS9505265  
;; GENERAL INFORMATION:  
;; APPLICANT: TULARIK, INC.  
;; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY  
;; NUMBER OF SEQUENCES: 74  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
;; STREET: 4 Embarcadero Center, Suite 3400  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94111-4187  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US95/05265  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/235,503  
;; FILING DATE: 29-APR-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Osman, Richard A

;;  
;; REGISTRATION NUMBER: 36,627  
;; REFERENCE/DOCKET NUMBER: PP-59232-PC/RAO  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 781-1989  
;; TELEFAX: (415) 398-3249  
;; TELEX: 910 277299  
;; INFORMATION FOR SEQ ID NO: 24:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cdna  
;; PCT-US95-05265-24

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 AGCAGATGGC 156  
|||  
Db 10 AGCAGATGGC 1

Search completed: January 17, 2007, 09:09:28  
Job time : 1 secs

This Page Blank (uspto)

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 17, 2007, 09:07:00 ; Search time 0.001 Seconds  
(without alignments)  
115.782 Million cell updates/sec

Title: US-10-528-631-1  
Perfect score: 2517  
Sequence: 1 gaatttagagtgcagctga.....gaaacgacttgcctccagta 2517

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 23 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 2 summaries

Database : estdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	0.5	13	1	AJ594173
2	10	0.4	10	1	AJ587884

#### ALIGNMENTS

**RESULT 1**  
AJ594173  
**LOCUS** Arabidopsis thaliana T-DNA flanking sequence, left border, clone 393H08, genomic survey sequence.  
**DEFINITION** AJ594173 13 bp DNA linear GSS 15-JAN-2004  
**ACCESSION** AJ594173  
**VERSION** AJ594173.1 GI:37943797  
**KEYWORDS** GSS; left border; T-DNA flanking sequence.  
**SOURCE** Arabidopsis thaliana (thale cress)  
**ORGANISM** Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

**REFERENCE**  
1 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)  
12446565

**AUTHORS** Balzerque, S.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

**COMMENT** PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

**FEATURES**  
Location/Qualifiers  
1..13  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="393H08"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Wassilewskija"  
misc\_feature 1..13  
/notes="T-DNA flanking sequence left border"

#### COMMENT

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

#### FEATURES

Location/Qualifiers  
1..13  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="393H08"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Wassilewskija"  
misc\_feature 1..13  
/notes="T-DNA flanking sequence left border"

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1371 TGCTGGTGAAGAT 1383  
|||||||  
Db 1 TGCTGGTGAAGAT 13

#### RESULT 2

AJ587884

**LOCUS** Arabidopsis thaliana T-DNA flanking sequence, left border, clone 336E10, genomic survey sequence.

**DEFINITION** AJ587884 10 bp DNA linear GSS 15-JAN-2004

**ACCESSION** AJ587884

**VERSION** AJ587884.1 GI:37937508

**KEYWORDS** GSS; left border; T-DNA flanking sequence.

**SOURCE** Arabidopsis thaliana (thale cress)

**ORGANISM** Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

#### REFERENCE

**AUTHORS** Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

#### TITLE

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)

12446565

**JOURNAL** PUBMED

**REFERENCE** 2 (bases 1 to 10)

Balzerque, S.

**TITLE** Direct Submission

**JOURNAL** Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

#### COMMENT

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

#### FEATURES

Location/Qualifiers

1..10

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

```

/db_xref="taxon:3702"
/clone="336E10"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
misc_feature 1..10
              /note="T-DNA flanking sequence
              left border"

Query Match
Best Local Similarity 0.4%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 AAATATTTT 330
   |||||
Db 1 AAATATTTT 10

```

Search completed: January 17, 2007, 09:07:01  
Job time : 1 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 17, 2007, 09:05:08 ; Search time 6 Seconds  
(without alignments)  
3.428 Million cell updates/sec

Title: US-10-528-631-1  
Perfect score: 2517  
Sequence: 1 gaatttagagtacgtga.....gaaagacttgctccagta 2517

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 387 seqs, 4086 residues

Total number of hits satisfying chosen parameters: 774

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 392 summaries

Database : ngsdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	0.5	12	1 AAN92501	DNA sequence encod
2	12	0.5	12	1 ABI118302	Oligonucleotide pr
3	12	0.5	12	1 ABH93849	Oligonucleotide pr
4	12	0.5	12	1 ABH93036	Oligonucleotide pr
5	12	0.5	12	1 ABH98700	Oligonucleotide pr
6	12	0.5	12	1 ABI02759	Oligonucleotide pr
7	12	0.5	12	1 ABH89860	Oligonucleotide pr
8	12	0.5	12	1 ABI47026	Oligonucleotide pr
9	12	0.5	12	1 ABI69350	Oligonucleotide pr
10	12	0.5	12	1 ABH86237	Oligonucleotide pr
11	12	0.5	12	1 ABI118972	Oligonucleotide pr
12	12	0.5	12	1 ABH90107	Oligonucleotide pr
13	12	0.5	12	1 ABI41148	Oligonucleotide pr
14	12	0.5	12	1 ABI76290	Oligonucleotide pr
15	12	0.5	12	1 ABI18995	Oligonucleotide pr
16	12	0.5	12	1 ABH71279	Oligonucleotide pr
17	12	0.5	12	1 ABI00878	Oligonucleotide pr
18	12	0.5	12	1 ABI26807	Oligonucleotide pr
19	12	0.5	12	1 ABI32572	Oligonucleotide pr
20	12	0.5	12	1 ABI67443	Oligonucleotide pr
21	12	0.5	12	1 ABI79368	Oligonucleotide pr
22	12	0.5	12	1 ABI05852	Oligonucleotide pr
23	12	0.5	12	1 ABI13911	Oligonucleotide pr
24	12	0.5	12	1 ABH89950	Oligonucleotide pr
25	12	0.5	12	1 ABI55519	Oligonucleotide pr
26	12	0.5	12	1 ABI65306	Oligonucleotide pr
27	12	0.5	12	1 ABH98644	Oligonucleotide pr
28	12	0.5	12	1 ABI27826	Oligonucleotide pr
29	12	0.5	12	1 ABI38730	Oligonucleotide pr
30	12	0.5	12	1 ABI48088	Oligonucleotide pr
31	12	0.5	12	1 ABH96978	Oligonucleotide pr
32	12	0.5	12	1 ABI02430	Oligonucleotide pr
33	12	0.5	12	1 ABI07725	Oligonucleotide pr

34	12	0.5	12	1 ABH87411	Oligonucleotide pr
35	12	0.5	12	1 ABI40919	Oligonucleotide pr
36	12	0.5	12	1 ABI44172	Oligonucleotide pr
37	12	0.5	12	1 ABI80293	Oligonucleotide pr
38	12	0.5	12	1 ABH68264	Oligonucleotide pr
39	12	0.5	12	1 ABH93996	Oligonucleotide pr
40	12	0.5	12	1 ABI19095	Oligonucleotide pr
41	12	0.5	12	1 ABI19660	Oligonucleotide pr
42	12	0.5	12	1 ABH71178	Oligonucleotide pr
43	12	0.5	12	1 ABI25898	Oligonucleotide pr
44	12	0.5	12	1 ABI37764	Oligonucleotide pr
45	12	0.5	12	1 ABI39700	Oligonucleotide pr
46	12	0.5	12	1 ABI81381	Oligonucleotide pr
47	12	0.5	12	1 ABH99816	Oligonucleotide pr
48	12	0.5	12	1 ABI11748	Oligonucleotide pr
49	12	0.5	12	1 ABI37940	Oligonucleotide pr
50	12	0.5	12	1 ABI51735	Oligonucleotide pr
51	12	0.5	12	1 ABI57986	Oligonucleotide pr
52	12	0.5	12	1 ABI58180	Oligonucleotide pr
53	12	0.5	12	1 ABI76136	Oligonucleotide pr
54	12	0.5	12	1 ABH78492	Oligonucleotide pr
55	12	0.5	12	1 ABI11150	Oligonucleotide pr
56	12	0.5	12	1 ABI11702	Oligonucleotide pr
57	12	0.5	12	1 ABI13561	Oligonucleotide pr
58	12	0.5	12	1 ABI57071	Oligonucleotide pr
59	12	0.5	12	1 ABI58265	Oligonucleotide pr
60	12	0.5	12	1 ABI79841	Oligonucleotide pr
61	12	0.5	12	1 ABH76905	Oligonucleotide pr
62	12	0.5	12	1 ABI33466	Oligonucleotide pr
63	12	0.5	12	1 ABI13329	Oligonucleotide pr
64	12	0.5	12	1 ABI67163	Oligonucleotide pr
65	12	0.5	12	1 ABI20661	Oligonucleotide pr
66	12	0.5	12	1 ABH99103	Oligonucleotide pr
67	12	0.5	12	1 ABI00978	Oligonucleotide pr
68	12	0.5	12	1 ABH76049	Oligonucleotide pr
69	12	0.5	12	1 ABH7824	Oligonucleotide pr
70	12	0.5	12	1 ABI34874	Oligonucleotide pr
71	12	0.5	12	1 ABI37478	Oligonucleotide pr
72	12	0.5	12	1 ABI42579	Oligonucleotide pr
73	12	0.5	12	1 ABI50631	Oligonucleotide pr
74	12	0.5	12	1 ABI57459	Oligonucleotide pr
75	12	0.5	12	1 ABI58854	Oligonucleotide pr
76	12	0.5	12	1 ABI59615	Oligonucleotide pr
77	12	0.5	12	1 ABI62520	Oligonucleotide pr
78	12	0.5	12	1 ABH75802	Oligonucleotide pr
79	12	0.5	12	1 ABI64629	Oligonucleotide pr
80	12	0.5	12	1 ABI80379	Oligonucleotide pr
81	12	0.5	12	1 ABI17880	Oligonucleotide pr
82	12	0.5	12	1 ABI04037	Oligonucleotide pr
83	12	0.5	12	1 ABI35858	Oligonucleotide pr
84	12	0.5	12	1 ABI37560	Oligonucleotide pr
85	12	0.5	12	1 ABI16545	Oligonucleotide pr
86	12	0.5	12	1 ABI55919	Oligonucleotide pr
87	12	0.5	12	1 ABI77927	Oligonucleotide pr
88	12	0.5	12	1 ABI80946	Oligonucleotide pr
89	12	0.5	12	1 ABH73109	Oligonucleotide pr
90	12	0.5	12	1 ABH78092	Oligonucleotide pr
91	12	0.5	12	1 ABI04010	Oligonucleotide pr
92	12	0.5	12	1 ABI31412	Oligonucleotide pr
93	12	0.5	12	1 ABI34210	Oligonucleotide pr
94	12	0.5	12	1 ABI14063	Oligonucleotide pr
95	12	0.5	12	1 ABI14566	Oligonucleotide pr
96	12	0.5	12	1 ABI78262	Oligonucleotide pr
97	12	0.5	12	1 ABH96028	Oligonucleotide pr
98	12	0.5	12	1 ABH73374	Oligonucleotide pr
99	12	0.5	12	1 ABI07752	Oligonucleotide pr
100	12	0.5	12	1 ABI11309	Oligonucleotide pr
101	12	0.5	12	1 ABH75997	Oligonucleotide pr
102	12	0.5	12	1 ABH69491	Oligonucleotide pr
103	12	0.5	12	1 ABI27318	Oligonucleotide pr
104	12	0.5	12	1 ABI06733	Oligonucleotide pr
105	12	0.5	12	1 ABI44961	Oligonucleotide pr
106	12	0.5	12	1 ABT14521	Rhesus monkey P-gi





253	10	0.4	10	1	AAF34405	Yeast NORF gene SA	C 326	10	0.4	10	1	ABK81525	Human CASP5 gene a
254	10	0.4	10	1	AAF36200	Yeast NORF gene SA	327	10	0.4	10	1	AAU43018	Human cerberus l (
255	10	0.4	10	1	AAF40125	Yeast NORF gene SA	328	10	0.4	10	1	AAU43018	MR 8 arbitrary pri
256	10	0.4	10	1	AAF41100	Yeast NORF gene SA	329	10	0.4	10	1	ABS64267	Tachykinin recepto
257	10	0.4	10	1	AAF33851	Yeast NORF gene SA	330	10	0.4	10	1	ABU45794	Human MMP13 gene a
258	10	0.4	10	1	AAF33954	Yeast NORF gene SA	331	10	0.4	10	1	AAS99221	Human NAT1 gene al
259	10	0.4	10	1	AAF35394	Yeast NORF gene SA	332	10	0.4	10	1	ACC41747	Zinc finger protei
260	10	0.4	10	1	AAF36420	Yeast NORF gene SA	333	10	0.4	10	1	ABT14371	Nucleic acid PCR a
261	10	0.4	10	1	AAF38893	Yeast NORF gene SA	334	10	0.4	10	1	AAD51658	Human CYP2E gene p
262	10	0.4	10	1	AAF39096	Yeast NORF gene SA	335	10	0.4	10	1	AAD60155	Human ARG energy m
263	10	0.4	10	1	AAF42788	Yeast NORF gene SA	336	10	0.4	10	1	AAD60119	Human androgen-reg
264	10	0.4	10	1	AAF43422	Yeast NORF gene SA	337	10	0.4	10	1	AAD60135	Human ARG genomic
265	10	0.4	10	1	AAF34490	Yeast NORF gene SA	338	10	0.4	10	1	AAL56084	Human BAGE 5 intro
266	10	0.4	10	1	AAF34724	Yeast NORF gene SA	339	10	0.4	10	1	ADH62228	Human transcriptio
267	10	0.4	10	1	AAF40070	Yeast NORF gene SA	340	10	0.4	10	1	ADH62244	Human ARG tag #4 u
268	10	0.4	10	1	AAF40280	Yeast NORF gene SA	341	10	0.4	10	1	ADH62264	Human energy metab
269	10	0.4	10	1	AAF41770	Yeast NORF gene SA	342	10	0.4	10	1	ADH78833	Human apical iodid
270	10	0.4	10	1	AAF33518	Yeast NORF gene SA	343	10	0.4	10	1	ACF57633	Human ALDOB gene a
271	10	0.4	10	1	AAF33852	Yeast NORF gene SA	344	10	0.4	10	1	ACA63212	Human ALDOB gene a
272	10	0.4	10	1	AAF34992	Yeast NORF gene SA	345	10	0.4	10	1	ADI110084	IL-1 activated HUV
273	10	0.4	10	1	AAF36344	Yeast NORF gene SA	346	10	0.4	10	1	ADK65348	Mismatch 1 DNA for
274	10	0.4	10	1	AAF36972	Yeast NORF gene SA	347	10	0.4	10	1	ADF91296	PCR primer for IL-
275	10	0.4	10	1	AAF37749	Yeast NORF gene SA	348	10	0.4	10	1	ADH14499	Human retinoblasto
276	10	0.4	10	1	AAF35013	Yeast NORF gene SA	349	10	0.4	10	1	ADI26560	Rat PIM1 antisense
277	10	0.4	10	1	AAF40110	Yeast NORF gene SA	350	10	0.4	10	1	ADK13018	Human glioma endot
278	10	0.4	10	1	AAF40228	Yeast NORF gene SA	351	10	0.4	10	1	ADL39551	Serial analysis of
279	10	0.4	10	1	AAF42124	Yeast NORF gene SA	352	10	0.4	10	1	ADL98325	trr-1 gene intron
280	10	0.4	10	1	AAF42124	Yeast NORF gene SA	353	10	0.4	10	1	ADL98324	trr-1 gene intron
281	10	0.4	10	1	AAF42175	Yeast NORF gene SA	354	10	0.4	10	1	ADN89109	Hyperlipidemia tre
282	10	0.4	10	1	AAF43867	Yeast NORF gene SA	355	10	0.4	10	1	ADN89109	Androgen-regulated
283	10	0.4	10	1	AAF33364	Yeast NORF gene SA	356	10	0.4	10	1	ADN89109	Androgen-regulated
284	10	0.4	10	1	AAF34673	Yeast NORF gene SA	357	10	0.4	10	1	ADQ39845	Androgen-regulated
285	10	0.4	10	1	AAF42142	Yeast NORF gene SA	358	10	0.4	10	1	ADQ39884	Human VRI exon la
286	10	0.4	10	1	AAF42886	Yeast NORF gene SA	359	10	0.4	10	1	ADR10674	Arbitrary decamer
287	10	0.4	10	1	AAF34324	Yeast NORF gene SA	360	10	0.4	10	1	ADR20657	Human oostrogen re
288	10	0.4	10	1	AAF34785	Yeast NORF gene SA	361	10	0.4	10	1	ADN89109	Breast cancer dete
289	10	0.4	10	1	AAF36117	Yeast NORF gene SA	362	10	0.4	10	1	ADN89109	Breast cancer dete
290	10	0.4	10	1	AAF38329	Yeast NORF gene SA	363	10	0.4	10	1	ADN89109	Breast cancer dete
291	10	0.4	10	1	AAF38661	Yeast NORF gene SA	364	10	0.4	10	1	ADN89109	Breast cancer dete
292	10	0.4	10	1	AAF39083	Yeast NORF gene SA	365	10	0.4	10	1	ADN89109	Breast cancer dete
293	10	0.4	10	1	AAF42120	Yeast NORF gene SA	366	10	0.4	10	1	ADN89109	Breast cancer dete
294	10	0.4	10	1	AAF43670	Yeast NORF gene SA	367	10	0.4	10	1	ADN89109	Breast cancer dete
295	10	0.4	10	1	AAF39602	Primer-extension o	368	10	0.4	10	1	ADN89109	Breast cancer dete
296	10	0.4	10	1	AAF39659	Primer-extension o	369	10	0.4	10	1	ADN89109	Breast cancer dete
297	10	0.4	10	1	AAF39533	Human Histamine H2	370	10	0.4	10	1	ADN89109	Hypoxia-related tu
298	10	0.4	10	1	ABL59309	Primer for platele	371	10	0.4	10	1	ADU19459	Hypoxia-related tu
299	10	0.4	10	1	ABK59954	Even-skipped homeo	372	10	0.4	10	1	ADU19459	Hypoxia-related tu
300	10	0.4	10	1	ABK5548	Selectin L Lymphoc	373	10	0.4	10	1	ADU19459	Hypoxia-related tu
301	10	0.4	10	1	ABK5548	Selectin L Lymphoc	374	10	0.4	10	1	ADU19459	Hypoxia-related tu
302	10	0.4	10	1	ABK1452	SCYA20 primer exte	375	10	0.4	10	1	ADU19459	Hypoxia-related tu
303	10	0.4	10	1	ABK17007	Pyridoxal (Pyridox	376	10	0.4	10	1	ADU19459	Hypoxia-related tu
304	10	0.4	10	1	ABK16990	Pyridoxal (Pyridox	377	10	0.4	10	1	ADU19459	Hypoxia-related tu
305	10	0.4	10	1	AAF95416	Human ICAM2 gene a	378	10	0.4	10	1	ADU19459	Novel nucleotide a
306	10	0.4	10	1	AAF95416	Human ICAM2 gene a	379	10	0.4	10	1	ADU19459	Rice oligonucleoti
307	10	0.4	10	1	AAF95416	UDP glycosyltransf	380	10	0.4	10	1	ADU19459	Immunomodulatory g
308	10	0.4	10	1	ABV78495	Human Thi cell pre	381	10	0.4	10	1	ADU19459	Sendai virus E seq
309	10	0.4	10	1	ABV84738	Human Thi cell pre	382	10	0.4	10	1	ADU19459	MR 8 PCR arbitrary
310	10	0.4	10	1	ABV84337	Human electron tra	383	10	0.4	10	1	ADU19459	Universal bacteria
311	10	0.4	10	1	ABV84317	Human NADH-ubiquin	384	10	0.4	10	1	ADU19459	Rat PIM-1 RNA frag
312	10	0.4	10	1	ABK3803	Human multiple chr	385	10	0.4	10	1	ADU19459	Muscleblind-like M
313	10	0.4	10	1	ABK3695	Transcript tag DNA	386	10	0.4	10	1	ADU19459	LNA-modified detec
314	10	0.4	10	1	ABK3740	Transcript tag DNA	387	10	0.4	10	1	ADU19459	Cystic disorder di
315	10	0.4	10	1	ABK3772	Transcript tag DNA	388	10	0.4	10	1	ADU19459	Let-7a-related oli
316	10	0.4	10	1	ABK28556	Paraoxonase 2 (PON	389	10	0.4	10	1	ADU19459	Cystic kidney up-r
317	10	0.4	10	1	ABK96317	EDG1 gene primer e	390	10	0.4	10	1	ADU19459	Mutant loxp site s
318	10	0.4	10	1	ADK43420	Human CYP3A5 gene	391	10	0.4	10	1	ADU19459	Mutant loxp site s
319	10	0.4	10	1	ABL45894	Human EDG6 gene al	392	10	0.4	10	1	ADU19459	Mutant loxp site s
320	10	0.4	10	1	ABK5562	Human IL8RB gene a							
321	10	0.4	10	1	ABK54475	Primer-extension o							
322	10	0.4	10	1	ABK64084	Human BF gene alle							
323	10	0.4	10	1	ABL58357	PNA label for CFTR							
324	10	0.4	10	1	ABL58352	PNA label for CFTR							
325	10	0.4	10	1	ABL58351	PNA label for CFTR							

ALIGNMENTS

RESULT 1

AA92501	AA92501 standard; DNA; 12 BP.
ID	AA92501 standard; DNA; 12 BP.
XX	
AC	AA92501;
XX	
DT	25-MAR-2003 (revised)
DT	10-MAY-1990 (first entry)
XX	
DE	DNA sequence encoding secretory signal peptide.
XX	
KW	Secretory signal peptide; anti-hyperlipidaemia agent;
KW	anti-arteriosclerosis agent.
XX	
OS	Escherichia coli.
XX	
PN	EP345155-A.
XX	
PD	06-DEC-1989.
XX	
PF	31-MAY-1989; 89EP-00401495.
XX	
PR	31-MAY-1988; 88JP-00133549.
PR	26-APR-1989; 89JP-00107027.
XX	
PA	(MITU ) MITSUBISHI KASEI CORP.
XX	
PI	Shibul T, Kamizono M, Teranishi Y;
XX	
DR	WPI; 1989-358519/49.
XX	
PT	Prodn. of natural human apolipoprotein E or related protein - using a
PT	vector contg. the coding sequence fused to a secretory signal peptide.
XX	
PS	Claim 6; Page 13; 32pp; English.
XX	
CC	vector contg. the coding sequence fused to a secretory signal peptide.
CC	This DNA sequence is inserted into a vector alongside a DNA fragment
CC	encoding human apolipoprotein E (I) or (I)-like protein downstream from a
CC	promoter. The resulting cultured (I) and (I)-like products are
CC	efficiently produced and (at least 1000 times greater than prior methods)
CC	and are not exposed to proteases. (I) includes apolipoproteins E2, E3 and
CC	E4 of which E3 may be used as an anti-hyperlipidaemia and anti-
CC	arteriosclerosis agent. (Updated on 25-MAR-2003 to correct PF field.)
CC	(Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC	correct PI field.)
XX	
SQ	Sequence 12 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
Query Match	0.5%; Score 12; DB 1; Length 12;
Best Local Similarity	100.0%; Pred. No. 43;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Qy	1159 AAGCTTATGGTA 1170
Db	1 AAGCTTATGGTA 12
RESULT 2	
ABI18302	
ID	ABI18302 standard; DNA; 12 BP.
XX	
AC	ABI18302;
XX	
DT	22-FEB-2002 (first entry)
XX	
DE	Oligonucleotide primer SEQ ID NO 318275 for detecting SNP TSC0028556.
XX	
KW	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	
OS	Homo sapiens.
XX	

```

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 293842; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC000010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 95 CAAAACTAAAC 106
Db 12 CAAAACTAAAC 1
XX
RESULT 4
ABH73036
ID ABH73036 standard; DNA; 12 BP.
XX
AC ABH73036;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 273021 for detecting SNP TSC0003016.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 273021; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
XX

```

```

CC oligomers are also used for detecting cell type differentiation. ABC000010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 899 TTGATCAAGATA 910
Db 1 TTGATCAAGATA 12
XX
RESULT 5
ABH98700
ID ABH98700 standard; DNA; 12 BP.
XX
AC ABH98700;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 298693 for detecting SNP TSC0018240.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 298693; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC000010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

```

[illegible]

```

XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX
PS Claim 1; SEQ ID NO 34999; 29pp + Sequence Listing; German.
XX XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX XX
SQ Sequence 12 BP; 3 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 933 AGGAAAGATT 944
Db 12 AGGAAAGATT 1
RESULT 9
ABI69350
ID ABI69350 standard; DNA; 12 BP.
XX AC ABI69350;
XX XX
DT 22-FEB-2002 (first entry)
XX XX
DE Oligonucleotide primer SEQ ID NO 369323 for detecting SNP TSC0057582.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
PN WO200177384-A2.
XX XX
PD 18-OCT-2001.
XX XX
PF 06-APR-2001; 2001WO-IB000713.
XX XX
PR 07-APR-2000; 2000DE-01019173.
XX XX
PA (EPIG-) EPIGENOMICS AG.
XX XX
PI Olek A, Piepenbrock C, Berlin K;
XX XX
DR WPI; 2001-657177/75.
XX XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX

```

```

PS Claim 1; SEQ ID NO 369323; 29pp + Sequence Listing; German.
XX XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX XX
SQ Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 92 CACCAAAACTA 103
Db 1 CACCAAAACTA 12
RESULT 10
ABH68237/c
ID ABH68237 standard; DNA; 12 BP.
XX AC ABH68237;
XX XX
DT 22-FEB-2002 (first entry)
XX XX
DE Oligonucleotide primer SEQ ID NO 268214 for detecting SNP TSC0000986.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
PN WO200177384-A2.
XX XX
PD 18-OCT-2001.
XX XX
PF 06-APR-2001; 2001WO-IB000713.
XX XX
PR 07-APR-2000; 2000DE-01019173.
XX XX
PA (EPIG-) EPIGENOMICS AG.
XX XX
PI Olek A, Piepenbrock C, Berlin K;
XX XX
DR WPI; 2001-657177/75.
XX XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX
PS Claim 1; SEQ ID NO 268214; 29pp + Sequence Listing; German.
XX XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX XX

```

```

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 ATTAATTAATAA 383
DB 12 ATTAATTAATAA 1

RESULT 11
AB118972/c
ID AB118972 standard; DNA; 12 BP.
XX
AC AB118972;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 318945 for detecting SNP TSC0028972.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-18000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PWPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 318945; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1855 ATTGTAGAAGGT 1866
DB 12 ATTGTAGAAGGT 1

RESULT 12
ABH90107/c
ID ABH90107 standard; DNA; 12 BP.
XX
AC ABH90107;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 290100 for detecting SNP TSC0014216.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-18000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PWPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 290100; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 898 TTTCATGAAGAT 909
DB 12 TTTCATGAAGAT 1

RESULT 13
ABI41148
ID ABI41148 standard; DNA; 12 BP.
XX
AC ABI41148;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 341121 for detecting SNP TSC0041869.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

```



CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 ATATTAAACAC 232

Db 1 ATATTAAACAC 12

RESULT 16

ABH71279

ID ABH71279 standard; DNA; 12 BP.

XX AC ABH71279;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 271256 for detecting SNP TSC0002442.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 271256; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 6 A; 0 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2162 AATTAAGATTAT 2173

Db 1 AATTAAGATTAT 12

RESULT 17

ABI00878/c

ID ABI00878 standard; DNA; 12 BP.

XX AC ABI00878;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 300851 for detecting SNP TSC0019220.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 300851; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 TTAACAACAAT 235

Db 12 TTAACAACAAT 1

RESULT 18

ABI26807

ID ABI26807 standard; DNA; 12 BP.

XX AC ABI26807;





PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PS Claim 1; SEQ ID NO 367416; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 12 BP; 4 A; 0 C; 2 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 319 GGAAATATTTT 330  
DB 1 GGAAATATTTT 12  
|||||  
RESULT 21  
ABI79368  
ID ABI79368 standard; DNA; 12 BP.  
XX  
XX ABI79368;  
AC  
XX  
XX 22-FEB-2002 (first entry)  
DT  
XX  
XX Oligonucleotide primer SEQ ID NO 379341 for detecting SNP TSC0004827.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PS Claim 1; SEQ ID NO 379341; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 12 BP; 4 A; 0 C; 2 G; 6 T; 0 U; 0 Other;  
SQ

CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;  
SQ

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 193 TATTCAAATAC 204  
DB 1 TATTCAAATAC 12  
|||||

RESULT 22  
ABI05852/c  
ID ABI05852 standard; DNA; 12 BP.  
XX  
XX AC  
XX ABI05852;  
AC  
XX  
XX 22-FEB-2002 (first entry)  
DT  
XX  
XX Oligonucleotide primer SEQ ID NO 305825 for detecting SNP TSC0021654.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PS Claim 1; SEQ ID NO 305825; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 12 BP; 1 A; 1 C; 1 G; 9 T; 0 U; 0 Other;  
SQ

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 64 GTAAAAACAAA 75  
|||||



XX (EPiG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 355492; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 12 BP; 5 A; 2 C; 0 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1347 AAGTGTTAAATT 1358  
 DB 12 AAGTGTTAAATT 1  
 |||||  
 RESULT 26  
 ABI65306  
 ID ABI65306 standard; DNA; 12 BP.  
 XX AC ABI65306;  
 XX 22-FEB-2002 (first entry)  
 XX Oligonucleotide primer SEQ ID NO 365279 for detecting SNP TSC0055022.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPiG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 365279; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 12 BP; 6 A; 0 C; 1 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 158 ATATTAAAGATT 169  
 DB 1 ATATTAAAGATT 12  
 |||||  
 RESULT 27  
 ABH98644/c  
 ID ABH98644 standard; DNA; 12 BP.  
 XX AC ABH98644;  
 XX 22-FEB-2002 (first entry)  
 XX Oligonucleotide primer SEQ ID NO 298637 for detecting SNP TSC0018205.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPiG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 298637; 29pp + Sequence Listing; German.  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

```

SQ Sequence 12 BP; 2 A; 0 C; 2 G; 8 T; 0 U; 0 Other;
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 ATTAAACACAA 234
DB 12 ATTAAACACAA 1

RESULT 28
ABI27826
ID ABI27826 standard; DNA; 12 BP.
XX AC
XX AB127826;
XX DT
XX 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 327799 for detecting SNP TSC0033909.
XX KW
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN
XX WO200177384-A2.
XX PD
XX 18-OCT-2001.
XX PP
XX 06-APR-2001; 2001WO-IB000713.
XX PR
XX 07-APR-2000; 2000DE-01019173.
XX PA
XX (EPIG-) EPIGENOMICS AG.
XX PI
XX Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX PT
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS
XX Claim 1; SEQ ID NO 327799; 29pp + Sequence Listing; German.
XX CC
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC ftp.wipo.int/pub/published_pct_sequences
XX CC
XX SQ Sequence 12 BP; 7 A; 0 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 AATATTAAAGAT 168
DB 1 AATATTAAAGAT 12

RESULT 29
ABI38730
ID ABI38730 standard; DNA; 12 BP.
XX AC
XX AB138730;
XX DT
XX 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 338703 for detecting SNP TSC0040634.
XX KW
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.
XX PN
XX WO200177384-A2.
XX PD
XX 18-OCT-2001.
XX PP
XX 06-APR-2001; 2001WO-IB000713.
XX PR
XX 07-APR-2000; 2000DE-01019173.
XX PA
XX (EPIG-) EPIGENOMICS AG.
XX PI
XX Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX PT
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS
XX Claim 1; SEQ ID NO 338703; 29pp + Sequence Listing; German.
XX CC
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC ftp.wipo.int/pub/published_pct_sequences
XX CC
XX SQ Sequence 12 BP; 9 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GTAAAAACAAA 75
DB 1 GTAAAAACAAA 12

RESULT 30
ABI48088/c
ID ABI48088 standard; DNA; 12 BP.
XX AC
XX AB148088;
XX DT
XX 22-FEB-2002 (first entry)
XX DE
XX Oligonucleotide primer SEQ ID NO 348061 for detecting SNP TSC0045417.
XX KW
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX Homo sapiens.

```

```

XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 296971; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH0010-ABH2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 5 A; 0 C; 2 G; 5 T; 0 U; 0 Other;
XX XX
XX Query Match 0.5%; Score 12; DB 1; Length 12;
XX XX Best Local Similarity 100.0%; Pred. No. 43;
XX XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 598 AATATCATTCAT 609
XX Db 12 AATATCATTCAT 1
XX XX
XX RESULT 31
XX ABH96978/c
XX ID ABH96978 standard; DNA; 12 BP.
XX AC
XX AC ABH96978;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide primer SEQ ID NO 296971 for detecting SNP TSC0017373.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 348061; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH0010-ABH2073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 5 A; 0 C; 2 G; 5 T; 0 U; 0 Other;
XX XX
XX Query Match 0.5%; Score 12; DB 1; Length 12;
XX XX Best Local Similarity 100.0%; Pred. No. 43;
XX XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 598 AATATCATTCAT 609
XX Db 12 AATATCATTCAT 1
XX XX
XX RESULT 31
XX ABH96978/c
XX ID ABH96978 standard; DNA; 12 BP.
XX AC
XX AC ABH96978;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide primer SEQ ID NO 296971 for detecting SNP TSC0017373.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 302403; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,

```

CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 CCAAAACTAAA 105

DB 12 CCAAAACTAAA 1

RESULT 33

ABI07725

ID ABI07725 standard; DNA; 12 BP.

XX AC

XX ABI07725;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 307698 for detecting SNP TSC0022646.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX PS Claim 1; SEQ ID NO 307698; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 8 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1175 AATATAAATAT 1186

DB 1 AATATAAATAT 12

RESULT 34

ABH87411

ID ABH87411 standard; DNA; 12 BP.

XX AC

XX ABH87411;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 287404 for detecting SNP TSC0013078.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX PS Claim 1; SEQ ID NO 287404; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 9 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1174 AATATAAATA 1185

DB 1 AATATAAATA 12

RESULT 35

ABI40919/c

ID ABI40919 standard; DNA; 12 BP.

XX AC

XX ABI40919;

XX DT 22-FEB-2002 (first entry)

```

XX DE Oligonucleotide primer SEQ ID NO 340892 for detecting SNP TSC0041738.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 340892; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AAATACAAAAC 2355
DB 12 AAATACAAAAC 1
|||||
RESULT 36
ABI44172
ID ABI44172 standard; DNA; 12 BP.
XX AC
XX AC ABI44172;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 344145 for detecting SNP TSC006614.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 340892; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AAATACAAAAC 2355
DB 12 AAATACAAAAC 1
|||||
RESULT 36
ABI44172
ID ABI44172 standard; DNA; 12 BP.
XX AC
XX AC ABI44172;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 380266 for detecting SNP TSC006614.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.

```

```

PF 06-APR-2001; 2001WO-IB000713.
XX XX
PR 07-APR-2000; 2000DE-01019173.
XX XX
XX (EPIG-) EPIGENOMICS AG.
XX XX
XX Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX XX
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 344145; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 0 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1425 AGAATATATAAT 1436
DB 1 AGAATATATAAT 12
|||||
RESULT 37
ABI80293/C
ID ABI80293 standard; DNA; 12 BP.
XX AC
XX AC ABI80293;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide primer SEQ ID NO 380266 for detecting SNP TSC006614.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.

```



XX PS Claim 1; SEQ ID NO 380266; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC CC range of diseases including immune system, gastrointestinal, respiratory, CC CC central nervous system, cardiovascular and metabolic disorders. The CC CC oligomers are also used for detecting cell type differentiation. ABC00010 CC CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC CC represent the oligomers described in the invention. NOTE: The sequence CC CC data for this patent did not form part of the printed specification, but CC CC was obtained in electronic format from WIPO at CC CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 6 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 601 ATCATTCATTAA 612  
                  |||||

Db 12 ATCATTCATTAA 1

RESULT 38  
ABH68264/c  
ID ABH68264 standard; DNA; 12 BP.

XX AC ABH68264;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 268241 for detecting SNP TSC0000998.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX PS Claim 1; SEQ ID NO 268241; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC CC range of diseases including immune system, gastrointestinal, respiratory, CC CC central nervous system, cardiovascular and metabolic disorders. The CC CC oligomers are also used for detecting cell type differentiation. ABC00010 CC CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC CC represent the oligomers described in the invention. NOTE: The sequence CC CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 4 A; 1 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 AGAATTAATTA 380  
                  |||||

Db 12 AGAATTAATTA 1

RESULT 39  
ABH93996/c  
ID ABH93996 standard; DNA; 12 BP.

XX AC ABH93996;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 293989 for detecting SNP TSC0015906.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX PS Claim 1; SEQ ID NO 293989; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC CC range of diseases including immune system, gastrointestinal, respiratory, CC CC central nervous system, cardiovascular and metabolic disorders. The CC CC oligomers are also used for detecting cell type differentiation. ABC00010 CC CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 CC CC represent the oligomers described in the invention. NOTE: The sequence CC CC data for this patent did not form part of the printed specification, but CC CC was obtained in electronic format from WIPO at CC CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 1 A; 0 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2034 CACCACCACTC 2045  
                  |||||

Db 12 CACCACCACTC 1



XX PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 271155; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 93 ACCAAAAAATAA 104  
 DB 12 ACCAAAAAATAA 1  
 RESULT 43  
 ABI25898  
 ID ABI25898 standard; DNA; 12 BP.  
 AC ABI25898;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide primer SEQ ID NO 325871 for detecting SNP TSC0032776.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 325871; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 909 TACCTTTTAAACAT 920  
 DB 1 TACCTTTTAAACAT 12  
 RESULT 44  
 ABI37764/C  
 ID ABI37764 standard; DNA; 12 BP.  
 XX ABI37764;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide primer SEQ ID NO 337737 for detecting SNP TSC0040047.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 337737; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 4 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

```

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 TTAATTAAAGGA 384
DB 12 TTAATTAAAGGA 1

RESULT 45
ABI39700/c
ID ABI39700 standard; DNA; 12 BP.
XX
AC ABI39700;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 339673 for detecting SNP TSC0041132.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 339673; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 497 TATTGGAAGGA 508
DB 12 TATTGGAAGGA 1

RESULT 46
ABI81381
ID ABI81381 standard; DNA; 12 BP.
XX

```

```

AC ABI81381;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 381354 for detecting SNP TSC006410;
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 381354; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 2 G; 6 T; 0 U; 0 Other;

Query Match          0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 TGGAAATATTTT 329
DB 1 TGGAAATATTTT 12

RESULT 47
ABH99816/c
ID ABH99816 standard; DNA; 12 BP.
XX
AC ABH99816;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 299809 for detecting SNP TSC0018756.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.

```

XX PD 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX DR WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 299809; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC000010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1581 CCAACTATACAA 1692  
 Db 12 CCAACTATACAA 1  
 |||||  
 RESULT 48  
 ABI11748  
 ID ABI11748 standard; DNA; 12 BP.  
 AC ABI11748;  
 XX 22-FEB-2002 (first entry)  
 DT Oligonucleotide primer SEQ ID NO 311721 for detecting SNP TSC0024649.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 311721; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC000010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1581 CCAACTATACAA 1692  
 Db 12 CCAACTATACAA 1  
 |||||  
 RESULT 48  
 ABI11748  
 ID ABI11748 standard; DNA; 12 BP.  
 AC ABI11748;  
 XX 22-FEB-2002 (first entry)  
 DT Oligonucleotide primer SEQ ID NO 311721 for detecting SNP TSC0024649.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 311721; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC000010

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.  
 XX Claim 1; SEQ ID NO 311721; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC000010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 198 AAAATACATACC 209  
 Db 1 AAAATACATACC 12  
 |||||  
 RESULT 49  
 ABI37940  
 ID ABI37940 standard; DNA; 12 BP.  
 AC ABI37940;  
 XX 22-FEB-2002 (first entry)  
 DT Oligonucleotide primer SEQ ID NO 337913 for detecting SNP TSC0040140.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 337913; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC000010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1167 GGATAGAAATA 1178  
 Db 1 GGATAGAAATA 12

RESULT 50  
 ABI51735/c  
 ID ABI51735 standard; DNA; 12 BP.  
 AC ABI51735;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 351708 for detecting SNP TSC0047446.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

PS Claim 1; SEQ ID NO 351708; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 12 BP; 4 A; 2 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 TCGATATTAAAA 229

Db 12 TCGATATTAAAA 1

RESULT 51  
 ABI57986/c  
 ID ABI57986 standard; DNA; 12 BP.  
 XX  
 AC ABI57986;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 357959 for detecting SNP TSC0050895.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 357959; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 12 BP; 4 A; 1 C; 0 G; 7 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 TATATAATAAGA 1440  
 Db 12 TATATAATAAGA 1

RESULT 52  
 ABI58180  
 ID ABI58180 standard; DNA; 12 BP.

XX  
 AC ABI58180;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX

DE Oligonucleotide primer SEQ ID NO 358153 for detecting SNP TSC0005054.

```

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PS 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 358153; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system and gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 88 AAACCACCAAAA 99
Db 1 AAACCACCAAAA 12
|||||
RESULT 53
ABI76136/c
ID ABI76136 standard; DNA; 12 BP.
XX AC ABI76136;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 376109 for detecting SNP TSC0061618.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PS Claim 1; SEQ ID NO 376109; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system and gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 88 AAACCACCAAAA 99
Db 1 AAACCACCAAAA 12
|||||
RESULT 53
ABI76136/c
ID ABI76136 standard; DNA; 12 BP.
XX AC ABI76136;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 376109 for detecting SNP TSC0061618.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PS Claim 1; SEQ ID NO 376109; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system and gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2018 CTTCAAAACCAAT 2029
Db 12 CTTCAAAACCAAT 1
|||||
RESULT 54
ABH78492
ID ABH78492 standard; DNA; 12 BP.
XX AC ABH78492;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 278485 for detecting SNP TSC0006051.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 278485; 29pp + Sequence Listing; German.

```

```

PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 376109; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2018 CTTCAAAACCAAT 2029
Db 12 CTTCAAAACCAAT 1
|||||
RESULT 54
ABH78492
ID ABH78492 standard; DNA; 12 BP.
XX AC ABH78492;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 278485 for detecting SNP TSC0006051.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 278485; 29pp + Sequence Listing; German.

```

```

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 8 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 TTAATTAATAAAA 384
Db 1 TTAATTAATAAAA 12

RESULT 55
AB111150
ID AB111150 standard; DNA; 12 BP.
AC AB111150;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 311123 for detecting SNP TSC0024322.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 311123; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

```

```

XX SQ Sequence 12 BP; 4 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 710 TCGTTAAGATAT 721
Db 1 TCGTTAAGATAT 12

RESULT 56
AB111702
ID AB111702 standard; DNA; 12 BP.
AC AB111702;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 311675 for detecting SNP TSC0024612.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 311675; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2025 CCAATCCATCAC 2036
Db 1 CCAATCCATCAC 12

RESULT 57

```





XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX Claim 1; SEQ ID NO 358238; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 6 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

XX Query Match 0.5%; Score 12; DB 1; Length 12;

XX Best Local Similarity 100.0%; Pred. No. 43;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 627 AATATATATG 638

DB 1 AATATATATG 12

RESULT 60

ABT9841

ID ABT9841 standard; DNA; 12 BP.

XX AC ABT9841;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 379814 for detecting SNP TSC0008223.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX Claim 1; SEQ ID NO 379814; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 8 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

XX Query Match 0.5%; Score 12; DB 1; Length 12;

XX Best Local Similarity 100.0%; Pred. No. 43;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 AAAAAATTAGAG 142

DB 1 AAAAAATTAGAG 12

RESULT 61

ABH76905

ID ABH76905 standard; DNA; 12 BP.

XX AC ABH76905;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 276898 for detecting SNP TSC000432.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX Claim 1; SEQ ID NO 276898; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT2073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 4 A; 0 C; 2 G; 6 T; 0 U; 0 Other;

XX Query Match 0.5%; Score 12; DB 1; Length 12;

XX Best Local Similarity 100.0%; Pred. No. 43;



```

XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 367136; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 AAAACCAACCAAA 98
Db 1 AAAACCAACCAAA 12

RESULT 65
ABI20661/c
ID ABI20661 standard; DNA; 12 BP.
XX AC ABI20661;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 320634 for detecting SNP TSC0029824.
XX SN: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine

```

```

PT methylation status.
XX Claim 1; SEQ ID NO 320634; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

```

```

SQ Sequence 12 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 AAAACCAACCAAA 98
Db 12 AAAACCAACCAAA 1

```

```

RESULT 66
ABH99103/c
ID ABH99103 standard; DNA; 12 BP.
XX AC ABH99103;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 299096 for detecting SNP TSC0018429
XX SN: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 299096; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence

```

CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 AACACCAACAAA 99  
 |||||  
 Db 12 AACACCAACAAA 1

## RESULT 67

AB100978/c  
 ID AB100978 standard; DNA; 12 BP.

AC AB100978;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 300951 for detecting SNP TSC0019272.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

PS Claim 1; SEQ ID NO 300951; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 AACACCAACAAA 100  
 |||||  
 Db 12 AACACCAACAAA 1

## RESULT 68

ABH76049  
 ID ABH76049 standard; DNA; 12 BP.

AC ABH76049;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 276042 for detecting SNP TSC0004073.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

PS Claim 1; SEQ ID NO 276042; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 12 BP; 8 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 AAAAACAACG 107

Db 1 AAAAACAACG 12

## RESULT 69

ABH77824  
 ID ABH77824 standard; DNA; 12 BP.

AC ABH77824;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 277817 for detecting SNP TSC0004978.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 277817; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 PS Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;  
 XX  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 93 ACCAAAAACTAA 104  
 Db 1 ACCAAAAACTAA 12  
 |||||  
 RESULT 70  
 ABI34874/c  
 ID ABI34874 standard; DNA; 12 BP.  
 XX  
 AC ABI34874;  
 XX  
 XX 22-FEB-2002 (first entry)  
 XX  
 XX Oligonucleotide primer SEQ ID NO 334847 for detecting SNP TSC0038439.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic

PA (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 334847; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 PS Sequence 12 BP; 2 A; 1 C; 2 G; 7 T; 0 U; 0 Other;  
 XX  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1324 CATAATAACGAA 1335  
 Db 12 CATAATAACGAA 1  
 |||||  
 RESULT 71  
 ABI37478  
 ID ABI37478 standard; DNA; 12 BP.  
 XX  
 AC ABI37478;  
 XX  
 XX 22-FEB-2002 (first entry)  
 XX  
 XX Oligonucleotide primer SEQ ID NO 337451 for detecting SNP TSC0039880.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 337451; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 12 BP; 7 A; 2 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1324 CATAATAACGAA 1335  
 DB 1 CATAATAACGAA 12  
 |||||

## RESULT 72

ABI42579  
 ID ABI42579 standard; DNA; 12 BP.  
 AC ABI42579;  
 DT 22-FEB-2002 (first entry)  
 DE Oligonucleotide primer SEQ ID NO 342552 for detecting SNP TSC0042596.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.

XX Claim 1; SEQ ID NO 342552; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 12 BP; 6 A; 1 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1562 ATACATATTATA 1573  
 DB 1 ATACATATTATA 12  
 |||||

## RESULT 73

ABI50631/C  
 ID ABI50631 standard; DNA; 12 BP.

XX AC ABI50631;

XX DT 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 350604 for detecting SNP TSC0046774.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.

XX Claim 1; SEQ ID NO 350604; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAATTTAGAGTG 12  
 DB 12 GAATTTAGAGTG 1  
 |||||

## RESULT 74

ABI57459  
 ID ABI57459 standard; DNA; 12 BP.





XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1: SEQ ID NO 359588; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC000010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 230 CACAAATCCGTAT 241  
DB 1 CACAAATCCGTAT 12  
|||||  
  
RESULT 77  
AB162520  
ID AB162520 standard; DNA; 12 BP.  
XX  
AC AB162520;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 362493 for detecting SNP TSC0053260.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1: SEQ ID NO 362493; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC000010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 230 CACAAATCCGTAT 241  
DB 1 CACAAATCCGTAT 12  
|||||  
  
RESULT 78  
ABH75802/c  
ID ABH75802 standard; DNA; 12 BP.  
XX  
AC ABH75802;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 275795 for detecting SNP TSC0004002.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1: SEQ ID NO 275795; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC000010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 0 G; 9 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC oligomers are also used for detecting cell type differentiation. ABC000010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1064 ACACAAAATCA 1075  
DB 1 ACACAAAATCA 12  
|||||  
  
RESULT 78  
ABH75802/c  
ID ABH75802 standard; DNA; 12 BP.  
XX  
AC ABH75802;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 275795 for detecting SNP TSC0004002.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1: SEQ ID NO 275795; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC000010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 0 G; 9 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1174 AAATATAAATA 1185
DB      12 AAATATAAATA 1

RESULT 79
ABI64629/c
ID      ABI64629 standard; DNA; 12 BP.
XX
AC      ABI64629;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 364602 for detecting SNP TSC0007151.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 364602; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 4 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1175 AAATATAAATAT 1186
DB      12 AAATATAAATAT 1

RESULT 80
ABI60379/c
ID      ABI60379 standard; DNA; 12 BP.
XX
AC      ABI60379;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 317853 for detecting SNP TSC000713.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PS      Claim 1; SEQ ID NO 380352; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 2 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      866 CGCTTAAACG 877
DB      12 CGCTTAAACG 1

RESULT 81
ABI17880/c
ID      ABI17880 standard; DNA; 12 BP.
XX
AC      ABI17880;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 317853 for detecting SNP TSC000713.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.

```

```

XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 317853; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2483 CCAAAACAAAAA 2494
DB 12 CCAAAACAAAAA 1
|||||||
RESULT 82
ABI04037/C
ID ABI04037 standard; DNA; 12 BP.
XX
AC ABI04037;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 304010 for detecting SNP TSC0020743.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX Oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 317853; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2483 CCAAAACAAAAA 2494
DB 12 CCAAAACAAAAA 1
|||||||
RESULT 82
ABI04037/C
ID ABI04037 standard; DNA; 12 BP.
XX
AC ABI04037;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 304010 for detecting SNP TSC0020743.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX Oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 317853; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2048 CAACGAAATCA 2059
DB 12 CAACGAAATCA 1
|||||||
RESULT 83
ABI35858
ID ABI35858 standard; DNA; 12 BP.
XX
AC ABI35858;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 335831 for detecting SNP TSC0039046.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 335831; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at

```

```

PS Claim 1; SEQ ID NO 304010; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 1 C; 3 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2048 CAACGAAATCA 2059
DB 12 CAACGAAATCA 1
|||||||
RESULT 83
ABI35858
ID ABI35858 standard; DNA; 12 BP.
XX
AC ABI35858;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 335831 for detecting SNP TSC0039046.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 335831; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at

```

```

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

  Query Match      0.5%; Score 12; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 TATATGATTATT 250
Db 1 TATATGATTATT 12

RESULT 84
ABI37560/c
ID ABI37560 standard; DNA; 12 BP.
XX
AC ABI37560;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 337533 for detecting SNP TSC0039915.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 337533; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 1 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match      0.5%; Score 12; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2095 GTCAAAAATAC 2106
Db 12 GTCAAAAATAC 1

RESULT 85
ABI16545/c
ID ABI16545 standard; DNA; 12 BP.
XX
AC ABI16545;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 316518 for detecting SNP TSC0049849.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 316518; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match      0.5%; Score 12; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 43;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1176 ATATAAAATATA 1187
Db 12 ATATAAAATATA 1

RESULT 86
ABI55919/c
ID ABI55919 standard; DNA; 12 BP.
XX
AC ABI55919;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 355892 for detecting SNP TSC0049849.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

```

```

XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 35892; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 2 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 627 AAATATAATGTC 638
Db 12 AAATATAATGTC 1
|||||

RESULT 87
ABI77927/c
ID ABI77927 standard; DNA; 12 BP.
XX AC ABI77927;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 377900 for detecting SNP TSC0006316.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 377900; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 2 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 627 AAATATAATGTC 638
Db 12 AAATATAATGTC 1
|||||

RESULT 88
ABI80946/c
ID ABI80946 standard; DNA; 12 BP.
XX AC ABI80946;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 380919 for detecting SNP TSC0064044
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 380919; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

```

```

PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 377900; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 498 ATTTGAAGCAT 509
Db 12 ATTTGAAGCAT 1
|||||

RESULT 88
ABI80946/c
ID ABI80946 standard; DNA; 12 BP.
XX AC ABI80946;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 380919 for detecting SNP TSC0064044
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 380919; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

```

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 12 BP; 4 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 371 AATTAATTAAAA 382  
 Db 12 AATTAATTAAAA 1

RESULT 89  
 ABH73109  
 ID ABH73109 standard; DNA; 12 BP.  
 XX  
 AC ABH73109;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 273094 for detecting SNP TSC0003043.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.

XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 273094; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 12 BP; 5 A; 0 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 240 AATGATTATTA 251  
 Db 1 AATGATTATTA 12

RESULT 90  
 ABH78092  
 ID ABH78092 standard; DNA; 12 BP.  
 XX  
 AC ABH78092;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 278085 for detecting SNP TSC0005590.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.

XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 278085; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 12 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2344 AATACAAAAAC 2355  
 Db 1 AATACAAAAAC 12

RESULT 91  
 ABI04010/C  
 ID ABI04010 standard; DNA; 12 BP.  
 XX  
 AC ABI04010;



PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 334183; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2032 ATCACCACCAAC 2043  
DB 12 ATCACCACCAAC 1  
  
RESULT 94  
ABI14063/C  
ID ABI14063 standard; DNA; 12 BP.  
XX  
AC ABI14063;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 314036 for detecting SNP TSC0036081.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 314036; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 319 GGAATATTTT 330  
DB 12 GGAATATTTT 1  
  
RESULT 95  
ABI41566/C  
ID ABI41566 standard; DNA; 12 BP.  
XX  
AC ABI41566;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 341539 for detecting SNP TSC0042092.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 341539; 29pp + Sequence Listing; German  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 999 TTTAATACATCC 1010  
DB 12 TTTAATACATCC 1  
  
RESULT 96  
ABI41566/C  
ID ABI41566 standard; DNA; 12 BP.  
XX  
AC ABI41566;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 341539 for detecting SNP TSC0042092.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 341539; 29pp + Sequence Listing; German  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073



```

Db      12 TTTAATACATCC 1
RESULT 96
ABI78262/c
AC      ABI78262 standard; DNA; 12 BP.
XX
AC      ABI78262;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 378235 for detecting SNP TSC0062683.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PP      07-APR-2000; 2000DE-01019173.
XX
PR      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
PI      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 378235; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
XX
Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      30 TGGTAGAGTAA 41
      |||||
Db      12 TGGTAGAGTAA 1

RESULT 97
ABH96028
ID      ABH96028 standard; DNA; 12 BP.
XX
AC      ABH96028;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 296021 for detecting SNP TSC0016856.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PP      07-APR-2000; 2000DE-01019173.
XX
PR      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
PI      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 378235; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
XX
Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      30 TGGTAGAGTAA 41
      |||||
Db      12 TGGTAGAGTAA 1

RESULT 98
ABH73374
ID      ABH73374 standard; DNA; 12 BP.
XX
AC      ABH73374;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 273359 for detecting SNP TSC0003150.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PP      07-APR-2000; 2000DE-01019173.
XX
PR      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
PI      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 296021; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2483 CCAAAAACAAAA 2494
      |||||
Db      1 CCAAAAACAAAA 12

RESULT 99
ABH73374
ID      ABH73374 standard; DNA; 12 BP.
XX
AC      ABH73374;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 273359 for detecting SNP TSC0003150.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PP      07-APR-2000; 2000DE-01019173.
XX
PR      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
PI      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 296021; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2483 CCAAAAACAAAA 2494
      |||||
Db      1 CCAAAAACAAAA 12

```

```

XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 273359; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 9 A; 1 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 12; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 43;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 961 ATTAACAAACAA 972
XX Db 1 ATTAACAAACAA 12
XX
XX RESULT 99
XX ID ABI07752/c
XX ID ABI07752 standard; DNA; 12 BP.
XX AC ABI07752;
XX XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 307725 for detecting SNP TSC0022655.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX
XX PR Oligonucleotide primer SEQ ID NO 307725 for detecting SNP TSC0022655.
XX
XX PA SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX PA peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX PA central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 307725; 29pp + Sequence Listing; German.
XX

```

```

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
CC SQ Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
CC
CC Query Match 0.5%; Score 12; DB 1; Length 12;
CC Best Local Similarity 100.0%; Pred. No. 43;
CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 2345 AATACAAAACCC 2356
CC Db 12 AATACAAAACCC 1
CC
CC RESULT 100
CC ID ABI11309
CC ID ABI11309 standard; DNA; 12 BP.
CC AC ABI11309;
CC XX
CC DT 22-FEB-2002 (first entry)
CC
CC DE Oligonucleotide primer SEQ ID NO 311282 for detecting SNP TSC0024190.
CC
CC KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
CC KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
CC KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
CC
CC OS Homo sapiens.
CC
CC PN WO200177384-A2.
CC
CC PD 18-OCT-2001.
CC
CC PF 06-APR-2001; 2001WO-IB0000713.
CC
CC PR 07-APR-2000; 2000DE-01019173.
CC
CC PA (EPIG-) EPIGENOMICS AG.
CC
CC PI Olek A, Piepenbrock C, Berlin K;
CC
CC DR WPI; 2001-657177/75.
CC
CC PT Set of oligonucleotides, useful for diagnosis and cell typing, is
CC PT designed to detect single-nucleotide polymorphisms and cytosine
CC PT methylation status.
CC
CC PS Claim 1; SEQ ID NO 311282; 29pp + Sequence Listing; German.
CC
CC CC This invention describes novel oligonucleotide primers or peptide nucleic
CC CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC CC range of diseases including immune system, gastrointestinal, respiratory,
CC CC central nervous system, cardiovascular and metabolic disorders. The
CC CC oligomers are also used for detecting cell type differentiation. ABC00010
CC CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC CC represent the oligomers described in the invention. NOTE: The sequence
CC CC data for this patent did not form part of the printed specification, but
CC CC was obtained in electronic format from WIPO at
CC CC ftp.wipo.int/pub/published_pct_sequences
CC
CC XX

```

```

SQ Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1728 TTACACCATTC 1739
DB 1 TTACACCATTC 12

RESULT 101
ABI75997
ID ABI75997 standard; DNA; 12 BP.
XX AC ABI75997;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 375970 for detecting SNP TSC0061543.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 375970; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 CCACCAAAACT 102
DB 1 CCACCAAAACT 12

RESULT 102
ABH69491
ID ABH69491 standard; DNA; 12 BP.
XX AC ABH69491;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 37299; for detecting SNP TSC0033541.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.

```

XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 327291; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 4 A; 2 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2161 GAATTAAGATTA 2172  
 DB 12 GAATTAAGATTA 1  
 RESULT 104  
 ABI06733/c  
 ID ABI06733 standard; DNA; 12 BP.  
 AC ABI06733;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide primer SEQ ID NO 306706 for detecting SNP TSC0022137.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 306706; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 12 BP; 3 A; 0 C; 3 G; 6 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1625 TCATCAAAATAC 1636  
 DB 12 TCATCAAAATAC 1  
 RESULT 105  
 ABI44961  
 ID ABI44961 standard; DNA; 12 BP.  
 AC ABI44961;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide primer SEQ ID NO 344934 for detecting SNP TSC0043787.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 344934; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1059 CAATTACACAAA 1070

Dd 1 CAATTACACAAA 12

RESULT 106

ABT14521/c

ID ABT14521 standard; DNA; 12 BP.

AC ABT14521;

DT 03-APR-2003 (first entry)

DE Rhesus monkey P-glycoprotein gene region #2.

KW Rhesus monkey; gene; ds; P-glycoprotein inhibitor; drug bioavailability;  
 KW P-glycoprotein; P-glycoprotein transporter-related disease.

OS Macaca mulatta.

XX WO200274048-A2.

XX 26-SEP-2002.

XX 19-MAR-2002; 2002WO-US008325.

XX 19-MAR-2001; 2001US-0277095P.

XX (GENT-) GENTEST CORP.

XX Crespi CL, Hanscom SR;

XX WPI; 2003-075423/07.

PT Isolated nucleic acid molecule encoding a P-glycoprotein of rhesus  
 PT monkey, useful in assays for evaluating bioavailability of drugs, as well  
 PT as for the optimization or discovery of drugs.

XX Example 1; Page 38; 103pp; English.

CC The invention comprises the amino acid and coding sequence of a rhesus  
 CC monkey (Macaca mulatta) P-glycoprotein and related P-glycoproteins. The  
 CC DNA and protein sequences of the invention are useful in assays for  
 CC evaluating the bioavailability of drugs, as well as the optimization or  
 CC discovery of drugs for the treatment of disease associated with P-  
 CC glycoprotein transporter activity. The present DNA sequence represents  
 CC part of the gene encoding the Rhesus monkey P-glycoprotein

SQ Sequence 12 BP; 2 A; 2 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1440 AGCTGAAAATAC 1451

Dd 12 AGCTGAAAATAC 1

RESULT 107

ACF03767/c

ID ACF03767 standard; RNA; 12 BP.

XX ACF03767;

XX 18-SEP-2003 (first entry)

DE HPIV1 P gene end RNA nucleotide sequence.

XX Parainfluenza virus; human parainfluenza virus 1; HPIV1; HPIV3; MP1V1;  
 KW human parainfluenza virus 3; murine parainfluenza virus 1; BPIV3; PIV;  
 KW bovine parainfluenza virus 3; immunogenic; immune response; pathogen;  
 KW infectious; self-replicating; major nucleocapsid protein; virulence;  
 KW recombinant human parainfluenza virus 1; nucleocapsid phosphoprotein;  
 KW large polymerase protein; vaccine; gene therapy; measles virus;  
 KW infection; immunisation; gene; ss.

OS Human parainfluenza virus 1.

XX WO2003043587-A2.

XX 30-MAY-2003.

XX 21-NOV-2002; 2002WO-US037688.

XX 21-NOV-2001; 2001US-0331961P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Murphy BR, Collins PL, Skiadopoulos MH, Newman JT;

XX WPI; 2003-457567/43.

XX New replicating, recombinant human parainfluenza virus type 1 (rHPIV1)  
 PT comprising parainfluenza virus (PIV) proteins and rHPIV1 (antigenome,  
 PT useful as vaccines against PIV and non-PIV pathogens, e.g. measles or  
 PT mumps viruses.

XX Example 1; Fig 3; 216pp; English.

CC The present invention describes an isolated, infectious, self-  
 CC replicating, recombinant human parainfluenza virus type 1 (HPIV1) (I),  
 CC which comprises a parainfluenza virus (PIV) major nucleocapsid (N)  
 CC protein, a PIV nucleocapsid phosphoprotein (P), a PIV large polymerase  
 CC protein (L), and a partial or complete recombinant HPIV1 genome or  
 CC antigenome. (I) has virucide activity and can be used in vaccines and in  
 CC gene therapy. The recombinant HPIV1, immunogenic compositions, and  
 CC methods from the present invention can be used for eliciting an immune  
 CC response in a subject (i.e. a human subject, preferably a newborn to a  
 CC four-month old human infant) against PIV (specifically HPIV2 and/or  
 CC HPIV3), or for eliciting a polyspecific immune response against multiple  
 CC human PIVs and/or against a human PIV and a non-PIV pathogen.

CC Specifically, they are useful for eliciting an immune response against  
 CC HPIV and measles virus; HPIV1 and HPIV3; HPIV1 or HPIV3, and measles  
 CC virus; or HPIV1 or HPIV3, and RSV. The recombinant HPIV1 or compositions  
 CC can be used for immunising human subjects against PIV and other  
 CC pathogens, e.g. measles virus, subgroup A and subgroup B of RSV, mumps  
 CC virus, human papilloma viruses, type 1 and type 2 human immunodeficiency  
 CC viruses, herpes simplex viruses, cytomegalovirus, rabies virus, Epstein  
 CC Barr virus, filoviruses, bunyaviruses, flaviviruses, alphaviruses, human  
 CC metapneumoviruses, or influenza viruses. ACF03754 to ACF03822 and  
 CC ABR81756 to ABR81811 represent sequences used in the exemplification of  
 CC the present invention

SQ Sequence 12 BP; 2 A; 1 C; 0 G; 0 T; 9 U; 0 Other;

Query Match 0.5%; Score 12; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AAAAGAATTAA 376

|||||||

```

Db      12 AAAAGAGATTAA 1
RESULT 108
ADQ30186
ID      ADQ30186 standard; DNA; 12 BP.
XX
AC      ADQ30186;
XX
DT      09-SEP-2004 (first entry)
XX
DE      Murine VR1 exon 1d transcription factor binding fragment #78.
XX
KW      de; VR1 receptor; vanilloid receptor type 1; modulator;
KW      pain transmission; primary sensory neuron; transcription factor;
KW      detection; MZFL; NPKappaB; NFAT; GATL; sensitivity disorder; analgesia;
KW      hypalgesia; hyperalgesia; neuralgia; myalgia; murine.
XX
OS      Mus sp.
XX
PN      WO2004053120-A2.
XX
PD      24-JUN-2004.
XX
PF      01-DEC-2003; 2003WO-EP013522.
XX
PR      09-DEC-2002; 2002DE-01057421.
XX
PA      (CHEF ) GRUENENTHAL GMBH.
XX
PI      Weihe E, Bieller A, Schaefer MKH;
XX
WPI; 2004-468868/44.
XX
PT      New nucleic acid that modulates expression of the vanilloid receptor-1,
PT      useful for control of pain or sensitivity disorders, comprises sequences
PT      from control regions of the receptor gene.
XX
PS      Disclosure; Page 50; 68pp; German.
XX
CC      This invention describes a novel nucleic acid containing a specific
CC      segment having at least one region that modulates expression of the VR1
CC      (vanilloid receptor type 1) receptor, or a functional derivative, allele
CC      or fragment of this region, or a sequence that hybridizes to it under
CC      standard conditions. The VR1 modulator is derived from one or more of
CC      positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or
CC      44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
CC      pain, particularly in primary sensory neurons. The invention also
CC      describes a vector that contains the VR1 modulator, host cells containing
CC      this vector (other than human germ or embryonal stem cells) and a method
CC      for modulating expression of the VR1 receptor by introducing the
CC      modulator or the vector into a cell that contains the VR1 gene. The
CC      products of the invention are used for detecting a transcription factor
CC      from its binding to a regulatory sequence (or a double-stranded
CC      oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
CC      linked immunosorbent assay, particularly for diagnosis of diseases
CC      associated with overexpression or underexpression of the transcription
CC      factor. The region that modulates VR1 receptor expression includes a
CC      binding site for a transcription factor, e.g. MZFL, NPKappaB, NFAT or
CC      GATL. The nucleic acids of the invention, or vectors containing them,
CC      are used for prevention or treatment of pain, also for treating
CC      sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
CC      neuralgia and myalgia, that are associated with activity of the VR1
CC      receptor. This sequence represents a fragment of murine VR1 exon 1d DNA
CC      which is capable of binding to a transcription factor.
XX
SQ      Sequence 12 BP; 6 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match      0.5%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      138 TAGAGGAAAAGC 149

```

---

```

Db      1 TAGAGGAAAAGC 12
|||||
RESULT 109
ABI34874
ID      ABI34874 standard; DNA; 12 BP.
XX
AC      ABI34874;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 334847 for detecting SNP TSC0038439.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO 18000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single nucleotide polymorphisms and cell
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 334847; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 2 A; 1 C; 2 G; 7 T; 0 U; 0 Other;

Query Match      0.4%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1225 TTCGTTATTAAAG 1236
|||||
Db      1 TTCGTTATTATG 12
|||||
RESULT 110
ABI37478/c
ID      ABI37478 standard; DNA; 12 BP.
XX
AC      ABI37478;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 337461 for detecting SNP TSN00000444

```

```

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 337451; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 7 A; 2 C; 1 G; 2 T; 0 U; 0 Other;
XX Query Match 0.4%; Score 10.4; DB 1; Length 12;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+02;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1225 TTCGTTATTAAAG 1236
XX Db 12 TTCGTTATTATG 1
XX
XX RESULT 111
XX ABI59615/C
XX ID ABI59615 standard; DNA; 12 BP.
XX AC ABI59615;
XX XX 22-FEB-2002 (first entry)
XX DT
XX DE Oligonucleotide primer SEQ ID NO 359588 for detecting SNP TSC0051670.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF
XX PR
XX PA

```

```

PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 359588; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
XX Query Match 0.4%; Score 10.4; DB 1; Length 12;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+02;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1742 ATACGGATTCGTG 1753
XX Db 12 ATACGGATTCGTG 1
XX
XX RESULT 112
XX AAQ31256/C
XX ID AAQ31256 standard; DNA; 10 BP.
XX AC AAQ31256;
XX XX 06-APR-1993 (first entry)
XX DT
XX DE Oligonucleotide d(CTAGxAXxCTAC) (x= deoxyxyl).
XX KW Deoxyxylonucleotide; anti-sense; therapy; antiviral; oligomer; ss.
XX OS Synthetic.
XX PH Key modified_base 5 Location/Qualifiers
XX FT /*tag= a
XX FT /note= "deoxyxylonucleotide A"
XX FT modified_base 6
XX FT /*tag= b
XX FT /note= "deoxyxylonucleotide A"
XX FT modified_base 7
XX FT /*tag= c
XX FT /note= "deoxyxylonucleotide C"
XX PN DE4117186-A.
XX XX 26-NOV-1992.
XX XX 25-MAY-1991; 91DE-04117186.
XX XX 25-MAY-1991; 91DE-04117186.
XX PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX

```

```

PI Seela F, Rosemeyer H, Muehlegger K, Von Der Eltz H;
XX WPI; 1992-399971/49.
XX
XX
XX New oligo-2-deoxy-nucleotide(s) for anti-sense therapy of viral infection
PT - contain 2-deoxy-beta-D-threo-penta-furanosyl gps., which partly or
PT wholly replace the 2-deoxy-beta-D-erythro-penta-furanosyl moieties.
XX
XX Example 11a; Page 8; 15pp; German.
XX
XX Example 11a describes the solid phase synthesis of this oligonucleotide.
CC Oligonucleotides contg. 2-deoxy-beta-D-threo-pentofuranosyl gps. are not
CC enzymatically degraded in eukaryotic cells, are simple to prepare and can
CC be used as antivirals according to the anti-sense principle
XX
XX Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2147 GTAGTTCTAC 2156
DB 10 GTAGTTCTAC 1
RESULT 113
AAQ97099
ID AAQ97099 standard; DNA; 10 BP.
XX
XX AAQ97099;
AC
XX
XX 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 LTR nucleotide deletion 81.
DE
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO9521912-A1.
PN
XX
XX 17-AUG-1995.
PD
XX
XX 14-FEB-1995; 95WO-AU0000063.
PF
XX
XX 14-FEB-1994; 94AU-00003864.
PR
XX 21-FEB-1994; 94AU-00004002.
PR
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA
XX (AURE-) AUSTRALIAN RED CROSS SOC.
PA
XX
XX Deacon NJ, Learmont JC, McPhee DA, Crowe S, Cooper D;
PI WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 14; Page 197; 301pp; English.
PS
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1233 TTAAGCCTCA 1242
DB 1 TTAAGCCTCA 10
RESULT 115
AAQ96807/c
ID AAQ96807 standard; DNA; 10 BP.
XX

```

```

SQ Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1232 TTAAGCCTCA 1241
DB 1 TTAAGCCTCA 10
RESULT 114
AAQ97100
ID AAQ97100 standard; DNA; 10 BP.
XX
XX AAQ97100;
AC
XX
XX 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 LTR nucleotide deletion 82.
DE
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO9521912-A1.
PN
XX
XX 17-AUG-1995.
PD
XX
XX 14-FEB-1995; 95WO-AU0000063.
PF
XX
XX 14-FEB-1994; 94AU-00003864.
PR
XX 21-FEB-1994; 94AU-00004002.
PR
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA
XX (AURE-) AUSTRALIAN RED CROSS SOC.
PA
XX
XX Deacon NJ, Learmont JC, McPhee DA, Crowe S, Cooper D;
PI WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 14; Page 197; 301pp; English.
PS
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1233 TAAGCCTCAA 1242
DB 1 TAAGCCTCAA 10
RESULT 115
AAQ96807/c
ID AAQ96807 standard; DNA; 10 BP.
XX

```



```

AC AAQ96807;
XX
XX
DT 16-OCT-2003 (revised)
DT 26-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 402.
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
XX Human immunodeficiency virus 1.
XX
XX WO9521912-A1.
XX
XX 17-AUG-1995.
XX
XX 14-FEB-1995; 95WO-AU000063.
XX
XX 14-FEB-1994; 94AU-00003864.
XX
XX 21-FEB-1994; 94AU-00004002.
XX
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX
XX infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 193; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX
XX resulting avirulent HIV strains are still capable of inducing an immune
XX
XX response in humans, and enable the generation of therapeutic, diagnostic
XX
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX
XX standardise OS field)
XX
XX Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 CAGTGGATAT 224
DB 10 CAGTGGATAT 1

RESULT 116
AAQ97017
ID AAQ97017 standard; DNA; 10 BP.
XX
XX AAQ97017;
XX
XX 16-OCT-2003 (revised)
XX
XX 26-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 612.
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
XX Human immunodeficiency virus 1.
XX
XX WO9521912-A1.
XX
XX 17-AUG-1995.
XX

```

```

PF 14-FEB-1995; 95WO-AU000063.
XX
XX 14-FEB-1994; 94AU-00003864.
XX
XX 21-FEB-1994; 94AU-00004002.
XX
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX
XX infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 196; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX
XX resulting avirulent HIV strains are still capable of inducing an immune
XX
XX response in humans, and enable the generation of therapeutic, diagnostic
XX
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX
XX standardise OS field)
XX
XX Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GAACTGCTGA 737
DB 1 GAACTGCTGA 10

RESULT 117
AAT29315
ID AAT29315 standard; DNA; 10 BP.
XX
XX AAT29315;
XX
XX 25-MAR-2003 (revised)
XX
XX 28-JUN-1996 (first entry)
XX
XX 5'-primer for mammalian G-protein coupled receptor coding sequences.
XX
XX 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;
XX
XX characterisation; biological samples; PCR amplification; indexing;
XX
XX identification; cloning; analysis; genes; genome mapping;
XX
XX disease diagnosis; ss.
XX
XX Synthetic.
XX
XX WO9531574-A1.
XX
XX 23-NOV-1995.
XX
XX 12-MAY-1995; 95WO-US006032.
XX
XX 16-MAY-1994; 94US-00242887.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Lopeznieto CE, Nigam SK;
XX
XX WPI; 1996-010958/01.
XX
XX Characterisation of nucleotide sequences using primer pairs - by PCR
XX
XX amplification and indexing of amplification prods. w.r.t. primers used
XX

```

PT for genome mapping and disease diagnosis.  
 PS Claim 46; Page 55; 72pp; English.  
 XX The 5'-primers AAT29262-382, and the complementary 3'-primers derived  
 CC from them, which target mammalian G-protein coupled receptor coding  
 CC sequences, together comprise a PCR primer kit. The kit is used in a new  
 CC method for the characterisation of nucleic acid sequences obtd. from  
 CC mammalian biological samples, which comprises PCR amplification and  
 CC indexing of the prods. w.r.t the primer pair that hybridised to its  
 CC delineating subsequences. The method may be used in the identification,  
 CC cloning and analysis of genes, e.g. in genome mapping, and disease  
 CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 406 CTCATCATC 415  
 Db 1 CTCATCATC 10  
 RESULT 118  
 AAV40086/c  
 ID AAV40086 standard; DNA; 10 BP.  
 XX  
 AC AAV40086;  
 XX  
 DT 09-NOV-1998 (first entry)  
 XX  
 DE Oligonucleotide P11 from WO9829453 Example 3.  
 XX  
 KW Drug; cell membrane-directed drug; phospholipid; lipid bilayer;  
 KW cell cortex; blood coagulation; inflammation; immunological disorder;  
 KW PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9829453-A1.  
 XX  
 XX 09-JUL-1998.  
 XX  
 XX 05-JAN-1998; 98WO-JP000002.  
 XX  
 XX 27-DEC-1996; 96JP-00359053.  
 XX  
 XX (MOCH ) MOCHIDA PHARM CO LTD.  
 XX  
 XX Kuriyama S, Hasegawa T;  
 XX WPI; 1998-388051/33.  
 XX  
 XX Drugs containing peptide(s) with specific affinity to phospholipid(s) -  
 PT such as phosphatidyl serine, for treatment of blood coagulation,  
 PT inflammatory and immunological disorders.  
 XX  
 XX Example 4; Fig 5; 117pp; Japanese.  
 PS  
 CC The present invention describes drug compositions which contain as an  
 CC active component a peptide which has specific affinity to particular  
 CC phospholipids (such as phosphatidyl ethanolamine or phosphatidyl serine),  
 CC especially to phospholipids which constitute a lipid bilayer of cellular  
 CC cortex and of which the concentration in the bilayer increases in cells  
 CC which are abnormal (e.g. through injury, denaturation or activation). In  
 CC particular, the peptide contains a sequence having phospholipid affinity  
 CC and a structure of formula (I): (A1)a-(A2)b-(A3)c, where (A1) is one of  
 CC two specific sequences (see AAW69516 and AAW69519), (A2) and (A3) are  
 CC TRYLRIRPQSHVQIALR, LRYLRIRPQSHVQIALR (see AAW69517) or MEVLGCEAQNLY  
 CC (see AAW69518); a = 0-5; b = 1-5, and c = 0-5. Preferred are the formulae

CC A1-A2-A3, A2-A3, A2-A2-A3, A2-A2 A2 A3 or A2 A2 (especially A2 A2 A1, A.  
 CC A2-A2-A3 or A2-A2). The sequence is linked to a peptide such as a blood  
 CC factor, especially thrombo-modulin, urina-statin or membrane cofactor  
 CC protein. The drugs are used for the treatment and prevention of diseases  
 CC involving blood coagulation, inflammatory and immunological disorders.  
 CC The present sequence represents an oligonucleotide used in an example  
 CC from the present invention  
 XX  
 SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 989 CTCACGAATG 998  
 Db 10 CTCACGAATG 1  
 RESULT 119  
 AAV34973  
 ID AAV34973 standard; DNA; 10 BP.  
 XX  
 AC AAV34973;  
 XX  
 DT 13-OCT-1998 (first entry)  
 XX  
 DE Synthetic Agaricus bisporus RAPD primer.  
 XX  
 KW Random amplified polymorphic DNA; primer; mushroom; RAPD; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9821975-A1.  
 XX  
 PD 28-MAY-1998.  
 XX  
 PF 19-NOV-1996; 96WO-US018686.  
 XX  
 PR 19-NOV-1996; 96WO-US018686.  
 XX  
 XX (AMYC-) AMYCEL INC.  
 XX  
 XX Loftus MG, Lodder SC, Legg EJ;  
 XX WPI; 1998-312054/27.  
 XX  
 XX New strains of Agaricus bisporus with improved cap whiteness - compared  
 XX with the U1 strain but retaining other desirable features of this strain.  
 XX  
 XX Disclosure; Page 10; 26pp; English.  
 XX  
 XX The sequence is that of an RAPD (random amplified DNA) primer which was  
 XX used in the isolation of an Agaricus bisporus mushroom strain which has  
 XX whiter caps, less scaling than known strains, particularly for mushrooms  
 XX produced in the first break, so it is more valuable (suitable for  
 XX marketing fresh rather than canning). It also retains the desirable  
 XX characteristics (good cap shape and shelf life, thick stem and veil) of  
 XX the U1 strain  
 XX  
 SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0;  
 QY 986 CAGCTCACGA 995  
 Db 1 CAGCTCACGA 10  
 RESULT 120  
 AAV50147/c

```

ID AAV50147 standard; DNA; 10 BP.
XX
AC AAV50147;
XX
DT 21-OCT-1998 (first entry)
XX
DE Yeast tag for additional NORF chromosome 10 tag position 392099.
XX
KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW eukaryotic cell; antifungal; SAGE tag; gene expression;
KW serial analysis of gene expression; probe; ss.
XX
OS Saccharomyces cerevisiae.
OS Synthetic.
XX
PN WO9832847-A2.
XX
PD 30-JUL-1998.
XX
PF 22-JAN-1998; 98WO-US001216.
XX
PR 23-JAN-1997; 97US-0035917P.
XX
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 1998-427943/36.
XX
XX
PT Yeast transcriptome - useful for modulating eukaryotic cell, for
PT screening antifungal agents, and for identifying genes in cell cycle
PT progression.
XX
PS Claim 1; Page 24; 44pp; English.
XX
CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
CC involved in cell cycle progression selected from the group of
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC tags for highly expressed genes and NORF genes are given in AAV50051 to
CC AAV50345. The present invention describes: (1) a method of using yeast
CC genes to modulate the cell cycle which comprises administering to a cell
CC an isolated DNA molecule comprising a yeast gene which is involved in
CC cell cycle progression selected from differentially expressed genes (SAGE
CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate
CC antifungal drugs which comprises contacting a test substance with a yeast
CC cell and monitoring expression of a yeast gene which is involved in cell
CC cycle progression; (3) a method of identifying human genes which are
CC involved in cell cycle progression which comprises hybridizing a probe
CC comprising at least 10 contiguous nucleotides of a yeast gene which is
CC differentially expressed between at least 2 phases selected from the log
CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
CC the phase in the cell cycle, where the probe comprises at least 14
CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
CC AAV50345), or as an array of probes on a solid support
XX
SQ Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1056 GTCCAAATTAC 1065
Db 10 GTCCAAATTAC 1

RESULT 121
AAV50073/c
ID AAV50073 standard; DNA; 10 BP.
XX
AC AAV50073;
XX
DT 21-OCT-1998 (first entry)
XX
DE Yeast tag for additional NORF chromosome 11 tag position 14426.
XX
KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW eukaryotic cell; antifungal; SAGE tag; gene expression;

```

```

XX Yeast tag for highly expressed gene PYK1.
DE
XX Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW eukaryotic cell; antifungal; SAGE tag; gene expression;
KW serial analysis of gene expression; probe; ss.
XX
OS Saccharomyces cerevisiae.
OS Synthetic.
XX
PN WO9832847-A2.
XX
PD 30-JUL-1998.
XX
PF 22-JAN-1998; 98WO-US001216.
XX
PR 23-JAN-1997; 97US-0035917P.
XX
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 1998-427943/36.
XX
XX
PT Yeast transcriptome - useful for modulating eukaryotic cell, for
PT screening antifungal agents, and for identifying genes in cell cycle
PT progression.
XX
PS Claim 1; Page 21; 44pp; English.
XX
CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
CC involved in cell cycle progression selected from the group of
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC tags for highly expressed genes and NORF genes are given in AAV50051 to
CC AAV50345. The present invention describes: (1) a method of using yeast
CC genes to modulate the cell cycle which comprises administering to a cell
CC an isolated DNA molecule comprising a yeast gene which is involved in
CC cell cycle progression selected from differentially expressed genes (SAGE
CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate
CC antifungal drugs which comprises contacting a test substance with a yeast
CC cell and monitoring expression of a yeast gene which is involved in cell
CC cycle progression; (3) a method of identifying human genes which are
CC involved in cell cycle progression which comprises hybridizing a probe
CC comprising at least 10 contiguous nucleotides of a yeast gene which is
CC differentially expressed between at least 2 phases selected from the log
CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
CC the phase in the cell cycle, where the probe comprises at least 14
CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
CC AAV50345), or as an array of probes on a solid support
XX
SQ Sequence 10 BP; 0 A; 1 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 970 AAAGAAAAAC 979
Db 10 AAAGAAAAAC 1

RESULT 122
AAV50301/c
ID AAV50301 standard; DNA; 10 BP.
XX
AC AAV50301;
XX
DT 21-OCT-1998 (first entry)
XX
DE Yeast tag for additional NORF chromosome 11 tag position 14426.
XX
KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW eukaryotic cell; antifungal; SAGE tag; gene expression;

```

```

KW serial analysis of gene expression; probe; ss.
XX Saccharomyces cerevisiae.
OS Synthetic.
PN WO9832847-A2.
XX 30-JUL-1998.
XX 22-JAN-1998; 98WO-US001216.
XX 23-JAN-1997; 97US-0035917P.
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 1998-427943/36.
XX Yeast transcriptome - useful for modulating eukaryotic cell, for
PT screening antifungal agents, and for identifying genes in cell cycle
PT progression.
XX Claim 1; Page 27; 44pp; English.
XX Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
CC involved in cell cycle progression selected from the group of
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC tags for highly expressed genes and NORF genes are given in AAV50051 to
CC AAV50345. The present invention describes: (1) a method of using yeast
CC genes to modulate the cell cycle which comprises administering to a cell
CC an isolated DNA molecule comprising a yeast gene which is involved in
CC cell cycle progression selected from differentially expressed genes (SAGE
CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate
CC antifungal drugs which comprises contacting a test substance with a yeast
CC cell and monitoring expression of a yeast gene which is involved in cell
CC cycle progression; (3) a method of identifying human genes which are
CC comprising at least 10 contiguous nucleotides of a yeast gene which is
CC differentially expressed between at least 2 phases selected from the log
CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
CC the phase in the cell cycle, where the probe comprises at least 14
CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
CC AAV50345), or as an array of probes on a solid support
XX Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1396 ATCAATAGAG 1405
DB 10 ATCAATAGAG 1
RESULT 123
AAV50338
ID AAV50338 standard; DNA; 10 BP.
XX AAV50338;
XX AAV50338;
XX 21-OCT-1998 (first entry)
DE Yeast tag for additional NORF chromosome 15 tag position 882567.
XX Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW eukaryotic cell; antifungal; SAGE tag; gene expression;
KW serial analysis of gene expression; probe; ss.
XX Saccharomyces cerevisiae.
OS Synthetic.
PN WO9832847-A2.
XX 30-JUL-1998.
XX 22-JAN-1998; 98WO-US001216.
XX 23-JAN-1997; 97US-0035917P.
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 1998-427943/36.
XX Yeast transcriptome - useful for modulating eukaryotic cell, for
PT screening antifungal agents, and for identifying genes in cell cycle
PT progression.
XX Claim 1; Page 27; 44pp; English.
XX Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
CC involved in cell cycle progression selected from the group of
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC tags for highly expressed genes and NORF genes are given in AAV50051 to
CC AAV50345. The present invention describes: (1) a method of using yeast
CC genes to modulate the cell cycle which comprises administering to a cell
CC an isolated DNA molecule comprising a yeast gene which is involved in
CC cell cycle progression selected from differentially expressed genes (SAGE
CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate
CC antifungal drugs which comprises contacting a test substance with a yeast
CC cell and monitoring expression of a yeast gene which is involved in cell
CC cycle progression; (3) a method of identifying human genes which are
CC comprising at least 10 contiguous nucleotides of a yeast gene which is
CC differentially expressed between at least 2 phases selected from the log
CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
CC the phase in the cell cycle, where the probe comprises at least 14
CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
CC AAV50345), or as an array of probes on a solid support
XX Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1396 ATCAATAGAG 1405
DB 10 ATCAATAGAG 1
RESULT 123
AAV50338
ID AAV50338 standard; DNA; 10 BP.
XX AAV50338;
XX AAV50338;
XX 21-OCT-1998 (first entry)
DE Human interleukin-1 forward primer OP117.
XX Human; cardiovascular disease; atherosclerosis; ischaemia; restenosis;
KW reperfusion; hypertension; arterial inflammation; diagnosis; rchd528;
KW primer; ss.
XX Synthetic.
OS Homo sapiens.
XX US5849578-A.
XX 15-DEC-1998.
XX 15-MAR-1996; 96US-00616844.

```

```

XX 10-FEB-1995; 95US-00386844.
PR 07-JUN-1995; 95US-00458873.
PR 09-FEB-1996; 96US-00599654.
XX (MILL-) MILLENNIUM PHARM INC.
XX Falb DA;
XX WPI; 1999-069743/06.
XX DNA encoding rchd528 polypeptide - associated with cardiovascular
PT disease.
XX Example; Col 101; 122pp; English.
XX The present invention describes rchd528 protein. A method has been
CC developed for producing the rchd528 gene product. The present invention
CC also describes methods and compositions for the treatment and diagnosis
CC of cardiovascular diseases, including: atherosclerosis; ischaemia;
CC restenosis; reperfusion; hypertension; and arterial inflammation. The
CC present sequence represents a primer used in an example from the present
CC invention
XX
SQ Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040
DB 10 CATCACCACC 1

RESULT 125
AAAX26264/c
ID AAX26264 standard; DNA; 10 BP.
AC AAX26264;
XX
XX 24-MAY-1999 (first entry)
DE Forward primer OP117.
XX
XX Fingerprinting gene; rchd502; transmembrane protein; cardiovascular;
KW fingerprint/target gene; up-regulated; endothelial cell; shear-stress;
KW atherosclerosis; ischemia; reperfusion; hypertension; restenosis; human;
KW PCR primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX US5882925-A.
XX
XX 16-MAR-1999.
PD
XX
XX 09-FEB-1996; 96US-00599654.
XX
XX 10-FEB-1995; 95US-00386844.
XX
XX 07-JUN-1995; 95US-00485573.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA Falb DA;
XX
XX WPI; 1999-214071/18.
XX
XX New polynucleotides consisting of residues 1-1929 of the rchd502 gene -
PT are differentially expressed in cardiovascular disease states, and can
PT therefore be used to treat and diagnose cardiovascular diseases.
XX
XX Disclosure; Col 10; 121pp; English.

```

```

XX The invention relates to a rchd502 target/fingerprint gene encoding a
CC transmembrane protein. The invention provides cDNAs contained in plasmids
CC pFCHD502SF (ATCC 69981) and pFCHD502SJ (ATCC 69982) that encode the
CC rchd502 polypeptide, and are differentially expressed in cardiovascular
CC disease states. Cultured genetically engineered host cell containing the
CC rchd502 polynucleotides in operative association with a nucleoside
CC regulatory element are used for producing a polypeptide rchd502 gene
CC product. Identifying that the fingerprint/target gene rchd502 is
CC differentially expressed (up-regulated) by endothelial cells subjected to
CC shear-stress, provides a tool for the diagnosis and treatment of
CC cardiovascular disease e.g. atherosclerosis, ischemia/reperfusion,
CC hypertension, restenosis. The fingerprint gene is useful for testing the
CC efficacy of candidate drugs in basic research and in clinical trials and
CC in imaging of a diseased cardiovascular tissue. The gene may also be used
CC in screening for ligands of target gene product receptor domains, as well
CC as antagonists of the ligand-receptor interaction
XX
SQ Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040
DB 10 CATCACCACC 1

RESULT 126
AAZ78100
ID AAZ78100 standard; DNA; 10 BP.
XX
XX AAZ78100;
XX
XX 10-APR-2000 (first entry)
DE Human dendritic cell SAGE tag, SEQ ID NO:528.
XX
XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL; antitumor; ss.
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
XX Homo sapiens.
XX
XX WO9965924-A2.
XX
XX 23-DEC-1999.
PD
XX
XX 18-JUN-1999; 99WO-US013800.
XX
XX 19-JUN-1998; 98US-0089833P.
XX
XX 19-JUN-1998; 98US-0089844P.
XX
XX 19-JUN-1998; 98US-0089853P.
XX
XX 19-JUN-1998; 98US-0089878P.
XX
XX 19-JUN-1998; 98US-0089911P.
XX
XX 19-JUN-1998; 98US-0089921P.
XX
XX 19-JUN-1998; 98US-0089933P.
XX
XX 19-JUN-1998; 98US-0089934P.
XX
XX 19-JUN-1998; 98US-0089977P.
XX
XX 19-JUN-1998; 98US-0089997P.
XX
XX 19-JUN-1998; 98US-0090000P.
XX
XX 19-JUN-1998; 98US-0090035P.
XX
XX 19-JUN-1998; 98US-0090036P.
XX
XX 19-JUN-1998; 98US-0090039P.
XX
XX 19-JUN-1998; 98US-0090040P.
XX
XX 19-JUN-1998; 98US-0090041P.
XX
XX 19-JUN-1998; 98US-0090042P.
XX
XX 19-JUN-1998; 98US-0090043P.
XX
XX 19-JUN-1998; 98US-0090044P.
XX
XX 19-JUN-1998; 98US-0090045P.
XX
XX 19-JUN-1998; 98US-0090047P.

```

```

PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 80; 130pp; English.
XX
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T-cell receptors is alone
XX insufficient to activate a robust cytotoxic immune response that can lyse
XX the tumour cells, immunostimulatory cofactors also being required for
XX efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX sequences identified using the SAGE tags have several potential uses.
XX They may be used in vaccines to induce an immune response, particularly
XX against a tumour antigen; to modulate the genotype of an APC; to screen
XX for agents that modulate expression of differentially expressed genes in
XX an APC; and as hybridisation probes/amplification primers for the
XX diagnosis, prognosis and monitoring of diseases related to abnormal
XX expression of these genes. Detection of the dendritic cell differentially
XX expressed genes, or of their encoded proteins, can be used to identify
XX cells as belonging to the monocyte lineage. Cells containing these genes
XX can be used in active immunotherapy (or to stimulate production of a
XX population of antigen-specific effector cells) and vectors containing
XX APC-associated costimulatory factors ensures adequate antigen
XX presentation to endogenous APCs and upregulates the APCs for the
XX presentation of co-stimulatory signals, migration to T cell-rich sites,
XX secretion of T cell growth factors and secretion of chemokines for
XX recruitment of immune effector cells
XX
XX Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred.No.1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1132 AGAATATCAG 1141
XX |||||
XX 1 AGAATATCAG 10
XX
XX RESULT 127
XX AAZ78164
XX ID AAZ78164 standard; DNA; 10 BP.
XX AC AAZ78164;
XX XX
XX 10-APR-2000 (first entry)

```

```

XX DE Human dendritic cell SAGE tag, SEQ ID NO:592.
XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX KW APC; monocyte-derived dendritic cell; differential gene expression;
XX KW immunostimulatory cofactor; costimulatory factor; CTL;
XX KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX OS Homo sapiens.
XX PN WO9965924-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013800.
XX PR 19-JUN-1998; 98US-0089833P.
XX PR 19-JUN-1998; 98US-0089844P.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089878P.
XX PR 19-JUN-1998; 98US-0089991P.
XX PR 19-JUN-1998; 98US-0089992P.
XX PR 19-JUN-1998; 98US-0089993P.
XX PR 19-JUN-1998; 98US-0089994P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0089999P.
XX PR 19-JUN-1998; 98US-0090000P.
XX PR 19-JUN-1998; 98US-0090003P.
XX PR 19-JUN-1998; 98US-0090006P.
XX PR 19-JUN-1998; 98US-0090007P.
XX PR 19-JUN-1998; 98US-0090008P.
XX PR 08-DEC-1998; 98US-0111715P.
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
XX WPI; 2000-106077/09.
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
XX Claim 1; Page 82; 130pp; English.
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T cell receptors is alone
XX insufficient to activate a robust cytotoxic immune response that can lyse
XX the tumour cells, immunostimulatory cofactors also being required for

```

CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
 CC sequences identified using the SAGE tags have several potential uses.  
 CC They may be used in vaccines to induce an immune response, particularly  
 CC against a tumour antigen; to modulate the genotype of an APC; to screen  
 CC for agents that modulate expression of differentially expressed genes in  
 CC an APC; and as hybridisation probes/amplification primers for the  
 CC diagnosis, prognosis and monitoring of diseases related to abnormal  
 CC expression of these genes. Detection of the dendritic cell differentially  
 CC expressed genes, or of their encoded proteins, can be used to identify  
 CC cells as belonging to the monocyte lineage. Cells containing these genes  
 CC can be used in active immunotherapy (or to stimulate production of a  
 CC population of antigen-specific effector cells) and vectors containing  
 CC them are used in gene therapy. Co-administration of tumour antigens and  
 CC APC-associated costimulatory factors ensures adequate antigen  
 CC presentation to endogenous APCs and upregulates the APCs for the  
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
 CC secretion of T cell growth factors and secretion of chemokines for  
 CC recruitment of immune effector cells  
 XX  
 SQ Sequence 10 BP; 6 A; 0 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 933 AGGAAAGAT 942

Db |||||  
 1 AGGAAAGAT 10

RESULT 128

AAZ79143/C

ID AAZ79143 standard; DNA; 10 BP.

XX AC AAZ79143;

XX 10-APR-2000 (first entry)

DE Human dendritic cell SAGE tag, SEQ ID NO:1571.

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
 KW APC; monocyte-derived dendritic cell; differential gene expression;  
 KW immunostimulatory cofactor; costimulatory factor; CTL; antitumor;  
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

OS Homo sapiens.

XX WO9965924-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

XX 19-JUN-1998; 98US-0089833P.

XX 19-JUN-1998; 98US-0089844P.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089878P.

XX 19-JUN-1998; 98US-0089919P.

XX 19-JUN-1998; 98US-0089922P.

XX 19-JUN-1998; 98US-0089933P.

XX 19-JUN-1998; 98US-0089944P.

XX 19-JUN-1998; 98US-0089977P.

XX 19-JUN-1998; 98US-0089999P.

XX 19-JUN-1998; 98US-0090000P.

XX 19-JUN-1998; 98US-0090035P.

XX 19-JUN-1998; 98US-0090036P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX 19-JUN-1998; 98US-0090041P.

XX 19-JUN-1998; 98US-0090042P.

XX 19-JUN-1998; 98US-0090043P.

XX 19-JUN-1998; 98US-0090044P.

XX 19-JUN-1998; 98US-0090045P.

PR 19-JUN-1998; 98US-0090047P.  
 PR 19-JUN-1998; 98US-0090048P.  
 PR 19-JUN-1998; 98US-0090072P.  
 PR 19-JUN-1998; 98US-0090076P.  
 PR 19-JUN-1998; 98US-0090077P.  
 PR 19-JUN-1998; 98US-0090078P.  
 PR 19-JUN-1998; 98US-0090079P.  
 PR 19-JUN-1998; 98US-0090080P.  
 PR 08-DEC-1998; 98US-0111715P..

(GENZ ) GENZYME CORP.

(ROBE/) ROBERTS B L.

(SHAN/) SHANKARA S.

Roberts BL, Shankara S;

WPI; 2000-106077/09.

Isolated polynucleotides differentially expressed in antigen-presenting  
 cells, useful in gene vaccines against cancer.

Claim 1; Page 110; 130pp; English.

Sequences AAZ77573-279709 represent SAGE (serial analysis of gene  
 expression) tags used to identify mRNA transcripts encoding  
 immunostimulatory cofactor proteins which are preferentially or  
 differentially expressed in monocyte-derived dendritic cells compared  
 with monocytes. Some of the transcripts correspond to known genes or ESTs  
 (expressed sequence tags) which were previously unknown to be  
 preferentially or differentially expressed in dendritic cells.  
 Other transcripts correspond to novel genes. Antigen-presenting cell;  
 (APC)-associated costimulatory factors play an important role in the  
 activation of the cytotoxic immune response, particularly against tumour  
 cells. Tumour antigen presentation via the MHC (major histocompatibility  
 complex) and subsequent recognition by T-cell receptors is alone  
 insufficient to activate a robust cytotoxic immune response that can lyse  
 the tumour cells, immunostimulatory cofactors also being required for  
 efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
 sequences identified using the SAGE tags have several potential uses.  
 They may be used in vaccines to induce an immune response, particularly  
 against a tumour antigen; to modulate the genotype of an APC; to screen  
 for agents that modulate expression of differentially expressed genes in  
 an APC; and as hybridisation probes/amplification primers for the  
 diagnosis, prognosis and monitoring of diseases related to abnormal  
 expression of these genes. Detection of the dendritic cell differentially  
 expressed genes, or of their encoded proteins, can be used to identify  
 cells as belonging to the monocyte lineage. Cells containing these genes  
 can be used in active immunotherapy (or to stimulate production of a  
 population of antigen-specific effector cells) and vectors containing  
 them are used in gene therapy. Co-administration of tumour antigens and  
 APC-associated costimulatory factors ensures adequate antigen  
 presentation to endogenous APCs and upregulates the APCs for the  
 presentation of co-stimulatory signals, migration to T cell-rich sites,  
 secretion of T cell growth factors and secretion of chemokines for  
 recruitment of immune effector cells

XX Sequence 10 BP; 2 A; 0 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1633 ATACATCAA 1642

Db |||||  
 10 ATACATCAA 1

RESULT 129

AAZ79622/C

ID AAZ79622 standard; DNA; 10 BP.

XX AAZ79622;

XX

DT 10-APR-2000 (first entry)  
 XX Human dendritic cell SAGE tag, SEQ ID NO:2050.  
 XX  
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
 KW APC; monocyte-derived dendritic cell; differential gene expression;  
 KW immunostimulatory cofactor; costimulatory factor; CTL;  
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9965924-A2.  
 XX  
 PD 23-DEC-1999.  
 XX  
 PF 18-JUN-1999; 99WO-US013800.  
 XX  
 PR 19-JUN-1998; 98US-0089833P.  
 PR 19-JUN-1998; 98US-0089844P.  
 PR 19-JUN-1998; 98US-0089853P.  
 PR 19-JUN-1998; 98US-0089878P.  
 PR 19-JUN-1998; 98US-0089911P.  
 PR 19-JUN-1998; 98US-0089922P.  
 PR 19-JUN-1998; 98US-0089933P.  
 PR 19-JUN-1998; 98US-0089954P.  
 PR 19-JUN-1998; 98US-0089977P.  
 PR 19-JUN-1998; 98US-0089999P.  
 PR 19-JUN-1998; 98US-0090000P.  
 PR 19-JUN-1998; 98US-0090035P.  
 PR 19-JUN-1998; 98US-0090036P.  
 PR 19-JUN-1998; 98US-0090039P.  
 PR 19-JUN-1998; 98US-0090040P.  
 PR 19-JUN-1998; 98US-0090041P.  
 PR 19-JUN-1998; 98US-0090042P.  
 PR 19-JUN-1998; 98US-0090043P.  
 PR 19-JUN-1998; 98US-0090044P.  
 PR 19-JUN-1998; 98US-0090045P.  
 PR 19-JUN-1998; 98US-0090047P.  
 PR 19-JUN-1998; 98US-0090048P.  
 PR 19-JUN-1998; 98US-0090072P.  
 PR 19-JUN-1998; 98US-0090076P.  
 PR 19-JUN-1998; 98US-0090077P.  
 PR 19-JUN-1998; 98US-0090078P.  
 PR 19-JUN-1998; 98US-0090079P.  
 PR 19-JUN-1998; 98US-0090080P.  
 PR 08-DEC-1998; 98US-0111715P.  
 XX  
 PA (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.  
 XX  
 PI Roberts BL, Shankara S;  
 XX  
 XX WPI; 2000-106077/09.  
 XX  
 XX Isolated polynucleotides differentially expressed in antigen-presenting  
 PT cells, useful in gene vaccines against cancer.  
 XX  
 XX Claim 1; Page 123; 130pp; English.  
 PS  
 XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene  
 CC expression) tags used to identify mRNA transcripts encoding  
 CC immunostimulatory cofactor proteins which are preferentially or  
 CC differentially expressed in monocyte-derived dendritic cells compared  
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
 CC (expressed sequence tags) which were previously unknown to be  
 CC preferentially or differentially expressed in dendritic cells, while  
 CC other transcripts correspond to novel genes. Antigen-presenting cell  
 CC (APC)-associated costimulatory factors play an important role in the  
 CC activation of the cytotoxic immune response, particularly against tumour  
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
 CC complex) and subsequent recognition by T-cell receptors is alone  
 CC insufficient to activate a robust cytotoxic immune response that can lyse

CC the tumour cells, immunostimulatory cofactors also being required for  
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
 CC sequences identified using the SAGE tags have several potential uses  
 CC They may be used in vaccines to induce an immune response, particularly  
 CC against a tumour antigen; to modulate the genotype of an APC; to screen  
 CC for agents that modulate expression of differentially expressed genes in  
 CC an APC; and as hybridisation probes/amplification primers for the  
 CC diagnosis, prognosis and monitoring of diseases related to abnormal  
 CC expression of these genes. Detection of the binding of differentially  
 CC expressed genes, or of their encoded proteins, can be used to identify  
 CC cells as belonging to the monocyte lineage. Cells containing these genes  
 CC can be used in active immunotherapy. The expression of these genes in a  
 CC population of antigen-specific effector cells, and various other cells,  
 CC them are used in gene therapy. To administer the genes to a cell, the  
 CC APC-associated costimulatory factors ensure adequate presentation of the  
 CC presentation to endogenous APCs and upregulates the APCs for the  
 CC presentation of co-stimulatory signals, migration to T cell rich areas,  
 CC secretion of T cell growth factors and secretion of chemokines for  
 CC recruitment of immune effector cells  
 XX  
 SQ Sequence 10 BP; 5 A; 1 C; 1 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1754 TGATTACATT 1763  
 Db 10 TGATTACATT 1  
 RESULT 130  
 AAZ77795/c  
 ID AAZ77795 standard; DNA; 10 BP.  
 XX  
 AC AAZ77795;  
 XX  
 XX 10-APR-2000 (first entry)  
 XX  
 DE Human dendritic cell SAGE tag, SEQ ID NO:223.  
 XX  
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
 KW APC; monocyte-derived dendritic cell; differential gene expression;  
 KW immunostimulatory cofactor; costimulatory factor; CTL;  
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9965924-A2.  
 XX  
 PD 23-DEC-1999.  
 XX  
 PF 18-JUN-1999; 99WO-US013800.  
 XX  
 PR 19-JUN-1998; 98US-0089833P.  
 PR 19-JUN-1998; 98US-0089844P.  
 PR 19-JUN-1998; 98US-0089853P.  
 PR 19-JUN-1998; 98US-0089878P.  
 PR 19-JUN-1998; 98US-0089911P.  
 PR 19-JUN-1998; 98US-0089922P.  
 PR 19-JUN-1998; 98US-0089933P.  
 PR 19-JUN-1998; 98US-0089954P.  
 PR 19-JUN-1998; 98US-0089977P.  
 PR 19-JUN-1998; 98US-0089999P.  
 PR 19-JUN-1998; 98US-0090000P.  
 PR 19-JUN-1998; 98US-0090035P.  
 PR 19-JUN-1998; 98US-0090036P.  
 PR 19-JUN-1998; 98US-0090039P.  
 PR 19-JUN-1998; 98US-0090040P.  
 PR 19-JUN-1998; 98US-0090041P.  
 PR 19-JUN-1998; 98US-0090042P.  
 PR 19-JUN-1998; 98US-0090043P.  
 PR 19-JUN-1998; 98US-0090044P.  
 PR 19-JUN-1998; 98US-0090045P.  
 PR 19-JUN-1998; 98US-0090047P.  
 PR 19-JUN-1998; 98US-0090048P.  
 PR 19-JUN-1998; 98US-0090072P.  
 PR 19-JUN-1998; 98US-0090076P.  
 PR 19-JUN-1998; 98US-0090077P.  
 PR 19-JUN-1998; 98US-0090078P.  
 PR 19-JUN-1998; 98US-0090079P.  
 PR 19-JUN-1998; 98US-0090080P.  
 PR 08-DEC-1998; 98US-0111715P.  
 XX  
 PA (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.  
 XX  
 PI Roberts BL, Shankara S;  
 XX  
 XX WPI; 2000-106077/09.  
 XX  
 XX Isolated polynucleotides differentially expressed in antigen-presenting  
 PT cells, useful in gene vaccines against cancer.  
 XX  
 XX Claim 1; Page 123; 130pp; English.  
 PS  
 XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene  
 CC expression) tags used to identify mRNA transcripts encoding  
 CC immunostimulatory cofactor proteins which are preferentially or  
 CC differentially expressed in monocyte-derived dendritic cells compared  
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
 CC (expressed sequence tags) which were previously unknown to be  
 CC preferentially or differentially expressed in dendritic cells, while  
 CC other transcripts correspond to novel genes. Antigen-presenting cell  
 CC (APC)-associated costimulatory factors play an important role in the  
 CC activation of the cytotoxic immune response, particularly against tumour  
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
 CC complex) and subsequent recognition by T-cell receptors is alone  
 CC insufficient to activate a robust cytotoxic immune response that can lyse



```

PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 70; 130pp; English.
XX
XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T-cell receptors is alone
XX insufficient to activate a robust cytotoxic immune response that can lyse
XX the tumour cells. Immunostimulatory cofactors also being required for
XX efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX sequences identified using the SAGE tags have several potential uses.
XX They may be used in vaccines to induce an immune response, particularly
XX against a tumour antigen; to modulate the genotype of an APC; to screen
XX for agents that modulate expression of differentially expressed genes in
XX an APC; and as hybridisation probes/amplification primers for the
XX diagnosis, prognosis and monitoring of diseases related to abnormal
XX expression of these genes. Detection of the dendritic cell differentially
XX expressed genes, or of their encoded proteins, can be used to identify
XX cells as belonging to the monocyte lineage. Cells containing these genes
XX can be used in active immunotherapy (or to stimulate production of a
XX population of antigen-specific effector cells) and vectors containing
XX them are used in gene therapy. Co-administration of tumour antigens and
XX APC-associated costimulatory factors ensures adequate antigen
XX presentation to endogenous APCs and upregulates the APCs for the
XX presentation of co-stimulatory signals, migration to T cell-rich sites,
XX secretion of T cell growth factors and secretion of chemokines for
XX recruitment of immune effector cells
XX
XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 345 ACCAGTAGCA 354
XX |||||
XX 10 ACCAGTAGCA 1
XX
XX RESULT 131
XX AA277747/c
XX ID AA277747 standard; DNA; 10 BP.
XX
XX AC AA277747;

```

```

XX
XX 10-APR-2000 (first entry)
XX
XX Human dendritic cell SAGE tag. SEQ ID NO:175.
XX
XX SAGE tag: serial analysis of gene expression; antigen-presenting cell;
XX APC; monocyte-derived dendritic cell; differential gene expression;
XX immunostimulatory cofactor; costimulatory factor; CTL;
XX cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anti-tumour; ss.
XX
XX Homo sapiens.
XX
XX WO9965924-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013800.
XX
XX 19-JUN-1998; 98US-0089833P.
XX 19-JUN-1998; 98US-0089844P.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089878P.
XX 19-JUN-1998; 98US-0089911P.
XX 19-JUN-1998; 98US-0089922P.
XX 19-JUN-1998; 98US-0089933P.
XX 19-JUN-1998; 98US-0089944P.
XX 19-JUN-1998; 98US-0089977P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090000P.
XX 19-JUN-1998; 98US-0090035P.
XX 19-JUN-1998; 98US-0090036P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090041P.
XX 19-JUN-1998; 98US-0090042P.
XX 19-JUN-1998; 98US-0090043P.
XX 19-JUN-1998; 98US-0090044P.
XX 19-JUN-1998; 98US-0090045P.
XX 19-JUN-1998; 98US-0090047P.
XX 19-JUN-1998; 98US-0090048P.
XX 19-JUN-1998; 98US-0090072P.
XX 19-JUN-1998; 98US-0090076P.
XX 19-JUN-1998; 98US-0090077P.
XX 19-JUN-1998; 98US-0090078P.
XX 19-JUN-1998; 98US-0090079P.
XX 19-JUN-1998; 98US-0090080P.
XX 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 69; 130pp; English.
XX
XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T-cell receptors is alone

```



AC AAZ78914;  
 XX  
 DT 10-APR-2000 (first entry)  
 XX  
 DE Human dendritic cell SAGE tag, SEQ ID NO:1342.  
 XX  
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
 KW APC; monocyte-derived dendritic cell; differential gene expression;  
 KW immunostimulatory cofactor; costimulatory factor; CTL; antitumor;  
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO965924-A2.  
 XX  
 PD 23-DEC-1999.  
 XX  
 PF 18-JUN-1999; 99WO-US013800.  
 XX  
 PR 19-JUN-1998; 98US-0089833P.  
 PR 19-JUN-1998; 98US-0089844P.  
 PR 19-JUN-1998; 98US-0089853P.  
 PR 19-JUN-1998; 98US-0089878P.  
 PR 19-JUN-1998; 98US-0089912P.  
 PR 19-JUN-1998; 98US-0089922P.  
 PR 19-JUN-1998; 98US-0089933P.  
 PR 19-JUN-1998; 98US-0089944P.  
 PR 19-JUN-1998; 98US-0089959P.  
 PR 19-JUN-1998; 98US-0089999P.  
 PR 19-JUN-1998; 98US-0090000P.  
 PR 19-JUN-1998; 98US-0090035P.  
 PR 19-JUN-1998; 98US-0090036P.  
 PR 19-JUN-1998; 98US-0090039P.  
 PR 19-JUN-1998; 98US-0090041P.  
 PR 19-JUN-1998; 98US-0090042P.  
 PR 19-JUN-1998; 98US-0090043P.  
 PR 19-JUN-1998; 98US-0090044P.  
 PR 19-JUN-1998; 98US-0090045P.  
 PR 19-JUN-1998; 98US-0090047P.  
 PR 19-JUN-1998; 98US-0090048P.  
 PR 19-JUN-1998; 98US-0090072P.  
 PR 19-JUN-1998; 98US-0090076P.  
 PR 19-JUN-1998; 98US-0090077P.  
 PR 19-JUN-1998; 98US-0090078P.  
 PR 19-JUN-1998; 98US-0090079P.  
 PR 19-JUN-1998; 98US-0090080P.  
 PR 08-DEC-1998; 98US-0111715P.  
 XX  
 PA (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.  
 XX  
 PI Roberts BL, Shankara S;  
 XX  
 XX WPI; 2000-106077/09.  
 XX  
 PT Isolated polynucleotides differentially expressed in antigen-presenting  
 PT cells, useful in gene vaccines against cancer.  
 XX  
 PS Claim 1; Page 103; 130pp; English.  
 XX  
 CC Sequences AAZ7573-279709 represent SAGE (serial analysis of gene  
 CC expression) tags used to identify mRNA transcripts encoding  
 CC immunostimulatory cofactor proteins which are preferentially or  
 CC differentially expressed in monocyte-derived dendritic cells compared  
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
 CC (expressed sequence tags) which were previously unknown to be  
 CC preferentially or differentially expressed in dendritic cells, while  
 CC other transcripts correspond to novel genes. Antigen-presenting cell  
 CC (APC)-associated costimulatory factors play an important role in the  
 CC activation of the cytotoxic immune response, particularly against tumour  
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility

CC complex) and subsequent recognition by T-cell receptors is alone  
 CC insufficient to activate a robust cytotoxic immune response that can lyse  
 CC the tumour cells, immunostimulatory cofactors also being required for  
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
 CC sequences identified using the SAGE tags have several potential uses.  
 CC They may be used in vaccines to induce an immune response, particularly  
 CC against a tumour antigen; to modulate the genotype of an APC; to screen  
 CC for agents that modulate expression of differentially expressed genes in  
 CC an APC; and as hybridisation probes/amplification primers for the  
 CC diagnosis, prognosis and monitoring of diseases related to abnormal  
 CC expression of these genes. Detection of the dendritic cell differentially  
 CC expressed genes, or of their encoded proteins, can be used to identify  
 CC cells as belonging to the monocyte lineage. Cells containing these genes  
 CC can be used in active immunotherapy (or to stimulate production of a  
 CC population of antigen-specific effector cells) and vectors containing  
 CC them are used in gene therapy. Co-administration of tumour antigens and  
 CC APC-associated costimulatory factors ensures adequate antigen  
 CC presentation to endogenous APCs and upregulates the APCs for the  
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
 CC secretion of T cell growth factors and secretion of chemokines for  
 CC recruitment of immune effector cells  
 XX  
 SQ Sequence 10 BP; 1 A; 3 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1 9e-02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 QY 759 TGAAGAGAGAA 768  
 Db 10 TGAAGAGAGAA 1  
 |||||  
 |||||  
 RESULT 134  
 AAZ79402  
 ID AAZ79402 standard; DNA; 10 BP.  
 XX  
 AC AAZ79402;  
 XX  
 DT 10-APR-2000 (first entry)  
 XX  
 DE Human dendritic cell SAGE tag, SEQ ID NO:1830.  
 XX  
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
 KW APC; monocyte-derived dendritic cell; differential gene expression;  
 KW immunostimulatory cofactor; costimulatory factor; CTL;  
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO965924-A2.  
 XX  
 PD 23-DEC-1999.  
 XX  
 PF 18-JUN-1999; 99WO-US013800.  
 XX  
 PR 19-JUN-1998; 98US-0089833P.  
 PR 19-JUN-1998; 98US-0089844P.  
 PR 19-JUN-1998; 98US-0089853P.  
 PR 19-JUN-1998; 98US-0089878P.  
 PR 19-JUN-1998; 98US-0089912P.  
 PR 19-JUN-1998; 98US-0089922P.  
 PR 19-JUN-1998; 98US-0089933P.  
 PR 19-JUN-1998; 98US-0089944P.  
 PR 19-JUN-1998; 98US-0089959P.  
 PR 19-JUN-1998; 98US-0089999P.  
 PR 19-JUN-1998; 98US-0090000P.  
 PR 19-JUN-1998; 98US-0090035P.  
 PR 19-JUN-1998; 98US-0090036P.  
 PR 19-JUN-1998; 98US-0090039P.  
 PR 19-JUN-1998; 98US-0090041P.  
 PR 19-JUN-1998; 98US-0090042P.

```

PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 117; 130pp; English.
XX
XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
XX Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 806 TCTTGGCATA 815
DB 1 TCTTGGCATA 10
RESULT 135
AAZ77986/c
ID AAZ77986 standard; DNA; 10 BP.

```

---

```

XX AC AAZ77986;
XX AC 10-APR-2000 (first entry)
XX DT Human dendritic cell SAGE tag, SEQ ID NO:414.
XX DE
XX KW SAGE tag; serial analysis of gene expression; antigen presentation; APC; monocyte-derived dendritic cell; differentially expressed; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; antitumor; ss
XX OS Homo sapiens.
XX KW WO9565924-A2.
XX PN 23-DEC-1999.
XX PD
XX PF 18-JUN-1999; 99WO US013807
XX PR 19-JUN-1998; 98US-0089833P.
XX PR 19-JUN-1998; 98US-0089844P.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089878P.
XX PR 19-JUN-1998; 98US-0089991P.
XX PR 19-JUN-1998; 98US-0089992P.
XX PR 19-JUN-1998; 98US-0089993P.
XX PR 19-JUN-1998; 98US-0089994P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0089999P.
XX PR 19-JUN-1998; 98US-0090000P.
XX PR 19-JUN-1998; 98US-0090035P.
XX PR 19-JUN-1998; 98US-0090036P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PR 19-JUN-1998; 98US-0090042P.
XX PR 19-JUN-1998; 98US-0090043P.
XX PR 19-JUN-1998; 98US-0090044P.
XX PR 19-JUN-1998; 98US-0090045P.
XX PR 19-JUN-1998; 98US-0090047P.
XX PR 19-JUN-1998; 98US-0090048P.
XX PR 19-JUN-1998; 98US-0090072P.
XX PR 19-JUN-1998; 98US-0090076P.
XX PR 19-JUN-1998; 98US-0090077P.
XX PR 19-JUN-1998; 98US-0090078P.
XX PR 19-JUN-1998; 98US-0090079P.
XX PR 19-JUN-1998; 98US-0090080P.
XX PR 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer
XX
XX Claim 1; Page 76; 130pp; English.
XX
XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
XX Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 806 TCTTGGCATA 815
DB 1 TCTTGGCATA 10
RESULT 135
AAZ77986/c
ID AAZ77986 standard; DNA; 10 BP.

```



XX ID AA277573 standard; DNA; 10 BP.
XX AC AA277573;
XX DT 10-APR-2000 (first entry)
XX DE Human dendritic cell SAGE tag, SEQ ID NO:1.
XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX KW APC; monocyte-derived dendritic cell; differential gene expression;
XX KW immunostimulatory cofactor; costimulatory factor; CTL;
XX KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX OS Homo sapiens.
XX PN WO965924-A2.
XX XX 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013800.
XX PR 19-JUN-1998; 98US-0089833P.
XX PR 19-JUN-1998; 98US-0089844P.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089878P.
XX PR 19-JUN-1998; 98US-0089911P.
XX PR 19-JUN-1998; 98US-0089922P.
XX PR 19-JUN-1998; 98US-0089933P.
XX PR 19-JUN-1998; 98US-0089944P.
XX PR 19-JUN-1998; 98US-0089978P.
XX PR 19-JUN-1998; 98US-0089999P.
XX PR 19-JUN-1998; 98US-0090000P.
XX PR 19-JUN-1998; 98US-0090035P.
XX PR 19-JUN-1998; 98US-0090036P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PR 19-JUN-1998; 98US-0090042P.
XX PR 19-JUN-1998; 98US-0090043P.
XX PR 19-JUN-1998; 98US-0090044P.
XX PR 19-JUN-1998; 98US-0090045P.
XX PR 19-JUN-1998; 98US-0090047P.
XX PR 19-JUN-1998; 98US-0090048P.
XX PR 19-JUN-1998; 98US-0090072P.
XX PR 19-JUN-1998; 98US-0090076P.
XX PR 19-JUN-1998; 98US-0090077P.
XX PR 19-JUN-1998; 98US-0090078P.
XX PR 19-JUN-1998; 98US-0090079P.
XX PR 19-JUN-1998; 98US-0090080P.
XX PR 08-DEC-1998; 98US-0111715P.
XX (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106077/09.
XX XX Isolated polynucleotides differentially expressed in antigen-presenting
XX PT cells, useful in gene vaccines against cancer.
XX XX Claim 1; Page 63; 130pp; English.
XX CC Sequences AA277573-279709 represent SAGE (serial analysis of gene
XX CC expression) tags used to identify mRNA transcripts encoding
XX CC immunostimulatory cofactor proteins which are preferentially or
XX CC differentially expressed in monocyte-derived dendritic cells compared
XX CC with monocytes. Some of the transcripts correspond to known genes or ESTs
XX CC (expressed sequence tags) which were previously unknown to be
XX CC preferentially or differentially expressed in dendritic cells, while
XX CC other transcripts correspond to novel genes. Antigen-presenting cell
XX CC (APC)-associated costimulatory factors play an important role in the

CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC, to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX Sequence 10 BP; 2 A; 1 C; 0 G; 7 T; 0 U; 0 Other.

Query Match 0.4%; Score 10; DB 1; Length 10.
Best Local Similarity 100.0%; Pred. No 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0.

QY 624 AGAAATATA 633
Db 10 AGAAATATA 1

RESULT 138
AA279124/C
ID AA279124 standard; DNA; 10 BP.
XX AC AA279124;
XX DT 10-APR-2000 (first entry)
XX DE Human dendritic cell SAGE tag, SEQ ID NO:1552.
XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX KW APC; monocyte-derived dendritic cell; differential gene expression;
XX KW immunostimulatory cofactor; costimulatory factor; CTL;
XX KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX OS Homo sapiens.
XX PN WO9965924-A2.
XX XX 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013800.
XX PR 19-JUN-1998; 98US-0089833P.
XX PR 19-JUN-1998; 98US-0089844P.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089878P.
XX PR 19-JUN-1998; 98US-0089901P.
XX PR 19-JUN-1998; 98US-0089922P.
XX PR 19-JUN-1998; 98US-0089933P.
XX PR 19-JUN-1998; 98US-0089944P.
XX PR 19-JUN-1998; 98US-0089978P.
XX PR 19-JUN-1998; 98US-0089999P.
XX PR 19-JUN-1998; 98US-0090000P.
XX PR 19-JUN-1998; 98US-0090035P.
XX PR 19-JUN-1998; 98US-0090036P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-00900041P.  
 PR 19-JUN-1998; 98US-00900042P.  
 PR 19-JUN-1998; 98US-00900043P.  
 PR 19-JUN-1998; 98US-00900044P.  
 PR 19-JUN-1998; 98US-00900045P.  
 PR 19-JUN-1998; 98US-00900047P.  
 PR 19-JUN-1998; 98US-00900048P.  
 PR 19-JUN-1998; 98US-00900072P.  
 PR 19-JUN-1998; 98US-00900076P.  
 PR 19-JUN-1998; 98US-00900077P.  
 PR 19-JUN-1998; 98US-00900078P.  
 PR 19-JUN-1998; 98US-00900079P.  
 PR 19-JUN-1998; 98US-00900080P.  
 PR 08-DEC-1998; 98US-0111715P.  
 XX  
 PA (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.  
 XX  
 PI Roberts BL, Shankara S;  
 XX  
 DR WPI; 2000-106077/09.  
 XX  
 PT Isolated polynucleotides differentially expressed in antigen-presenting  
 PT cells, useful in gene vaccines against cancer.  
 XX  
 PS Claim 1; Page 109; 130pp; English.  
 XX  
 CC Sequences AA277573-279709 represent SAGE (serial analysis of gene  
 CC expression) tags used to identify mRNA transcripts encoding  
 CC immunostimulatory cofactor proteins which are preferentially or  
 CC differentially expressed in monocyte-derived dendritic cells compared  
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
 CC (expressed sequence tags) which were previously unknown to be  
 CC preferentially or differentially expressed in dendritic cells, while  
 CC other transcripts correspond to novel genes. Antigen-presenting cell  
 CC (APC)-associated costimulatory factors play an important role in the  
 CC activation of the cytotoxic immune response, particularly against tumour  
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
 CC complex) and subsequent recognition by T-cell receptors is alone  
 CC insufficient to activate a robust cytotoxic immune response that can lyse  
 CC the tumour cells, immunostimulatory cofactors also being required for  
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
 CC sequences identified using the SAGE tags have several potential uses.  
 CC They may be used in vaccines to induce an immune response, particularly  
 CC against a tumour antigen; to modulate the genotype of an APC; to screen  
 CC for agents that modulate expression of differentially expressed genes in  
 CC an APC; and as hybridisation probes/amplification primers for the  
 CC diagnosis, prognosis and monitoring of diseases related to abnormal  
 CC expression of these genes. Detection of the dendritic cell differentially  
 CC expressed genes, or of their encoded proteins, can be used to identify  
 CC cells as belonging to the monocyte lineage. Cells containing these genes  
 CC can be used in active immunotherapy (or to stimulate production of a  
 CC population of antigen-specific effector cells) and vectors containing  
 CC them are used in gene therapy. Co-administration of tumour antigens and  
 CC APC-associated costimulatory factors ensures adequate antigen  
 CC presentation to endogenous APCs and upregulates the APCs for the  
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
 CC secretion of T cell growth factors and secretion of chemokines for  
 CC recruitment of immune effector cells  
 XX  
 SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 508 ATCACTCTCAG 517  
 Db |||||  
 10 ATCACTCTCAG 1  
 RESULT 139

AA278501  
 ID AA278501 standard; DNA; 10 BP.  
 XX  
 AC AA278501;  
 XX  
 DT 10-APR-2000 (first entry)  
 XX  
 DE Human dendritic cell SAGE tag, SEQ ID NO:929.  
 XX  
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
 KW APC; monocyte-derived dendritic cell; differential gene expression;  
 KW immunostimulatory cofactor; costimulatory factor; CTL;  
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9965924-A2.  
 XX  
 PD 23-DEC-1999.  
 XX  
 PF 18-JUN-1999; 99WO-US013800.  
 XX  
 PR 19-JUN-1998; 98US-0089833P.  
 PR 19-JUN-1998; 98US-0089844P.  
 PR 19-JUN-1998; 98US-0089853P.  
 PR 19-JUN-1998; 98US-0089878P.  
 PR 19-JUN-1998; 98US-0089911P.  
 PR 19-JUN-1998; 98US-0089992P.  
 PR 19-JUN-1998; 98US-0089993P.  
 PR 19-JUN-1998; 98US-0089994P.  
 PR 19-JUN-1998; 98US-0089997P.  
 PR 19-JUN-1998; 98US-0089999P.  
 PR 19-JUN-1998; 98US-0090000P.  
 PR 19-JUN-1998; 98US-0090035P.  
 PR 19-JUN-1998; 98US-0090036P.  
 PR 19-JUN-1998; 98US-0090039P.  
 PR 19-JUN-1998; 98US-0090040P.  
 PR 19-JUN-1998; 98US-0090041P.  
 PR 19-JUN-1998; 98US-0090042P.  
 PR 19-JUN-1998; 98US-0090043P.  
 PR 19-JUN-1998; 98US-0090044P.  
 PR 19-JUN-1998; 98US-0090045P.  
 PR 19-JUN-1998; 98US-0090047P.  
 PR 19-JUN-1998; 98US-0090048P.  
 PR 19-JUN-1998; 98US-0090072P.  
 PR 19-JUN-1998; 98US-0090076P.  
 PR 19-JUN-1998; 98US-0090077P.  
 PR 19-JUN-1998; 98US-0090078P.  
 PR 19-JUN-1998; 98US-0090079P.  
 PR 19-JUN-1998; 98US-0090080P.  
 PR 08-DEC-1998; 98US-0111715P.  
 XX  
 PA (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.  
 XX  
 PI Roberts BL, Shankara S;  
 XX  
 DR WPI; 2000-106077/09.  
 XX  
 PT Isolated polynucleotides differentially expressed in antigen-presenting  
 PT cells, useful in gene vaccines against cancer.  
 XX  
 PS Claim 1; Page 92; 130pp; English.  
 XX  
 CC Sequences AA277573-279709 represent SAGE (serial analysis of gene  
 CC expression) tags used to identify mRNA transcripts encoding  
 CC immunostimulatory cofactor proteins which are preferentially or  
 CC differentially expressed in monocyte-derived dendritic cells compared  
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
 CC (expressed sequence tags) which were previously unknown to be  
 CC preferentially or differentially expressed in dendritic cells, while  
 CC other transcripts correspond to novel genes. Antigen-presenting cell

CC (APC)-associated costimulatory factors play an important role in the  
 CC activation of the cytotoxic immune response, particularly against tumour  
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
 CC complex) and subsequent recognition by T-cell receptors is alone  
 CC insufficient to activate a robust cytotoxic immune response that can lyse  
 CC the tumour cells. Immunostimulatory cofactors also being required for  
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
 CC sequences identified using the SAGE tags have several potential uses.  
 CC They may be used in vaccines to induce an immune response, particularly  
 CC against a tumour antigen; to modulate the genotype of an APC; to screen  
 CC for agents that modulate expression of differentially expressed genes in  
 CC an APC; and as hybridisation probes/amplification primers for the  
 CC diagnosis, prognosis and monitoring of diseases related to abnormal  
 CC expression of these genes. Detection of the dendritic cell differentially  
 CC expressed genes, or of their encoded proteins, can be used to identify  
 CC cells as belonging to the monocyte lineage. Cells containing these genes  
 CC can be used in active immunotherapy (or to stimulate production of a  
 CC population of antigen-specific effector cells) and vectors containing  
 CC them are used in gene therapy. Co-administration of tumour antigens and  
 CC APC-associated costimulatory factors ensures adequate antigen  
 CC presentation to endogenous APCs and upregulates the APCs for the  
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
 CC secretion of T cell growth factors and secretion of chemokines for  
 CC recruitment of immune effector cells

XX Sequence 10 BP; 4 A; 1 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;

QY 420 ATTGATCAAT 429

DB 1 ATTGATCAAT 10

RESULT 140

AAZ78501/C

ID AAZ78501 standard; DNA; 10 BP.

AC AAZ78501;

DT 10-APR-2000 (first entry)

XX Human dendritic cell SAGE tag, SEQ ID NO:929.

DE SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
 KW APC; monocyte-derived dendritic cell; differential gene expression;  
 KW immunostimulatory cofactor; costimulatory factor; CTL;  
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX Homo sapiens.

XX WO9965924-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

XX 19-JUN-1998; 98US-0089833P.

XX 19-JUN-1998; 98US-0089844P.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089878P.

XX 19-JUN-1998; 98US-0089919P.

XX 19-JUN-1998; 98US-0089922P.

XX 19-JUN-1998; 98US-0089933P.

XX 19-JUN-1998; 98US-0089934P.

XX 19-JUN-1998; 98US-0089957P.

XX 19-JUN-1998; 98US-0089999P.

XX 19-JUN-1998; 98US-0090000P.

XX 19-JUN-1998; 98US-0090035P.

XX 19-JUN-1998; 98US-0090036P.

XX 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.  
 PR 19-JUN-1998; 98US-0090041P.  
 PR 19-JUN-1998; 98US-0090042P.  
 PR 19-JUN-1998; 98US-0090043P.  
 PR 19-JUN-1998; 98US-0090044P.  
 PR 19-JUN-1998; 98US-0090045P.  
 PR 19-JUN-1998; 98US-0090047P.  
 PR 19-JUN-1998; 98US-0090048P.  
 PR 19-JUN-1998; 98US-0090072P.  
 PR 19-JUN-1998; 98US-0090076P.  
 PR 19-JUN-1998; 98US-0090077P.  
 PR 19-JUN-1998; 98US-0090078P.  
 PR 19-JUN-1998; 98US-0090079P.  
 PR 19-JUN-1998; 98US-0090080P.  
 PR 08-DEC-1998; 98US 0111715P

(GENZ ) GENZYME CORP.

(ROBE/) ROBERTS B L.

(SHAN/) SHANKARA S.

Roberts BL, Shankara S;

WPI; 2000-106077/09.

Isolated polynucleotides differentially expressed in antigen presenting cells, useful in gene vaccines against cancer.

Claim 1; Page 92; 130pp; English.

Sequences AAZ77573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells. Immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co administration of tumour antigen and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

Sequence 10 BP; 4 A; 1 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 ATTGATCAAT 429

DB 10 ATTGATCAAT 1



```

RESULT 141
AAZ78980
ID AAZ78980 standard; DNA; 10 BP.
XX AC
XX AAZ78980;
XX 10-APR-2000 (first entry)
DT XX
XX Human dendritic cell SAGE tag, SEQ ID NO:1408.
DE XX
XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX XX
OS Homo sapiens.
XX XX
XX WO9965924-A2.
XX PD
XX 23-DEC-1999.
XX PF
XX 18-JUN-1999; 99WO-US013800.
XX PR
XX 19-JUN-1998; 98US-0089833P.
XX PR
XX 19-JUN-1998; 98US-0089844P.
XX PR
XX 19-JUN-1998; 98US-0089853P.
XX PR
XX 19-JUN-1998; 98US-0089878P.
XX PR
XX 19-JUN-1998; 98US-0089912P.
XX PR
XX 19-JUN-1998; 98US-0089922P.
XX PR
XX 19-JUN-1998; 98US-0089933P.
XX PR
XX 19-JUN-1998; 98US-0089944P.
XX PR
XX 19-JUN-1998; 98US-0089977P.
XX PR
XX 19-JUN-1998; 98US-0089999P.
XX PR
XX 19-JUN-1998; 98US-0090035P.
XX PR
XX 19-JUN-1998; 98US-0090044P.
XX PR
XX 19-JUN-1998; 98US-0090045P.
XX PR
XX 19-JUN-1998; 98US-0090047P.
XX PR
XX 19-JUN-1998; 98US-0090048P.
XX PR
XX 19-JUN-1998; 98US-0090072P.
XX PR
XX 19-JUN-1998; 98US-0090076P.
XX PR
XX 19-JUN-1998; 98US-0090077P.
XX PR
XX 19-JUN-1998; 98US-0090078P.
XX PR
XX 19-JUN-1998; 98US-0090079P.
XX PR
XX 19-JUN-1998; 98US-0090080P.
XX PR
XX 08-DEC-1998; 98US-0111715P.
XX PA
XX (GENZ ) GENZYME CORP.
XX PA
XX (ROBE/) ROBERTS B L.
XX PA
XX (SHAN/) SHANKARA S.
XX PI
XX Roberts BL, Shankara S;
XX PF
XX WPI; 2000-106077/09.
XX XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
XX XX
XX Claim 1; Page 105; 130pp; English.
XX XX
XX Sequences AAZ77573-737909 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while

```

```

CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is a major
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX XX
SQ Sequence 10 BP; 5 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
QY 1582 AAGGAAAGTG 1591
Db 1 AAGGAAAGTG 10
|||||||
RESULT 142
AAZ78339/C
ID AAZ78339 standard; DNA; 10 BP.
XX AC
XX AAZ78339;
XX 10-APR-2000 (first entry)
DT XX
XX Human dendritic cell SAGE tag, SEQ ID NO:767.
DE XX
XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX XX
XX Homo sapiens.
XX XX
XX WO9965924-A2.
XX PD
XX 23-DEC-1999.
XX PF
XX 18-JUN-1999; 99WO-US013800.
XX PR
XX 19-JUN-1998; 98US-0089833P.
XX PR
XX 19-JUN-1998; 98US-0089844P.
XX PR
XX 19-JUN-1998; 98US-0089853P.
XX PR
XX 19-JUN-1998; 98US-0089878P.
XX PR
XX 19-JUN-1998; 98US-0089912P.
XX PR
XX 19-JUN-1998; 98US-0089922P.
XX PR
XX 19-JUN-1998; 98US-0089933P.
XX PR
XX 19-JUN-1998; 98US-0089944P.
XX PR
XX 19-JUN-1998; 98US-0089977P.
XX PR
XX 19-JUN-1998; 98US-0089999P.
XX PR
XX 19-JUN-1998; 98US-0090035P.
XX PR
XX 19-JUN-1998; 98US-0090044P.
XX PR
XX 19-JUN-1998; 98US-0090045P.
XX PR
XX 19-JUN-1998; 98US-0090047P.
XX PR
XX 19-JUN-1998; 98US-0090048P.
XX PR
XX 19-JUN-1998; 98US-0090072P.
XX PR
XX 19-JUN-1998; 98US-0090076P.
XX PR
XX 19-JUN-1998; 98US-0090077P.
XX PR
XX 19-JUN-1998; 98US-0090078P.
XX PR
XX 19-JUN-1998; 98US-0090079P.
XX PR
XX 19-JUN-1998; 98US-0090080P.
XX PR
XX 08-DEC-1998; 98US-0111715P.
XX PA
XX (GENZ ) GENZYME CORP.
XX PA
XX (ROBE/) ROBERTS B L.
XX PA
XX (SHAN/) SHANKARA S.
XX PI
XX Roberts BL, Shankara S;
XX PF
XX WPI; 2000-106077/09.
XX XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
XX XX
XX Claim 1; Page 105; 130pp; English.
XX XX
XX Sequences AAZ77573-737909 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while

```

```

PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 87; 130pp; English.
XX
XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T-cell receptors is alone
XX insufficient to activate a robust cytotoxic immune response that can lyse
XX the tumour cells, immunostimulatory cofactors also being required for
XX efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX sequences identified using the SAGE tags have several potential uses.
XX They may be used in vaccines to induce an immune response, particularly
XX against a tumour antigen, to modulate the genotype of an APC; to screen
XX for agents that modulate expression of differentially expressed genes in
XX an APC; and as hybridisation probes/amplification primers for the
XX diagnosis, prognosis and monitoring of diseases related to abnormal
XX expression of these genes. Detection of the dendritic cell differentially
XX expressed genes, or of their encoded proteins, can be used to identify
XX cells as belonging to the monocyte lineage. Cells containing these genes
XX can be used in active immunotherapy (or to stimulate production of a
XX population of antigen-specific effector cells) and vectors containing
XX them are used in gene therapy. Co-administration of tumour antigens and
XX APC-associated costimulatory factors ensures adequate antigen
XX presentation to endogenous APCs and upregulates the APCs for the
XX presentation of co-stimulatory signals, migration to T cell-rich sites,
XX secretion of T cell growth factors and secretion of chemokines for
XX recruitment of immune effector cells
XX
XX Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 803 GGTCTTGGC 812
XX |||||
XX 10 GGTCTTGGC 1
XX

```

```

RESULT 143
AA279250
ID AA279250 standard; DNA; 10 BP.
XX
XX AC AA279250;
XX
XX DT 10-APR-2000 (first entry)
XX
XX DE Human dendritic cell SAGE tag, SEQ ID NO:1678.
XX
XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX APC; monocyte-derived dendritic cell; differential gene expression;
XX immunostimulatory cofactor; costimulatory factor; CTL;
XX cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965924-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013800.
XX
XX PR 19-JUN-1998; 98US-0089833P.
XX PR 19-JUN-1998; 98US-0089844P.
XX PR 19-JUN-1998; 98US-0089851P.
XX PR 19-JUN-1998; 98US-0089878P.
XX PR 19-JUN-1998; 98US-0089991P.
XX PR 19-JUN-1998; 98US-0089992P.
XX PR 19-JUN-1998; 98US-0089993P.
XX PR 19-JUN-1998; 98US-0089994P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0089999P.
XX PR 19-JUN-1998; 98US-0090000P.
XX PR 19-JUN-1998; 98US-0090035P.
XX PR 19-JUN-1998; 98US-0090036P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090042P.
XX PR 19-JUN-1998; 98US-0090043P.
XX PR 19-JUN-1998; 98US-0090044P.
XX PR 19-JUN-1998; 98US-0090045P.
XX PR 19-JUN-1998; 98US-0090047P.
XX PR 19-JUN-1998; 98US-0090048P.
XX PR 19-JUN-1998; 98US-0090072P.
XX PR 19-JUN-1998; 98US-0090076P.
XX PR 19-JUN-1998; 98US-0090077P.
XX PR 19-JUN-1998; 98US-0090078P.
XX PR 19-JUN-1998; 98US-0090079P.
XX PR 19-JUN-1998; 98US-0090080P.
XX PR 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 113; 130pp; English.
XX
XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T-cell receptors is alone
XX insufficient to activate a robust cytotoxic immune response that can lyse
XX the tumour cells, immunostimulatory cofactors also being required for
XX efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX sequences identified using the SAGE tags have several potential uses.
XX They may be used in vaccines to induce an immune response, particularly
XX against a tumour antigen, to modulate the genotype of an APC; to screen
XX for agents that modulate expression of differentially expressed genes in
XX an APC; and as hybridisation probes/amplification primers for the
XX diagnosis, prognosis and monitoring of diseases related to abnormal
XX expression of these genes. Detection of the dendritic cell differentially
XX expressed genes, or of their encoded proteins, can be used to identify
XX cells as belonging to the monocyte lineage. Cells containing these genes
XX can be used in active immunotherapy (or to stimulate production of a
XX population of antigen-specific effector cells) and vectors containing
XX them are used in gene therapy. Co-administration of tumour antigens and
XX APC-associated costimulatory factors ensures adequate antigen
XX presentation to endogenous APCs and upregulates the APCs for the
XX presentation of co-stimulatory signals, migration to T cell-rich sites,
XX secretion of T cell growth factors and secretion of chemokines for
XX recruitment of immune effector cells
XX
XX Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 803 GGTCTTGGC 812
XX |||||
XX 10 GGTCTTGGC 1
XX

```

preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells. Immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

Sequence 10 BP; 4 A; 1 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 999 TTTAATACAT 1008  
Db 1. TTTAATACAT 10

RESULT 144  
AAZ79438/c

ID AAZ79438 standard; DNA; 10 BP.

XX AAZ79438;

DT 10-APR-2000 (first entry)

XX Human dendritic cell SAGE tag, SEQ ID NO:1866.

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

OS Homo sapiens.

XX WO9965924-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

PR 19-JUN-1998; 98US-0089833P.

PR 19-JUN-1998; 98US-0089844P.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089878P.

PR 19-JUN-1998; 98US-0089991P.

PR 19-JUN-1998; 98US-0089992P.

PR 19-JUN-1998; 98US-0089993P.

PR 19-JUN-1998; 98US-0089994P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090000P.

PR 19-JUN-1998; 98US-0090035P.

PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.

XX (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B. L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

PI WPI; 2000-106077/09.

XX Isolated polynucleotides differentially expressed in antigen presenting cells, useful in gene vaccines against cancer

PT Claim 1; Page 118; 130pp; English.

PS Sequences AAZ77573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 831 GCTGTCAACCA 840

Db 10 GCTGTCAACCA 1

```

RESULT 145
AAA88601/c
ID AAA88601 standard; DNA; 10 BP.
XX
XX
AC AAA88601;
XX
DT 05-FEB-2001 (first entry)
XX
DE Forward primer OP117 used in differential display.
XX
XX Human; rchd036 gene; differential expression; HUVEC; endothelial cell;
KW cardiovascular disease; diagnosis; therapy; primer; ss.
XX
XX Homo sapiens.
XX
XX US6124433-A.
PN
XX
XX 26-SEP-2000.
PD
XX
XX 06-OCT-1997; 97US-00944496.
PF
XX
XX 10-FEB-1995; 95US-00386844.
PR
XX 07-JUN-1995; 95US-00485573.
PR
XX 09-FEB-1996; 96US-00599654.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Gimbrone MA, Falb DA;
PI
XX
XX WPI; 2000-611017/58.
DR
XX
XX Novel isolated rchd036 polypeptides, differentially expressed in response
PT to endothelial cell shear stress, used for diagnosis, monitoring clinical
PT trails, and treating cardiovascular diseases such as ischemia.
PT
XX
XX Example 8.2; Col 9; 123pp; English.
PS
XX
XX This oligonucleotide was used as forward primer, with the reverse primer
CC given in AAA88595, in a differential display analysis of interleukin-1
CC activated HUVEC. mRNA prepared from control HUVEC and from HUVEC treated
CC for 1 or 6 hr with 10 U/ml IL-1 was subjected to analysis. The novel
CC human gene rchd036 (see AAA88583) was identified, which is up-regulated
CC in IL-1 activated HUVEC. rchd036 is 1 of 8 novel human genes of the
CC invention (see AAA88576-83) characterised as being differentially
CC expressed in cardiovascular disease states, and which are of diagnostic
CC or therapeutic use
XX
XX Sequence 10 BP; 1'A; 0 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2031 CATCACCACC 2040
DB 10 CATCACCACC 1
RESULT 146
AAZ82640
ID AAZ82640 standard; DNA; 10 BP.
XX
XX
AC AAZ82640;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1874.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX

```

---

```

KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9965928-A2.
PN
XX
XX 23-DEC-1999.
PD
XX
XX 18-JUN-1999; 99WO-US013647.
PF
XX
XX 19-JUN-1998; 98US-0089851P.
PR
XX 19-JUN-1998; 98US-0089997P.
PR
XX 19-JUN-1998; 98US-0090039P.
PR
XX 19-JUN-1998; 98US-0090040P.
PR
XX 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
PA
XX (ROBE/) ROBERTS B L.
PA
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
PI
XX
XX WPI; 2000-106079/09.
DR
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
PT
XX
XX Claim 1; Page 109; 219pp; English.
PS
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types,
CC e.g. therapeutic genes (also ribozymes or antisense sequences).
CC particularly an antigen-encoding sequence for use in gene or cell based
CC vaccines. Polypeptides encoded by the transcripts are also useful as
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or in other applications.
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other.
SQ
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1874 AAAGCCAAGA 1883
DB 1 AAAGCCAAGA 10
RESULT 147
AAZ83728/c
ID AAZ83728 standard; DNA; 10 BP.
XX
XX
AC AAZ83728;
XX
XX 07-APR-2000 (first entry)
DT
XX
XX Metastatic breast tumour cell upregulated transcript tag #2962.
DE
XX

```

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.  
 OS Homo sapiens.  
 XX WO9965928-A2.  
 PN 23-DEC-1999.  
 PD 18-JUN-1999; 99WO-US013647.  
 PF 19-JUN-1998; 98US-0089853P.  
 PR 19-JUN-1998; 98US-0089997P.  
 PR 19-JUN-1998; 98US-0090039P.  
 PR 19-JUN-1998; 98US-0090040P.  
 PR 19-JUN-1998; 98US-0090041P.  
 XX (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.  
 XX Roberts BL, Shankara S;  
 XX WPI; 2000-106079/09.  
 DR Isolated polynucleotides differentially expressed between metastatic and  
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 XX treatment of cancer.  
 XX Claim 1; Page 138; 219pp; English.  
 CC AZ80767 to AZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AZ83942  
 CC to AZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1980 CGCCATCACT 1989  
 |||||  
 Db 10 CGCCATCACT 1  
 RESULT 148  
 AAZ81610  
 ID AAZ81610 standard; DNA; 10 BP.  
 XX AAZ81610;  
 AC  
 XX 07-APR-2000 (first entry)  
 DT  
 XX

DE Metastatic breast tumour cell upregulated transcript tag #844.  
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.  
 OS Homo sapiens.  
 XX WO9965928-A2.  
 PN 23-DEC-1999.  
 PD 18-JUN-1999; 99WO-US013647.  
 PF 19-JUN-1998; 98US-0089853P.  
 PR 19-JUN-1998; 98US-0089997P.  
 PR 19-JUN-1998; 98US-0090039P.  
 PR 19-JUN-1998; 98US-0090040P.  
 PR 19-JUN-1998; 98US-0090041P.  
 XX (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.  
 XX Roberts BL, Shankara S;  
 XX WPI; 2000-106079/09.  
 DR Isolated polynucleotides differentially expressed between metastatic and  
 XX non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 XX treatment of cancer.  
 XX Claim 1; Page 81; 219pp; English.  
 CC AZ80767 to AZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AZ83942  
 CC to AZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX Sequence 10 BP; 3 A; 2 C; 0 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1903 AATTACTTC 1912  
 |||||  
 Db 1 AATTACTTC 10  
 RESULT 149  
 AAZ85267/c  
 ID AAZ85267 standard; DNA; 10 BP.  
 XX AAZ85267;  
 AC  
 XX

```

DT 07-APR-2000 (first entry)
XX Metastatic breast tumour cell downregulated transcript tag #4501.
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
OS Homo sapiens.
XX WO965928-A2.
PN 23-DEC-1999.
XX 18-JUN-1999; 99WO-US013647.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
PI WPI; 2000-106079/09.
DR Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX Claim 1; Page 179; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1837 GAAACCACT 1846
DB 10 GAAACCACT 1

RESULT 150
AAZ84513
ID AAZ84513 standard; DNA; 10 BP.
XX

```

```

AC AAZ84513;
XX 07-APR-2000 (first entry)
XX Metastatic breast tumour cell downregulated transcript tag #1747.
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX WO965928-A2.
PN 23-DEC-1999.
XX 18-JUN-1999; 99WO-US013647.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
PI WPI; 2000-106079/09.
DR Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX Claim 1; Page 184; 219pp; English.
XX AAZ80767 to AAZ81941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ81942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
XX cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
XX Sequence 10 BP; 4 A; 1 C; 1 G; 4 T; 0 U; 0 Other.

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 ATTGATCAAT 429
DB 1 ATTGATCAAT 10

RESULT 151
AAZ84513/c

```

```

ID AAZ84513 standard; DNA; 10 BP.
XX
AC AAZ84513;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3747.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX
OS antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
XX
PR 19-JUN-1998; 98US-0089997P.
XX
PR 19-JUN-1998; 98US-0090039P.
XX
PR 19-JUN-1998; 98US-0090040P.
XX
XX 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 158; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 4 A; 1 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 420 ATTGATCAAT 429
DB 10 ATTGATCAAT 1

```

---

```

RESULT 152
AAZ84587/C
ID AAZ84587 standard; DNA; 10 BP.
XX
AC AAZ84587;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3821.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX
OS antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
XX
PR 19-JUN-1998; 98US-0089997P.
XX
PR 19-JUN-1998; 98US-0090039P.
XX
PR 19-JUN-1998; 98US-0090040P.
XX
XX 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 160; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 1 C; 1 G; 6 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1092 AAAATACAGT 1101
DB 10 AAAATACAGT 1

```

```

RESULT 153
AAZ86223
ID AAZ86223 standard; DNA; 10 BP.
XX
AC AAZ86223;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #5457.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
(GENZ ) GENZYME CORP.
(PA (ROBE//) ROBERTS B L.
(PA (SHAN//) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
PI WPI; 2000-106079/09.
XX
DR
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 203; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 4 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2259 ATGTAAGTG 2268

```

```

Db 1 ATGTAAGTG 10
|||||
RESULT 154
AAZ86551
ID AAZ86551 standard; DNA; 10 BP
XX
AC AAZ86551;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #5457.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
(GENZ ) GENZYME CORP.
(PA (ROBE//) ROBERTS B L.
(PA (SHAN//) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
PI WPI; 2000-106079/09.
XX
DR
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 211; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 4 A; 0 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



QY 2256 TGTATGTAAA 2265  
 Db 1 TGTATGTAAA 10

RESULT 155  
 AAZ81597/c  
 ID AAZ81597 standard; DNA; 10 BP.  
 XX AC AAZ81597;  
 XX DT 07-APR-2000 (first entry)  
 XX DE Metastatic breast tumour cell upregulated transcript tag #831.  
 XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.  
 OS Homo sapiens.  
 XX WO9965928-A2.  
 XX 23-DEC-1999.  
 XX 18-JUN-1999; 99WO-US013647.  
 PR 19-JUN-1998; 98US-0089853P.  
 PR 19-JUN-1998; 98US-0089997P.  
 PR 19-JUN-1998; 98US-0090039P.  
 PR 19-JUN-1998; 98US-0090040P.  
 PR 19-JUN-1998; 98US-0090041P.  
 XX (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.  
 PI Roberts BL, Shankara S;  
 XX WPI; 2000-106079/09.  
 XX Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.  
 XX Claim 1; Page 80; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.  
 CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred No. 1.9e-02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 668 TCATCGATTT 677  
 Db 10 TCATCGATTT 1

RESULT 156  
 AAZ84444/c  
 ID AAZ84444 standard; DNA; 10 BP.  
 XX AC AAZ84444;  
 XX DT 07-APR-2000 (first entry)  
 XX DE Metastatic breast tumour cell downregulated transcript tag #674  
 XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.  
 OS Homo sapiens.  
 XX WO9965928-A2.  
 XX 23-DEC-1999.  
 XX 18-JUN-1999; 99WO-US013647.  
 PR 19-JUN-1998; 98US-0089853P.  
 PR 19-JUN-1998; 98US-0089997P.  
 PR 19-JUN-1998; 98US-0090039P.  
 PR 19-JUN-1998; 98US-0090040P.  
 PR 19-JUN-1998; 98US-0090041P.  
 XX (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.  
 PI Roberts BL, Shankara S;  
 XX WPI; 2000-106079/09.  
 XX Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.  
 XX Claim 1; Page 157; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.  
 CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX Sequence 10 BP; 1 A; 0 C; 1 G; 8 T; 0 U; 0 Other;

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AAATACAAA 2353
Db 10 AAATACAAA 1

RESULT 157
AAZ82092
ID AAZ82092 standard; DNA; 10 BP.
XX
AC AAZ82092;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1326.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
(GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
WPI; 2000-106079/09.
XX
Isolated polynucleotides differentially expressed between metastatic and
non-metastatic breast cancer cells, useful for diagnosis, prevention and
treatment of cancer.
XX
Claim 1; Page 94; 219pp; English.
XX
AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
to AAZ86677 represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
the transcripts are used to direct expression, in selected cell types, of
e.g. therapeutic genes (also ribozymes or antisense sequences),
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines. Polypeptides encoded by the transcripts are also useful in
vaccines; for diagnosing breast cancer and for raising specific
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides can be used to expand
and isolate populations of educated, antigen-specific immune effector
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy

```

---

```

XX Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
SO
Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 528 AATGTCCGAA 537
Db 1 AATGTCCGAA 10

RESULT 158
AAZ82215/c
ID AAZ82215 standard; DNA; 10 BP.
XX
AC AAZ82215;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1449.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
(GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
WPI; 2000-106079/09.
XX
Isolated polynucleotides differentially expressed between metastatic and
non-metastatic breast cancer cells, useful for diagnosis, prevention and
treatment of cancer.
XX
Claim 1; Page 97; 219pp; English.
XX
AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the metastatic breast tumour
tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
to AAZ86677 represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
the transcripts are used to direct expression, in selected cell types, of
e.g. therapeutic genes (also ribozymes or antisense sequences),
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines. Polypeptides encoded by the transcripts are also useful in
vaccines; for diagnosing breast cancer and for raising specific
antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
agents. Host cells that produce the polypeptides can be used to expand
and isolate populations of educated, antigen-specific immune effector
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
immunotherapy

```

CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1238 CTCAAAGTGC 1247  
 Db 10 CTCAAAGTGC 1

RESULT 159  
 AAZ85947/c  
 ID AAZ85947 standard; DNA; 10 BP.  
 XX AC AAZ85947;  
 XX DT 07-APR-2000 (first entry)  
 XX DE Metastatic breast tumour cell downregulated transcript tag #5181.  
 XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.  
 XX OS Homo sapiens.  
 XX PN WO9965928-A2.  
 XX PD 23-DEC-1999.  
 XX PF 18-JUN-1999; 99WO-US013647.  
 XX PR 19-JUN-1998; 98US-0089853P.  
 XX PR 19-JUN-1998; 98US-0089997P.  
 XX PR 19-JUN-1998; 98US-0090039P.  
 XX PR 19-JUN-1998; 98US-0090040P.  
 XX PR 19-JUN-1998; 98US-0090041P.  
 XX (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.  
 XX Roberts BL, Shankara S;  
 PI WPI; 2000-106079/09.  
 XX Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.  
 XX Claim 1; Page 196; 219pp; English.

CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.  
 CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic

CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2031 CATCACCACC 2040  
 Db 10 CATCACCACC 1

RESULT 160  
 AAZ82060  
 ID AAZ82060 standard; DNA; 10 BP.  
 XX AC AAZ82060;  
 XX DT 07-APR-2000 (first entry)  
 XX DE Metastatic breast tumour cell upregulated transcript tag #1294.  
 XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.  
 XX OS Homo sapiens.  
 XX PN WO9965928-A2.  
 XX PD 23-DEC-1999.  
 XX PF 18-JUN-1999; 99WO-US013647.  
 XX PR 19-JUN-1998; 98US-0089853P.  
 XX PR 19-JUN-1998; 98US-0089997P.  
 XX PR 19-JUN-1998; 98US-0090039P.  
 XX PR 19-JUN-1998; 98US-0090040P.  
 XX PR 19-JUN-1998; 98US-0090041P.  
 XX (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.  
 XX Roberts BL, Shankara S;  
 PI WPI; 2000-106079/09.  
 XX Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.  
 XX Claim 1; Page 93; 219pp; English.

CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.  
 CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic

CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy

XX Sequence 10 BP; 4 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2295 ATGGTTAAAG 2304  
 |||||  
 Db 1 ATGGTTAAAG 10

## RESULT 161

AAZ83635/C  
 ID AAZ83635 standard; DNA; 10 BP.

XX AC AAZ83635;

XX DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell upregulated transcript tag #2869.

XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;

XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;

XX KW antimetastatic; vaccine; diagnosis; sb.

XX OS Homo sapiens.

XX PN WO9965928-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013647.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX PA (GENZ ) GENZYME CORP.

XX PA (ROBE/) ROBERTS B L.

XX PA (SHAN/) SHANKARA S.

XX PI Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.

XX Claim 1; Page 135; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.

XX Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),

CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy

XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other.

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 742 CGCGCTCCAG 751  
 |||||  
 Db 10 CGCGCTCCAG 1

## RESULT 162

AAZ83758/C  
 ID AAZ83758 standard; DNA; 10 BP.

XX AC AAZ83758;

XX DT 07-APR-2000 (first entry)

XX DE Metastatic breast tumour cell upregulated transcript tag #2992.

XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;

XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;

XX KW antimetastatic; vaccine; diagnosis; sb.

XX OS Homo sapiens.

XX PN WO9965928-A2.

XX PD 23-DEC-1999.

XX PF 18-JUN-1999; 99WO-US013647.

XX PR 19-JUN-1998; 98US-0089853P.

XX PR 19-JUN-1998; 98US-0089997P.

XX PR 19-JUN-1998; 98US-0090039P.

XX PR 19-JUN-1998; 98US-0090040P.

XX PR 19-JUN-1998; 98US-0090041P.

XX PA (GENZ ) GENZYME CORP.

XX PA (ROBE/) ROBERTS B L.

XX PA (SHAN/) SHANKARA S.

XX PI Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.

XX Claim 1; Page 139; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.

XX Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from

CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX  
 SQ Sequence 10 BP; 6 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 464 TCTTAATATT 473  
 |||||  
 Db 10 TCTTAATATT 1

## RESULT 163

AAZ82636/c  
 ID AAZ82636 standard; DNA; 10 BP.

XX  
 AC AAZ82636;

XX  
 DT 07-APR-2000 (first entry)

XX  
 DE Metastatic breast tumour cell upregulated transcript tag #1870.

XX  
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.

XX  
 OS Homo sapiens.

XX  
 PN WO9965928-A2.

XX  
 PD 23-DEC-1999.

XX  
 PF 18-JUN-1999; 99WO-US013647.

XX  
 PR 19-JUN-1998; 98US-0089853P.

XX  
 PR 19-JUN-1998; 98US-0089997P.

XX  
 PR 19-JUN-1998; 98US-0090039P.

XX  
 PR 19-JUN-1998; 98US-0090040P.

XX  
 PR 19-JUN-1998; 98US-0090041P.

XX  
 PA (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX  
 PI Roberts BL, Shankara S;

XX  
 WPI; 2000-106079/09.

XX  
 DR Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.

XX  
 PS Claim 1; Page 109; 219pp; English.

XX  
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX  
 SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1043 CTGCACTCAA 1052  
 |||||  
 Db 10 CTGCACTCAA 1

## RESULT 164

AAZ85859/c

ID AAZ85859 standard; DNA; 10 BP.

XX  
 AC AAZ85859;

XX  
 DT 07-APR-2000 (first entry)

XX  
 DE Metastatic breast tumour cell downregulated transcript tag #5093.

XX  
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.

XX  
 OS Homo sapiens.

XX  
 PN WO9965928-A2.

XX  
 PD 23-DEC-1999.

XX  
 PF 18-JUN-1999; 99WO-US013647.

XX  
 PR 19-JUN-1998; 98US-0089853P.

XX  
 PR 19-JUN-1998; 98US-0089997P.

XX  
 PR 19-JUN-1998; 98US-0090039P.

XX  
 PR 19-JUN-1998; 98US-0090040P.

XX  
 PR 19-JUN-1998; 98US-0090041P.

XX  
 PA (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX  
 PI Roberts BL, Shankara S;

XX  
 WPI; 2000-106079/09.

XX  
 DR Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.

XX  
 PS Claim 1; Page 194; 219pp; English.

XX  
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and

CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.  
 CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX  
 SQ Sequence 10 BP; 2 A; 0 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1628 TACAAATACA 1637  
 Db 10 TACAAATACA 1

RESULT 165  
 AAZ82115/C  
 ID AAZ82115 standard; DNA; 10 BP.  
 XX  
 AC AAZ82115;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #1349.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.  
 XX WO9965928-A2.  
 XX

PD 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.  
 PR 19-JUN-1998; 98US-0089997P.  
 PR 19-JUN-1998; 98US-0090039P.  
 PR 19-JUN-1998; 98US-0090040P.  
 PR 19-JUN-1998; 98US-0090041P.

XX (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.

XX Claim 1; Page 94; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour

CC tissue (i.e. are downregulated in metastatic breast tumour cells. These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.  
 CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX

SQ Sequence 10 BP; 5 A; 1 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1754 TGATTACATT 1763  
 Db 10 TGATTACATT 1

RESULT 166  
 AAZ86534/C  
 ID AAZ86534 standard; DNA; 10 BP.  
 XX  
 AC AAZ86534;

DT 07-APR-2000 (first entry)

XX Metastatic breast tumour cell; downregulated transcript tag #1349.  
 DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

PD 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.  
 PR 19-JUN-1998; 98US-0089997P.  
 PR 19-JUN-1998; 98US-0090039P.  
 PR 19-JUN-1998; 98US-0090040P.  
 PR 19-JUN-1998; 98US-0090041P.

XX (GENZ ) GENZYME CORP.  
 PA (ROBE/) ROBERTS B L.  
 PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.

XX Claim 1; Page 210; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour

CC to AA286677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.  
 CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX  
 SQ Sequence 10 BP; 2 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 661 GTAAACTCA 670  
 |||||  
 Db 10 GTAAACTCA 1

## RESULT 167

AAZ82316/c  
 ID AAZ82316 standard; DNA; 10 BP.

XX AAZ82316;  
 XX

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #1550.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX 19-JUN-1998; 98US-0090041P.

XX (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.

XX Claim 1; Page 99; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts

CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.  
 CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX

SQ Sequence 10 BP; 2 A; 1 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 624 AGAAATATA 633

|||||

Db 10 AGAAATATA 1

## RESULT 168

AAZ82944/c

ID AAZ82944 standard; DNA; 10 BP.

XX AAZ82944;  
 AC

XX 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #2178.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX 19-JUN-1998; 98US-0090041P.

XX (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.

XX Claim 1; Page 118; 219pp; English.

XX AA280767 to AA283941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942  
 CC to AA286677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.  
 CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX  
 SQ Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 738 GTTTCGGCT 747  
 |||||  
 Db 10 GTTTCGGCT 1

RESULT 169  
 AA282341/c  
 ID AA282341 standard; DNA; 10 BP.

XX AA282341;

AC 07-APR-2000 (first entry)

DT Metastatic breast tumour cell upregulated transcript tag #1575.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

OS WO9965928-A2.

PN 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

XX (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

PI WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

PT non-metastatic breast cancer cells, useful for diagnosis, prevention and

PT treatment of cancer.

XX Claim 1; Page 100; 219pp; English.  
 XX AA280767 to AA283941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942  
 CC to AA286677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.  
 CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy  
 XX  
 SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 CGTTGTAGGG 307  
 |||||  
 Db 10 CGTTGTAGGG 1

RESULT 170  
 AA282593/c  
 ID AA282593 standard; DNA; 10 BP.

XX AA282593;

AC 07-APR-2000 (first entry)

DT Metastatic breast tumour cell upregulated transcript tag #1827.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

OS WO9965928-A2.

PN 23-DEC 1999.

XX 18-JUN-1999; 99WO-US013647.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

XX (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

PI WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

PT non-metastatic breast cancer cells, useful for diagnosis, prevention and

PT treatment of cancer.



PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.

PS Claim 1; Page 108; 219pp; English.

XX AZ80767 to AZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AZ83942  
 CC to AZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.  
 CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy

XX Sequence 10 BP; 0 A; 0 C; 1 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 AAAAAACAAA 75  
 Db 10 AAAAAACAAA 1

RESULT 171

AZ84709  
 ID AZ84709 standard; DNA; 10 BP.

AC AZ84709;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell downregulated transcript tag #3943.

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;

XX antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO9965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US013647.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089977P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PA (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

DR WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and  
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
 PT treatment of cancer.

XX Claim 1; Page 163; 219pp; English.

XX AZ80767 to AZ83941 represent tags corresponding to distinct transcripts  
 CC that are preferentially transcribed in the metastatic breast tumour  
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AZ83942  
 CC to AZ86677 represent tags corresponding to distinct transcripts that are  
 CC preferentially transcribed in the primary or non-metastatic breast tumour  
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
 CC transcripts can be used for diagnosis, prognosis, monitoring and  
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
 CC by standard immunoassays or hybridisation/amplification reactions.  
 CC Compounds that modulate expression of the transcripts are potentially  
 CC useful for treatment of (metastatic) breast cancer, while promoters from  
 CC the transcripts are used to direct expression, in selected cell types, of  
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
 CC particularly an antigen-encoding sequence for use in gene or cell-based  
 CC vaccines. Polypeptides encoded by the transcripts are also useful in  
 CC vaccines; for diagnosing breast cancer and for raising specific  
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
 CC agents. Host cells that produce the polypeptides can be used to expand  
 CC and isolate populations of educated, antigen-specific immune effector  
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
 CC immunotherapy

XX Sequence 10 BP; 3 A; 1 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 896 ACTTTGATGA 905

Db 1 ACTTTGATGA 10

RESULT 172

AZ85118/C

ID AZ85118 standard; DNA; 10 BP.

AC AZ85118;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell downregulated transcript tag #4352.  
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;

XX antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO9965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US013647.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089977P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PA (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

```

XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX
XX Claim 1; Page 175; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX
XX Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 819 TCTTCTGAGT 828
XX Db TCTTCTGAGT 1
XX
XX RESULT 173
XX AAZ85314
XX ID AAZ85314 standard; DNA; 10 BP.
XX AC AAZ85314;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Metastatic breast tumour cell downregulated transcript tag #4548.
XX
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013647.
XX
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997B.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B. L.
XX PA (SHAN/) SHANKARA S.

```

```

XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX
XX Claim 1; Page 181; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX
XX Sequence 10 BP; 7 A; 1 C; 1 G; 1 T; 0 U; 0 Other.
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 128 GCAAAAAAAT 137
XX Db GCAAAAAAAT 10
XX
XX RESULT 174
XX AAZ86557
XX ID AAZ86557 standard; DNA; 10 BP.
XX AC AAZ86557;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Metastatic breast tumour cell downregulated transcript tag #5791.
XX
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US013647.
XX
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B. L.
XX PA (SHAN/) SHANKARA S.

```

```

PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
FI Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX
XX Claim 1; Page 211; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful as
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 0 A; 1 C; 3 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1655 TGTGCTGTTT 1664
Db 1 TGTGCTGTTT 10
|||||

RESULT 175
AAZ83190/c
ID AAZ83190 standard; DNA; 10 BP.
XX
XX AAZ83190;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell upregulated transcript tag #2424.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.

```

```

XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX
XX Claim 1; Page 124; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful as
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 803 GTGCTTGGC 812
Db 10 GTGCTTGGC 1
|||||

RESULT 176
AAZ84261/c
ID AAZ84261 standard; DNA; 10 BP.
XX
XX AAZ84261;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell downregulated transcript tag #3495.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.

```

```

PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 152; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 0 C; 1 G; 8 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 65 TAAAAACAAA 74
Db 10 TAAAAACAAA 1
RESULT 177
AAZ85291
ID AAZ85291 standard; DNA; 10 BP.
XX
AC AAZ85291;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell downregulated transcript tag #4525.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
PR

```

---

```

PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 180; 219pp; English
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 6 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 933 AGGAAACAGAT 942
Db 1 AGGAAACAGAT 10
RESULT 178
AAZ82395
ID AAZ82395 standard; DNA; 10 BP.
XX
AC AAZ82395;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell downregulated transcript tag #4525.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO9965928-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013647.
XX
XX 18-JUN-1999; 99WO-US013647.
PR

```

```

XX 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX Claim 1; Page 102; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX Sequence 10 BP; 0 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 796 GCTGTGGTG 805
Db 1 GCTGTGGTG 10
RESULT 179
AAZ82662
ID AAZ82662 standard; DNA; 10 BP.
XX AAZ82662;
XX 07-APR-2000 (first entry)
XX Metastatic breast tumour cell upregulated transcript tag #1896.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
OS WO9965928-A2.
XX 23-DEC-1999.
PD

XX 18-JUN-1999; 99WO-US013647.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX Claim 1; Page 110; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX Sequence 10 BP; 4 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 999 TTTAATACAT 1008
Db 1 TTTAATACAT 10
RESULT 180
AAZ82891
ID AAZ82891 standard; DNA; 10 BP.
XX AAZ82891;
XX 07-APR-2000 (first entry)
XX Metastatic breast tumour cell upregulated transcript tag #2125.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
OS WO9965928-A2.
XX 23-DEC-1999.
PD

```

```

XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX PI WPI; 2000-106079/09.
XX DR
XX DR Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 116; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 3 A; 2 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1941 TCATTTCACA 1950
Db 1 TCATTTCACA 10
|||||
|

RESULT 181
AAZ83628/c
ID AAZ83628 standard; DNA; 10 BP.
XX AC AAZ83628;
XX AC
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #2862.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.

```

```

XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX PI WPI; 2000-106079/09.
XX DR
XX DR Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 135; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 5 A; 0 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 ACATTTCATTC 197
Db 10 ACATTTCATTC 1
|||||
|

RESULT 182
AAZ85057
ID AAZ85057 standard; DNA; 10 BP.
XX AC AAZ85057;
XX AC
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #429.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.

```

```

XX OS Homo sapiens.
XX OS
XX PN WO9965928-A2.
XX XX
XX PD 23-DEC-1999.
XX XX
XX PF 18-JUN-1999; 99WO-US013647.
XX XX
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX XX
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX XX
XX PI Roberts BL, Shankara S;
XX XX
XX DR WPI; 2000-106079/09.
XX XX
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 173; 219pp; English.
XX XX
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ8677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX XX
XX SQ Sequence 10 BP; 5 A; 2 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2109 CAATAAAGCT 2118
DB 1 CAATAAAGCT 10
RESULT 183
AAZ85761
ID AAZ85761 standard; DNA; 10 BP.
XX AC
XX AC AAZ85761;
XX XX
XX DT 07-APR-2000 (first entry)
XX XX
XX DE Metastatic breast tumour cell downregulated transcript tag #4995.
XX XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;

```

```

KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW anti-metastatic; vaccine; diagnosis; ss.
XX OS
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX XX
XX PD 23-DEC-1999.
XX XX
XX PF 18-JUN-1999; 99WO-US013647.
XX XX
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX XX
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX XX
XX PI Roberts BL, Shankara S;
XX XX
XX DR WPI; 2000-106079/09.
XX XX
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 192; 219pp; English.
XX XX
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ8677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX XX
XX SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2397 TGCTGGAGAA 2406
DB 1 TGCTGGAGAA 10
RESULT 184
AAZ74090/C
ID AAC74090 standard; cDNA; 10 BP.
XX AC
XX AC AAC74090;
XX XX
XX DT 02-FEB-2001 (first entry)
XX XX Human dendritic cell and monocyte expressed gene oligonucleotide #177.

```

```

XX KW Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
XX KW autoimmune disease; tumour; ss.
XX OS
XX OS Homo sapiens.
XX PN WO2000060074-A1.
XX PD 12-OCT-2000.
XX PF
XX PF 30-MAR-2000; 2000WO-JP002019.
XX PR 01-APR-1999; 99JP-00095481.
XX PR (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PA Hashimoto S, Matsushima K, Suzuki T;
XX PI WPI; 2000-619172/59.
XX DR
XX XX Groups of genes expressed in human dendritic cells at a greater or lesser
XX PT extent than in monocytes for investigation and diagnosis of autoimmune
XX PT disease and tumors.
XX PS Claim 10; Page 13; 95pp; Japanese.
XX XX The present invention describes a group of genes consisting of 100 genes
XX CC which are highly expressed in human dendritic cells; a group of genes
XX CC which are expressed at a higher frequency in human dendritic cells than
XX CC in human monocytes; and a group of genes which are expressed at lower
XX CC frequency in human dendritic cells than in human monocytes. Each group of
XX CC genes are characterised in that cDNAs of these genes respectively have
XX CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
XX CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
XX CC to AAC74213), each is continuous with the base sequence 5'-CATG-3'
XX CC located most closely to the poly-A region. The sequences can be used for
XX CC the investigation of the role and mechanism of the involvement of
XX CC dendritic cells in the immune system and for the study and diagnosis of
XX CC diseases in which dendritic cells play a significant role, e.g. cancers
XX CC and autoimmune diseases
XX SQ Sequence 10 BP; 2 A; 1 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 624 AGAAATATA 633
Db 10 AGAAATATA 1

RESULT 185
AAZ89813/c
ID AAZ89813 standard; cDNA; 10 BP.
XX AC
XX AC AAZ89813;
XX DT
XX DT 05-MAY-2000 (first entry)
XX DE Differential display primer OP117 used in rchd036 cloning.
XX KW Differentially expressed; cardiovascular disease; atherosclerosis;
XX KW ischaemia; reperfusion; hypertension; restenosis; arterial inflammation;
XX KW rchd036; transmembrane protein; ss.
XX OS Synthetic.
XX PN US6020463-A.
XX PD
XX PD 01-FEB-2000.
XX PF
XX PF 06-OCT-1997; 97US-00944423.

```

```

XX 10-FEB-1995; 95US-00386844.
XX PR 07-JUN-1995; 95US-00485573.
XX PR 09-FEB-1996; 96US-00599654.
XX XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Gimbrone MA, Falb DA;
XX XX WPI; 2000-146911/13.
XX DR
XX XX Marker proteins for the diagnosis of cardiovascular diseases such as
XX PT atherosclerosis and hypertension, comprising peptide sequences derived
XX PT from the rchd523 transmembrane protein.
XX PS Disclosure; Col 10; 121pp; English.
XX XX This sequence represents a differential display primer used in the
XX CC cloning of rchd036. Rchd036 is related to the rchd523 transmembrane
XX CC polypeptide (see AA78506) encoded by cDNA isolated from the rchd523
XX CC pchd523. The rchd523 protein is differentially expressed in diseased
XX CC cells compared to healthy cells. The rchd523 protein may be used as a
XX CC marker protein for the diagnosis of cardiovascular diseases such as
XX CC atherosclerosis, ischaemia, reperfusion, hypertension, restenosis and
XX CC arterial inflammation. rchd523 peptides may be used as antigens in the
XX CC production of antibodies specific for rchd523. The anti rchd523
XX CC antibodies may then be used in diagnostic assays to quantitatively
XX CC peptides in samples
XX SQ Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040
Db 10 CATCACCACC 1

RESULT 186
AAAL5243
ID AAAL5243 standard; DNA; 10 BP.
XX AC
XX AC AAAL5243;
XX DT
XX DT 04-SEP-2000 (first entry)
XX DE Primer MR8 for modified differential display of tumour antigens.
XX KW Epitope; tumour specific epitope; antigen; vaccine; tumour antigens;
XX KW cancer; infection; primer; ss.
XX OS Synthetic.
XX PN WO200028016-A1.
XX PD 18-MAY-2000.
XX PF
XX PF 10-NOV-1998; 98WO-US024029.
XX PR 10-NOV-1998; 98WO-US024029.
XX PA (UYRP ) UNIV ROCHESTER.
XX PI Zauderer M;
XX DR WPI; 2000-376533/32.
XX XX Novel method of identifying target epitopes or antigens specific for
XX PT human tumors, cancers and infected cells involving screening expression
XX PT library products of a cell expressing the target epitope.

```



XX PS Disclosure; Page 68; 132pp; English.

XX CC AAA15239-50 represent arbitrary primers which are used for modified differential display of tumour antigens, in the method of the invention. The specification describes a method for identifying a target epitope. CC CC The method comprises screening the products of an expression library from a cell expressing the target epitope with cytotoxic T cells generated against the cell to identify DNA clones expressing the target epitope. CC CC The method may also comprise providing a cytotoxic T cell specific for a gene product differentially expressed by a cell and measuring the cross-reactivity of the cytotoxic T cell. The methods are useful for CC CC identifying tumour specific target epitopes and antigens which are useful in immunogenic compositions or vaccines to induce the regression of CC CC tumors, cancers or infections in mammals. The genes expressed in a panel of tumour cells that are derived from single immortalised, non-tumourigenic cell line are used to generate HLA restricted cytotoxic T cells which are evaluated for activity against tumour cells. The method is useful to identify potential antigens expressed not only by the pathogen but also by the host cells whose gene expression is altered as a result of infection. The differential gene expression strategies can be applied to identify immunogenic molecules of cells infected with virus, CC CC fungus or mycobacterium

XX SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 TACTATGGC 1458  
Db 1 TACTATGGC 10  
|||||

RESULT 187  
AAZ88025/c  
ID AAZ88025 standard; DNA; 10 BP.  
AC AAZ88025;  
XX 19-APR-2000 (first entry)  
XX Human umbilical vein endothelial cell rchd036 primer SEQ ID NO:25.  
XX Cardiovascular disease; diagnosis; atherosclerosis; ischaemia;  
KW reperfusion; hypertension; restenosis; arterial inflammation;  
KW antiarteriosclerotic; vasotropic; hypotensive; PCR primer; ss.  
XX Homo sapiens.  
XX US6018025-A.  
XX 25-JAN-2000.  
XX 06-OCT-1997; 97US-00944868.  
XX 10-FEB-1995; 95US-00386844.  
PR 07-JUN-1995; 95US-00485573.  
PR 09-FEB-1996; 96US-00599654.  
XX (MILL-) MILLENIUM PHARM INC.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
XX Falb DA, Gimbrone MA;  
XX WPI; 2000-136704/12.  
XX Isolated polypeptide for treating and diagnosing cardiovascular disease,  
PT such as, atherosclerosis, ischemia/reperfusion, hypertension, restenosis  
PT and arterial inflammation.  
XX Example; Col 10; 122pp; English.

XX CC The present invention describes an isolated polypeptide (I) comprising either the amino acid sequence of 1481 residues, given in AAY68447, or an CC amino acid sequence encoded by the cDNA contained in plasmids pFCHD528A (ATCC 69985), pFCHD528B (ATCC 69986) and pFCHD528C (ATCC 69987). The CC polypeptide is useful in the treatment and diagnosis of cardiovascular CC disease, such as, atherosclerosis, ischaemia/reperfusion, hypertension, CC restenosis and arterial inflammation. AAZ88001 to AAZ88040, and AAY68444 CC to AAY68457 represent sequences used in the exemplification of the CC present invention

XX SQ Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACCACC 2040  
Db 10 CATCACCACC 1  
|||||

RESULT 188  
AAH55376/c  
ID AAH55376 standard; DNA; 10 BP.  
XX AAH55376;  
AC AAH55376;  
XX 03-SEP-2001 (first entry)  
XX Genomic DNA methylation parallel detection associated DNA fragment #278.  
XX DNA methylation; parallel detection; 5-unmethylated cytosine; CpG; CpNpG;  
KW amplification; transcription regulation; genetic imprinting;  
KW tumorigenesis; primer; ss.  
XX Unidentified.  
XX WO200142493-A2.  
XX 14-JUN-2001.  
XX 06-DEC-2000; 2000WO-DE004381.  
XX 06-DEC-1999; 99DE-01059691.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C;  
XX WPI; 2001-381705/40.  
XX Parallel detection of the methylation pattern of many genomic DNA  
PT regions, useful for detecting aberrant methylation, includes multiple  
PT amplification of chemically modified DNA.  
XX Claim 18; Page 22; 63pp; German.  
XX This invention describes a novel method for the parallel detection of the CC methylation status of genomic DNA (I) which involves a (i) sample being CC treated chemically to convert 5-unmethylated cytosine to uracil, CC thymidine or some other base having hybridization behavior different from CC that of C, then amplifying simultaneously at least 10 different fragments CC (of fewer than 2 kb) using synthetic oligonucleotide (ON) primers. These CC primers are based on regulatory, transcribed and/or translated segments CC present in the sample after chemical treatment. The sequence context of CC all, or some, of the CpG and CpNpG motifs in the amplified products is CC then determined. The method is used to detect aberrant methylation CC patterns in the genome, these are implicated in regulation of CC transcription, genetic imprinting and tumorigenesis. Many target regions CC in the genome can be analyzed simultaneously and it is not essential to CC know the sequence context of all targeted regions. Primers may be CC designed for preferential amplification of particular segments of

CC interest (e.g. promoters and exons)  
 XX Sequence 10 BP; 4 A; 0 C; 0 G; 6 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 371 AATTAATTAA 380  
 DB 10 AATTAATTAA 1  
 |||||

RESULT 189  
 AAH55375  
 ID AAH55375 standard; DNA; 10 BP.  
 AC AAH55375;  
 DT 03-SEP-2001 (first entry)  
 XX Genomic DNA methylation parallel detection associated DNA fragment #277.  
 XX DNA methylation; parallel detection; 5-unmethylated cytosine; CpG; CpnpG;  
 KW amplification; transcription regulation; genetic imprinting;  
 KW tumorigenesis; primer; ss.  
 XX Unidentified.  
 OS  
 XX  
 XX WO200142493-A2.  
 PN  
 XX  
 PD 14-JUN-2001.  
 XX  
 XX 06-DEC-2000; 2000WO-DE004381.  
 PF  
 XX  
 PR 06-DEC-1999; 99DE-01059691.  
 XX  
 PA (EPiG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C;  
 PI  
 XX WPI; 2001-381705/40.  
 DR  
 XX  
 XX Parallel detection of the methylation pattern of many genomic DNA  
 PT regions, useful for detecting aberrant methylation, includes multiple  
 PT amplification of chemically modified DNA.  
 XX  
 PS Claim 18; Page 22; 63pp; German.  
 XX  
 CC This invention describes a novel method for the parallel detection of the  
 CC methylation status of genomic DNA (I) which involves a (I) sample being  
 CC treated chemically to convert 5-unmethylated cytosine to uracil,  
 CC thymidine or some other base having hybridization behavior different from  
 CC that of C, then amplifying simultaneously at least 10 different fragments  
 CC (of fewer than 2 kb) using synthetic oligonucleotide (ON) primers. These  
 CC primers are based on regulatory, transcribed and/or translated segments  
 CC present in the sample after chemical treatment. The sequence context of  
 CC all, or some, of the CpG and CpnpG motifs in the amplified products is  
 CC then determined. The method is used to detect aberrant methylation  
 CC patterns in the genome, these are implicated in regulation of  
 CC transcription, genetic imprinting and tumorigenesis. Many target regions  
 CC in the genome can be analyzed simultaneously and it is not essential to  
 CC know the sequence context of all targeted regions. Primers may be  
 CC designed for preferential amplification of particular segments of  
 CC interest (e.g. promoters and exons)  
 XX  
 SQ Sequence 10 BP; 6 A; 0 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 371 AATTAATTAA 380

DB 1 AATTAATTAA 10  
 |||||

RESULT 190  
 AAH19969/c  
 ID AAH19969 standard; DNA; 10 BP.  
 AC AAH19969;  
 XX  
 XX 07-AUG-2001 (first entry)  
 DE Mouse Treg immunoregulatory network related tag #40.  
 XX  
 KW Mouse; EST; expressed sequence tag; contig; immunoregulation;  
 KW immunosuppression; Treg immunoregulatory network; inflammatory;  
 KW immune disorder; T regulatory lymphocyte; T helper cell; dermatological;  
 KW antiinflammatory; immunosuppressive; antiarteriosclerotic; antiallergic;  
 KW antidiabetic; neuroprotective; osteopathic; antiarthritic; anti-ulcer;  
 KW rheumatoid arthritis; osteoarthritis; glomerular nephritis; diabetes;  
 KW inflammatory bowel disease; vascular disease; atherosclerosis; psoriasis;  
 KW vasculitis; skin disease; dermatitis; Crohn's disease; lung disease;  
 KW ulcerative colitis; lupus erythematosus; autoimmune disorder; emphysema;  
 KW hypersensitivity; multiple sclerosis; chronic bronchitis; asthma;  
 KW idiopathic pulmonary fibrosis; primer; probe; tag; ss.  
 XX  
 OS Mus musculus.  
 OS Synthetic.  
 XX  
 XX WO200127267-A2.  
 PN  
 XX  
 PD 19-APR-2001.  
 XX  
 XX 06-OCT-2000; 2000WO-GB003821.  
 PF  
 XX  
 PR 08-OCT-1999; 99GB-00023790.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD  
 XX  
 PI Adams E, Waldmann H, Cobbold S, Ziegler WH;  
 XX  
 XX WPI; 2001-300216/31.  
 DR  
 XX  
 XX Isolated genes differentially expressed in T helper 1 Th1 and Th2  
 PT and T regulatory (Treg) lymphocytes useful in prophylaxis, diagnosis and  
 PT therapy of inflammatory and immune diseases.  
 XX  
 PS Example 4; Page 4; 29pp; English.  
 XX  
 CC The present invention describes an isolated gene (I) obtainable by: (a)  
 CC comparing the expression of one or more genes in populations of T helper  
 CC 1 lymphocytes (Th1)-, Th2- and T regulatory cells (Treg)-enriched cell  
 CC populations to identify a gene which is differentially expressed in the  
 CC populations; and (b) isolating the gene. (I) can have dermatological,  
 CC antiinflammatory, immunosuppressive, antiarteriosclerotic, antiallergic,  
 CC antidiabetic, neuroprotective, osteopathic, antiarthritic and anti-ulcer  
 CC activities. (I) can be used in anti-inflammatory and immunoregulatory  
 CC compositions for use in therapy, prophylaxis, or diagnosis and/or in a  
 CC pharmaceutical excipient, a unit dosage form or in a form suitable for  
 CC local or systemic administration. Methods from the present invention can  
 CC be used for detecting Th1 and/or Th2 and/or Treg cells in a biological  
 CC sample, for cell typing or for determining the number of Th1 and/or Th2  
 CC and/or Treg cells in a biological sample. Diseases which may be treated  
 CC by compositions of the invention include rheumatoid and osteoarthritis,  
 CC glomerular nephritis, diabetes, inflammatory bowel disease, vascular  
 CC diseases e.g. atherosclerosis and vasculitis, skin diseases such as  
 CC psoriasis and dermatitis, Crohn's disease, ulcerative colitis, lupus  
 CC erythematosus, autoimmune disorders, hypersensitivity, multiple  
 CC sclerosis, and lung diseases e.g. chronic bronchitis, emphysema,  
 CC idiopathic pulmonary fibrosis and asthma. The invention is also useful  
 CC for analysis of serum, urine and biopsy material. The invention is also  
 CC therapy for multiple sclerosis. AAH19969 is a DNA fragment which  
 CC represent sequence used in the exemplified method of the present invention.

```

XX SQ Sequence 10 BP; 4 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2256 TGTATGTAAA 2265
DB 10 TGTATGTAAA 1

RESULT 191
AAH63332/c
ID AAH63332 standard; cDNA; 10 BP.
XX AC AAH63332;
XX DT 20-SEP-2001 (first entry)
XX DE Human melanocyte specific transcriptome sequence SEQ ID NO: 172.
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;
XX KW cancer diagnosis; cell specific gene expression; ss.
XX OS Homo sapiens.
XX PN WO200138577-A2.
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US031922.
XX PR 24-NOV-1999; 99US-00448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velulescu VE, Vogelstein B, Kinzler KW;
XX PP WPI; 2001-367706/38.
XX PT New isolated polynucleotides, useful for identifying specific cell type,
XX PT such as cancer cell, comprises transcriptomes expressed in particular
XX PT cell types.
XX PS Claim 1; Page 43; 94pp; English.
XX SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 886 TGTGACTGGG 895
DB 10 TGTGACTGGG 1

RESULT 192
AAH63847
ID AAH63847 standard; cDNA; 10 BP.
XX AC AAH63847;
XX DT 20-SEP-2001 (first entry)
XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 313.
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;
XX KW cancer diagnosis; cell specific gene expression; ss.
XX OS Homo sapiens.
XX PN WO200138577-A2.
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US031922.
XX PR 24-NOV-1999; 99US-00448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.

```

```

DT 20-SEP-2001 (first entry)
XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 587.
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;
XX KW cancer diagnosis; cell specific gene expression; ss.
XX OS Homo sapiens.
XX PN WO200138577-A2.
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US031922.
XX PR 24-NOV-1999; 99US-00448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velulescu VE, Vogelstein B, Kinzler KW;
XX PP WPI; 2001-367706/38.
XX PT New isolated polynucleotides, useful for identifying specific cell type,
XX PT such as cancer cell, comprises transcriptomes expressed in particular
XX PT cell types.
XX PS Claim 13; Page 55; 94pp; English.
XX SQ Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1874 AAAGCCAAGA 1883
DB 1 AAAGCCAAGA 10

RESULT 193
AAH63473/c
ID AAH63473 standard; cDNA; 10 BP.
XX AC AAH63473;
XX DT 20-SEP-2001 (first entry)
XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 313.
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;
XX KW cancer diagnosis; cell specific gene expression; ss.
XX OS Homo sapiens.
XX PN WO200138577-A2.
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US031922.
XX PR 24-NOV-1999; 99US-00448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.

```

```

XX PI Velculescu VE, Vogelstein B, Kinzler KW;
XX DR WPI; 2001-367706/38.
XX PT New isolated polynucleotides, useful for identifying specific cell type,
XX PT such as cancer cell, comprises transcriptomes expressed in particular
XX PT cell types.
XX PS Claim 13; Page 46; 94pp; English.
XX CC The present invention describes a method of identifying the type of cell
XX CC in a sample, involving determining which of the sequences AAH63161-
XX CC AAH64724 is expressed by the cell. The transcriptomes described in the
XX CC invention are cell-type specific, cancer specific or ubiquitously
XX CC expressed in humans. They can also be used to screen for drugs, reduce
XX CC cancer specific gene expression, standardise expression and restore the
XX CC function of a diseased cell or tissue. The present sequence is one of the
XX CC transcriptomes described in the exemplification of the invention
XX SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 ACCAGTAGCA 354
DB 10 ACCAGTAGCA 1

RESULT 194
AAH63223/c
ID AAH63223 standard; cDNA; 10 BP.
XX AC AAH63223;
XX DT 20-SEP-2001 (first entry)
XX DE Human colon epithelium specific transcriptome sequence SEQ ID NO: 63.
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;
XX KW cancer diagnosis; cell specific gene expression; ss.
XX OS Homo sapiens.
XX PN WO200138577-A2.
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US031922.
XX PR 24-NOV-1999; 99US-00448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu VE, Vogelstein B, Kinzler KW;
XX DR WPI; 2001-367706/38.
XX PT New isolated polynucleotides, useful for identifying specific cell type,
XX PT such as cancer cell, comprises transcriptomes expressed in particular
XX PT cell types.
XX PS Claim 13; Page 40; 94pp; English.
XX CC The present invention describes a method of identifying the type of cell
XX CC in a sample, involving determining which of the sequences AAH63161-
XX CC AAH64724 is expressed by the cell. The transcriptomes described in the
XX CC invention are cell-type specific, cancer specific or ubiquitously
XX CC expressed in humans. They can also be used to screen for drugs, reduce
XX CC cancer specific gene expression, standardise expression and restore the
XX CC function of a diseased cell or tissue. The present sequence is one of the

```

```

CC transcriptomes described in the exemplification of the invention
XX SQ Sequence 10 BP; 3 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1727 ATTACACCAT 1736
DB 10 ATTACACCAT 1

RESULT 195
AAH64367/c
ID AAH64367 standard; cDNA; 10 BP.
XX AC AAH64367;
XX DT 20-SEP-2001 (first entry)
XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 195.
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;
XX KW cancer diagnosis; cell specific gene expression; ss.
XX OS Homo sapiens.
XX PN WO200138577-A2.
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US031922.
XX PR 24-NOV-1999; 99US-00448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu VE, Vogelstein B, Kinzler KW;
XX DR WPI; 2001-367706/38.
XX PT New isolated polynucleotides, useful for identifying specific cell type,
XX PT such as cancer cell, comprises transcriptomes expressed in particular
XX PT cell types.
XX PS Claim 13; Page 66; 94pp; English.
XX CC The present invention describes a method of identifying the type of cell
XX CC in a sample, involving determining which of the sequences AAH63161-
XX CC AAH64724 is expressed by the cell. The transcriptomes described in the
XX CC invention are cell-type specific, cancer specific or ubiquitously
XX CC expressed in humans. They can also be used to screen for drugs, reduce
XX CC cancer specific gene expression, standardise expression and restore the
XX CC function of a diseased cell or tissue. The present sequence is one of the
XX CC transcriptomes described in the exemplification of the invention
XX SQ Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 819 TCTTCTGAGT 828
DB 10 TCTTCTGAGT 1

RESULT 196
AAH64148
ID AAH64148 standard; cDNA; 10 BP.
XX AC AAH64148;

```

XX DT 20-SEP-2001 (first entry)

XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 988.

XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;

XX KW cancer diagnosis; cell specific gene expression; ss.

XX OS Homo sapiens.

XX FN WO200138577-A2.

XX PD 31-MAY-2001.

XX PF 21-NOV-2000; 2000WO-US031922.

XX PR 24-NOV-1999; 99US-00448480.

XX PA (UWJO ) UNIV JOHNS HOPKINS.

XX PI Velculescu VE, Vogelstein B, Kinzler KW;

XX DR WPI; 2001-367706/38.

XX PT New isolated polynucleotides, useful for identifying specific cell type,

XX PT such as cancer cell, comprises transcriptomes expressed in particular

XX PT cell types.

XX PS Claim 13; Page 61; 94pp; English.

XX CC The present invention describes a method of identifying the type of cell

XX CC in a sample, involving determining which of the sequences AAH63161-

XX CC AAH64724 is expressed by the cell. The transcriptomes described in the

XX CC invention are cell-type specific, cancer specific or ubiquitously

XX CC expressed in humans. They can also be used to screen for drugs, reduce

XX CC cancer specific gene expression, standardise expression and restore the

XX CC function of a diseased cell or tissue. The present sequence is one of the

XX CC transcriptomes described in the exemplification of the invention

XX SQ Sequence 10 BP; 5 A; 2 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2109 CAATAAACTG 2118

Db 1 CAATAAACTG 10

RESULT 197

AAF69643

ID AAF69643 standard; DNA; 10 BP.

AC AAF69643;

DT 18-APR-2001 (first entry)

DE Human IL4Ralpha gene probe #283.

XX KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;

XX KW allergic disease; probe; ss.

XX OS Homo sapiens.

XX FN WO200104270-A1.

XX PD 18-JAN-2001.

XX PF 13-JUL-2000; 2000WO-US019094.

XX PR 13-JUL-1999; 99US-0143435P.

PA (GENA-) GENAISSANCE PHARM INC.

XX Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;

PI Windemuth AK;

XX WPI; 2001-103078/11.

XX PT New isolated polynucleotide useful for the identification of therapeutics

XX PT in allergic diseases is new.

XX PS Disclosure; Page 46; 188pp; English.

XX CC The present invention relates to polymorphisms of the human interleukin 4

XX CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference

XX CC sequence). Polynucleotides comprising polymorphic gene variants are

XX CC useful for therapeutic purposes. For example, where a patient may benefit

XX CC from expression of a particular IL4Ralpha protein isoform, an expression

XX CC vector encoding the isoform may be administered to the patient. It may

XX CC desirable to decrease or block expression of a particular IL4Ralpha

XX CC isogene, which may be done by turning off by transforming a targeted

XX CC organ, tissue or cell population with an expression vector that expresses

XX CC high levels of untranslatable mRNA for the isogene. Specific therapeutics

XX CC identified by these methods may be useful for allergic diseases. The

XX CC present sequence is a probe for human IL4R-alpha

XX SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1211 AACGAGCTCC 1220

Db 1 AACGAGCTCC 10

RESULT 198

AAF55786/c

ID AAF55786 standard; DNA; 10 BP.

AC AAF55786;

DT 19-APR-2001 (first entry)

XX Peptide nucleic acid #3.

XX Peptide nucleic acid; dendrimer; PNA; ss.

XX Unidentified.

XX Key Location/Qualifiers

PH modified\_base 1

FT /tag= a

FT /mod\_base= OTHER

FT /note= "Carboxyfluoresceinyl-T"

FT modified\_base 10

FT /tag= b

FT /mod\_base= OTHER

FT /note= "T-linker-Lys-NH2, where linker is

FT NH(CH2)20(CH2)20CH2C(O)-"

XX WO200102861-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-DK000351.

XX 29-JUN-1999; 99DK-00000934.

XX (DAKO-) DAKO AS.

XX Lohse J;

DR WPI; 2001-168366/17.  
 XX  
 PT New dendrimers or their protected forms which provide spacing between  
 PT terminal peripheral functional groups to which various compounds are  
 PT attached, useful as a detection or signal amplification system for  
 PT detecting nucleic acids, etc.  
 XX  
 PS Example 21; Page 68; 131pp; English.  
 XX  
 CC The present invention relates to dendrimers or their protected forms  
 CC which provide spacing between terminal peripheral functional groups to  
 CC which various compounds are attached e.g. peptide nucleic acids (PNA).  
 CC The dendrimer can be used as a detection system or as a signal  
 CC amplification system for detecting the presence of compounds in  
 CC biological samples and for labelling compounds. The present sequence is a  
 CC peptide nucleic acid used in the present invention  
 XX  
 SQ Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 124 ACTGGCAAAA 133  
 Db 10 ACTGGCAAAA 1  
 RESULT 199  
 AAF33290/c  
 ID AAF33290 standard; DNA; 10 BP.  
 XX  
 AC AAF33290;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast highly expressed gene SAGE tag oligonucleotide SEQ ID NO:29.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velulescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX  
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle..  
 XX  
 PS Example; Page 21; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substrate with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle; the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 0 A; 1 C; 1 G; 8 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 970 AAGAGAAAAAC 979  
 Db 10 AAGAGAAAAAC 1  
 RESULT 200  
 AAF34153/c  
 ID AAF34153 standard; DNA; 10 BP.  
 XX  
 AC AAF34153;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:89.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velulescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX  
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 PS Example; Page 31; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention.

XX  
 SQ Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0;

QY 407 TTCATCATCC 416  
 |||||  
 Db 10 TTCATCATCC 1

## RESULT 201

AAF34326/c  
 ID AAF34326 standard; DNA; 10 BP.

XX  
 AC AAF34326;

XX  
 DT 23-MAR-2001 (first entry)

XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1065.

XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX  
 OS Saccharomyces cerevisiae.

XX  
 FN WO200077214-A2.

XX  
 PD 21-DEC-2000.

XX  
 PF 14-JUN-2000; 2000WO-US016223.

XX  
 PR 16-JUN-1999; 99US-00335032.

XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.

XX  
 PI Velculescu V, Vogelstein B, Kinzler K;

XX  
 DR WPI; 2001-061874/07.

XX  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX  
 PS Example; Page 38; 419pp; English.

XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF; genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. At least  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate phases of the cell cycle. The  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention.

XX  
 SQ Sequence 10 BP; 6 A; 1 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0;

QY 323 ATATTTTTC 332  
 |||||  
 Db 10 ATATTTTTC 1

## RESULT 202

AAF35035  
 ID AAF35035 standard; DNA; 10 BP.

XX  
 AC AAF35035;

XX  
 DT 23-MAR-2001 (first entry)

XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1774.

XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX  
 OS Saccharomyces cerevisiae.

XX  
 FN WO200077214-A2.

XX  
 PD 21-DEC-2000.

XX  
 PF 14-JUN-2000; 2000WO-US016223.

XX  
 PR 16-JUN-1999; 99US-00335032.

XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.

XX  
 PI Velculescu V, Vogelstein B, Kinzler K;

XX  
 DR WPI; 2001-061874/07.

XX  
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX  
 PS Example; Page 63; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate phases which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1122 ACCACTTGGG 1131  
 Db 1 ACCACTTGGG 10  
 RESULT 203  
 AAF35364  
 ID AAF35364 standard; DNA; 10 BP.  
 AC AAF35364;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2103.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UWJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX  
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.  
 XX  
 PS Example; Page 75; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate phases which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 3 A; 1 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1902 TAAATTTACTT 1911  
 Db 1 TAAATTTACTT 10  
 RESULT 204  
 AAF35749/c  
 ID AAF35749 standard; DNA; 10 BP.  
 XX  
 AC AAF35749;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO: 4444  
 XX  
 KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae  
 XX  
 PN WO200077214 A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UWJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX  
 DR



XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT Gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
XX Example; Page 88; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
XX Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1886 AGCAGAGATT 1895  
Db 10 AGCAGAGATT 1  
|||  
RESULT 205  
AAF36005/C  
ID AAF36005 standard; DNA; 10 BP.  
XX  
AC AAF36005;  
XX  
XX 23-MAR-2001 (first entry)  
XX  
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2744.  
XX  
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;  
XX serial analysis of gene expression; antifungal; tag; identification;  
XX linker; PCR primer; ds.  
XX  
XX Saccharomyces cerevisiae.  
XX  
XX WO200077214-A2.  
XX  
XX 21-DEC-2000.  
XX  
XX 14-JUN-2000; 2000WO-US016223.  
XX  
XX 16-JUN-1999; 99US-00335032.  
XX  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX

PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
XX  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
XX Example; Page 98; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
XX Sequence 10 BP; 3 A; 0 C; 2 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 195 TTCAAAATAC 204  
Db 10 TTCAAAATAC 1  
|||  
RESULT 206  
AAF36878  
ID AAF36878 standard; DNA; 10 BP.  
XX  
AC AAF36878;  
XX  
XX 23-MAR-2001 (first entry)  
XX  
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1617  
XX  
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;  
XX serial analysis of gene expression; antifungal; tag; identification;  
XX linker; PCR primer; ds.  
XX  
XX Saccharomyces cerevisiae.  
XX  
XX WO200077214-A2.  
XX  
XX 21-DEC-2000.  
XX  
XX 14-JUN-2000; 2000WO-US016223.  
XX  
XX 16-JUN-1999; 99US-00335032.  
XX  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX

```

XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX XX
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 129; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate phases which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention.
XX SQ Sequence 10 BP; 9 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 379 AAAAAAGAAA 388
Db 1 AAAAAAGAAA 10
|||||
AAAF37302
ID AAF37302 standard; DNA; 10 BP.
XX
XX AAF37302;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4041.
XX
XX Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX KW serial analysis of gene expression; antifungal; tag; identification;
XX KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX OS WO200077214-A2.
XX PN 21-DEC-2000.
XX PD
XX

```

```

PF 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K.
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 144; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate phases which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33262 to AAF33267
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention.
XX SQ Sequence 10 BP; 6 A; 0 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 61 ATTGTAAAAA 70
Db 1 ATTGTAAAAA 10
|||||
AAAF40032/C
ID AAF40032 standard; DNA; 10 BP.
XX
XX AAF40032;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6771.
XX
XX Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX KW serial analysis of gene expression; antifungal; tag; identification;
XX KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX OS WO200077214-A2.
XX PN

```

```

XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX FI Velculescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX XX
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 241; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 213 ACCAGTGGAT 222
Db |||||
10 ACCAGTGGAT 1
RESULT 209
AAF42219
ID AAF42219 standard; DNA; 10 BP.
XX AC AAF42219;
XX XX
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8958.
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX KW serial analysis of gene expression; antifungal; tag; identification;
XX KW linker; PCR primer; ds.

```

```

OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX XX
XX PD 21-DEC-2000.
XX XX
XX PF 14-JUN-2000; 2000WO-US016223.
XX XX
XX PR 16-JUN-1999; 99US-00335032.
XX XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX XX
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX XX WPI; 2001-061874/07.
XX DR
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 319; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 4 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1854 GATTGTAGAA 1863
Db |||||
1 GATTGTAGAA 10
RESULT 210
AAF35568
ID AAF35568 standard; DNA; 10 BP.
XX AC AAF35568;
XX XX
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2307
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

```

KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 OS Saccharomyces cerevisiae.  
 PN WO200077214-A2.  
 XX 21-DEC-2000.  
 XX 14-JUN-2000; 2000WO-US016223.  
 PF 16-JUN-1999; 99US-00335032.  
 PR (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI WPI; 2001-061874/07.  
 DR Yeast gene coding sequences comprising NORF genes with serial analysis of  
 XX gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Example; Page 82; 419pp; English.  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention.  
 XX Sequence 10 BP; 5 A; 0 C; 2 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 935 GAAAGATTTT 944  
 Db 1 GAAAGATTTT 10  
 RESULT 211  
 AAF36681  
 ID AAF36681 standard; DNA; 10 BP.  
 XX AAF36681;  
 AC AAF36681;  
 XX 23-MAR-2001 (first entry)  
 DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3420.  
 DE

XX Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX Saccharomyces cerevisiae.  
 OS WO200077214-A2.  
 XX 21-DEC-2000.  
 XX 14-JUN-2000; 2000WO US016223.  
 PF 16-JUN-1999; 99US-00335032.  
 PR (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI WPI; 2001-061874/07.  
 DR Yeast gene coding sequences comprising NORF genes with serial analysis of  
 XX gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Example; Page 122; 419pp; English.  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention.  
 XX Sequence 10 BP; 3 A; 0 C; 3 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 78 GTTGTGAAA 87  
 Db 1 GTTGTGAAA 10  
 RESULT 212  
 AAF39705  
 ID AAF39705 standard; DNA; 10 BP.  
 XX AAF39705;  
 AC AAF39705;  
 XX

```

DT 23-MAR-2001 (first entry)
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6444.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
OS WO200077214-A2.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 230; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression of
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2441 AGGAACAAG 2450
DB 1 AGGAACAAG 10
RESULT 213
AAF34344/C
ID AAF34344 standard; DNA; 10 BP.

```

```

XX AAF34344;
XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1083.
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
OS WO200077214-A2.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 38; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression of
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX Sequence 10 BP; 2 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1129 GGAAGAATAT 1138
DB 10 GGAAGAATAT 1

```

RESULT 214  
 AAF34715/C  
 ID AAF34715 standard; DNA; 10 BP.  
 XX AC AAF34715;  
 XX DT 23-MAR-2001 (first entry)  
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1454.  
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.  
 XX PN WO200077214-A2.  
 XX PD 21-DEC-2000.  
 XX PF 14-JUN-2000; 2000WO-US016223.  
 XX PR 16-JUN-1999; 99US-00335032.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Example; Page 51; 419pp; English.  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF3262 to AAF3267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX Sequence 10 BP; 3 A; 3 C; 0 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TGAATAATGTG 27  
 |||||

Db 10 TGAATAATGTG 1  
 RESULT 215  
 AAF34978/C  
 ID AAF34978 standard; DNA; 10 BP.  
 XX AC AAF34978;  
 XX DT 23-MAR-2001 (first entry)  
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1717.  
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.  
 XX PN WO200077214-A2.  
 XX PD 21-DEC-2000.  
 XX PF 14-JUN-2000; 2000WO-US016223.  
 XX PR 16-JUN-1999; 99US-00335032.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Example; Page 61; 419pp; English.  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF3262 to AAF3267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX Sequence 10 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TGAATAATGTG 27  
 |||||

```

QY      1056 GTCCAATTAC 1065
Db      |||||
        10 GTCCAATTAC 1

RESULT 216
AAF35422
ID      AAF35422 standard; DNA; 10 BP.
AC      AAF35422;
XX      23-MAR-2001 (first entry)
XX      Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2161.
XX      Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW      nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW      serial analysis of gene expression; antifungal; tag; identification;
KW      linker; PCR primer; ds.
XX      Saccharomyces cerevisiae.
XX      WO200077214-A2.
XX      21-DEC-2000.
XX      14-JUN-2000; 2000WO-US016223.
XX      16-JUN-1999; 99US-00335032.
XX      (UYJO ) UNIV JOHNS HOPKINS.
XX      Velulescu V, Vogelstein B, Kinzler K;
XX      WPI; 2001-061874/07.
XX      Yeast gene coding sequences comprising NORF genes with serial analysis of
PT      gene expression (SAGE) tags, useful for studying, monitoring and
PT      affecting phases of the cell cycle.
XX      Example; Page 77; 419pp; English.
XX      The present invention describes an isolated DNA molecule comprising a
CC      coding sequence of a yeast gene selected from a group of 745 NORF (not
CC      previously assigned open reading frame; or nonannotated ORF) genes
CC      comprising a SAGE (serial analysis of gene expression) tag. Also
CC      described are: (1) a method (M1) of using NORF genes to affect the cell
CC      cycle comprising administering a NORF gene whose expression varies by at
CC      least 10% between any two phases of the cell cycle selected from log
CC      phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC      antifungal drugs comprising: (a) contacting a test substance with a yeast
CC      cell; and (b) monitoring expression of a NORF gene whose expression
CC      varies as in M1, where a test substance which modifies the expression of
CC      the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC      identifying human genes which are involved in cell cycle progression
CC      comprising contacting human DNA with a probe which comprises at least 10
CC      contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC      and (4) a method (M4) for identifying a candidate drug as a member of a
CC      class of drugs having a characteristic effect on gene expression in a
CC      yeast cell comprising contacting a yeast cell with a candidate drug and
CC      monitoring expression in the yeast cell of at least 1 NORF gene whose
CC      expression is affected by the class of drugs. The NORF genes may be used
CC      to study, monitor and affect phases of the cell cycle, the differentially
CC      expressed genes may be used as markers of phases of the cell cycle. The
CC      methods may be used to identify candidate drugs which affect the cell
CC      cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC      represent SAGE tags used in the exemplification of the present invention.
CC      AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC      method, in the exemplification of the present invention
XX      Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

```

---

```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1838 AAACACGCTG 1847
Db      |||||
        1 AAACACGCTG 10

RESULT 217
AAF35685
ID      AAF35685 standard; DNA; 10 BP.
AC      AAF35685;
XX      23-MAR-2001 (first entry)
XX      Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2424.
XX      Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW      nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW      serial analysis of gene expression; antifungal; tag; identification;
KW      linker; PCR primer; ds.
XX      Saccharomyces cerevisiae.
XX      WO200077214-A2.
XX      21-DEC-2000.
XX      14-JUN-2000; 2000WO-US016223.
XX      16-JUN-1999; 99US-00335032.
XX      (UYJO ) UNIV JOHNS HOPKINS.
XX      Velulescu V, Vogelstein B, Kinzler K;
XX      WPI; 2001-061874/07.
XX      Yeast gene coding sequences comprising NORF genes with serial analysis of
PT      gene expression (SAGE) tags, useful for studying, monitoring and
PT      affecting phases of the cell cycle.
XX      Example; Page 86; 419pp; English.
XX      The present invention describes an isolated DNA molecule comprising a
CC      coding sequence of a yeast gene selected from a group of 745 NORF (not
CC      previously assigned open reading frame; or nonannotated ORF) genes
CC      comprising a SAGE (serial analysis of gene expression) tag. Also
CC      described are: (1) a method (M1) of using NORF genes to affect the cell
CC      cycle comprising administering a NORF gene whose expression varies by at
CC      least 10% between any two phases of the cell cycle selected from log
CC      phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC      antifungal drugs comprising: (a) contacting a test substance with a yeast
CC      cell; and (b) monitoring expression of a NORF gene whose expression
CC      varies as in M1, where a test substance which modifies the expression of
CC      the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC      identifying human genes which are involved in cell cycle progression
CC      comprising contacting human DNA with a probe which comprises at least 10
CC      contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC      and (4) a method (M4) for identifying a candidate drug as a member of a
CC      class of drugs having a characteristic effect on gene expression in a
CC      yeast cell comprising contacting a yeast cell with a candidate drug and
CC      monitoring expression in the yeast cell of at least 1 NORF gene whose
CC      expression is affected by the class of drugs. The NORF genes may be used
CC      to study, monitor and affect phases of the cell cycle, the differentially
CC      expressed genes may be used as markers of phases of the cell cycle. The
CC      methods may be used to identify candidate drugs which affect the cell
CC      cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC      represent SAGE tags used in the exemplification of the present invention.
CC      AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC      method, in the exemplification of the present invention

```

XX SQ Sequence 10 BP; 6 A; 1 C; 2 G; 1 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 TGGCAAAAAA 135  
 |||||  
 DB 1 TGGCAAAAAA 10

RESULT 218  
 AAF36782/c  
 ID AAF36782 standard; DNA; 10 BP.  
 XX AC AAF36782;  
 XX DT 23-MAR-2001 (first entry)  
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3521.  
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.  
 XX PN WO200077214-A2.  
 XX PD 21-DEC-2000.  
 XX PF 14-JUN-2000; 2000WO-US016223.  
 XX PR 16-JUN-1999; 99US-00335032.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX PS Example; Page 125; 419pp; English.  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression  
 CC of the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX SQ Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1328 ATAACGAAGA 1337  
 |||||  
 DB 10 ATAACGAAGA 1

RESULT 219  
 AAF36869/c  
 ID AAF36869 standard; DNA; 10 BP.  
 XX AC AAF36869;  
 XX DT 23-MAR-2001 (first entry)  
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:414H  
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.  
 XX PN WO200077214-A2.  
 XX PD 21-DEC-2000.  
 XX PF 14-JUN-2000; 2000WO-US016223.  
 XX PR 16-JUN-1999; 99US-00335032.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX PS Example; Page 128; 419pp; English.  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression  
 CC of the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially



CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 0 A; 0 C; 1 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 AAAAAACAAA 75  
 |||||  
 Db 10 AAAAAACAAA 1

RESULT 220  
 AAF40273  
 ID AAF40273 standard; DNA; 10 BP.

XX AC AAF40273;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7012.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI Velculescu V, Vogelstein B, Kinzler K;

XX DR WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 250; 419pp; English.

CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX

SQ Sequence 10 BP; 6 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 ATTAGAAGAA 267  
 |||||  
 Db 1 ATTAGAAGAA 10

RESULT 221

AAF42240

ID AAF42240 standard; DNA; 10 BP.

XX AC AAF42240;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8979.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI Velculescu V, Vogelstein B, Kinzler K;

XX DR WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 320; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention

XX  
 SQ Sequence 10 BP; 3 A; 1 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 940 GATTTTATCA 949  
 |||||  
 Db 1 GATTTTATCA 10

RESULT 222  
 AAF43436  
 ID AAF43436 standard; DNA; 10 BP.

AC AAF43436;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11575.

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

PF 14-JUN-2000; 2000WO-US016223.

PR 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 363; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 1;  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention

SQ Sequence 10 BP; 4 A; 1 C; 0 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1352 TTAAATTCAT 1361  
 |||||  
 Db 1 TTAAATTCAT 10

RESULT 223  
 AAF39999/c

ID AAF39999 standard; DNA; 10 BP.

AC AAF39999;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11575.

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

PF 14-JUN-2000; 2000WO-US016223.

PR 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 240; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 2 A; 1 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 623 CAGAAATAT 632  
 Db 10 CAGAAATAT 1

## RESULT 224

AAF41653  
 ID AAF41653 standard; DNA; 10 BP.

AC AAF41653;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8392.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velulescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 299; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX

SQ Sequence 10 BP; 7 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 GAAAAAACCA 93

Db 1 GAAAAAACCA 10

## RESULT 225

AAF41771

ID AAF41771 standard; DNA; 10 BP.

AC AAF41771;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8510.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velulescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 303; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes

comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 GAACGTGGTGC 281  
|||||||  
DB 1 GAACGTGGTGC 10

RESULT 226  
AAF42620/c  
ID AAF42620 standard; DNA; 10 BP.

AC AAF42620;

XX 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10759.

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.

PS Example; Page 334; 419pp; English.

XX

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle, the methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 4 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1894 TTATCACATA 1903  
|||||||  
DB 10 TTATCACATA 1

RESULT 227

AAF34095/c

ID AAF34095 standard; DNA; 10 BP.

XX AAF34095;

XX 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:834.

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032;

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.

XX PS Example; Page 29; 419pp; English.

XX CC The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression,

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX SQ Sequence 10 BP; 0 A; 1 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 970 AAGGAAAC 979

DB 10 AAGGAAAC 1

RESULT 228

AAF37233

ID AAF37233 standard; DNA; 10 BP.

AC AAF37233;

XX 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3972.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PF 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

PA Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX

PT Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX Example; Page 141; 419pp; English.

XX CC The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression,

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX SQ Sequence 10 BP; 3 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ATCACCTATT 63

DB 1 ATCACCTATT 10

RESULT 229

AAF38377/c

ID -AAF38377 standard; DNA; 10 BP.

AC AAF38377;

XX 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5116.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PF 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

PA Velculescu V, Vogelstein B, Kinzler K;

XX



```

XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velulescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 244; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC antifungal drug comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention.
XX PT Sequence 10 BP; 4 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
XX PT
XX PT Query Match 0.4%; Score 10; DB 1; Length 10;
XX PT Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX PT Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 159 TATTAAAGAT 168
DB 10 TATTAAAGAT 1
RESULT 232
AAF41625
ID AAF41625 standard; DNA; 10 BP.
AC AAF41625;
XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8364.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX OS WO200077214-A2.
XX PN
XX

```

```

PD XX 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX XX 16-JUN-1999; 99US-00335032.
XX XX (UYJO ) UNIV JOHNS HOPKINS.
XX PA Velulescu V, Vogelstein B, Kinzler K;
XX PI WPI; 2001-061874/07.
XX DR Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 298; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention.
XX PT Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
XX PT
XX PT Query Match 0.4%; Score 10; DB 1; Length 10;
XX PT Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX PT Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1493 CTTTGCCAAA 1502
DB 1 CTTTGCCAAA 10
RESULT 233
AAF37203/C
ID AAF37203 standard; DNA; 10 BP.
XX AAF37203;
XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3942.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX OS

```

```

XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PF 16-JUN-1999; 99US-00335032.
XX PF (UYJO ) UNIV JOHNS HOPKINS.
XX PA Velculescu V, Vogelstein B, Kinzler K;
XX PI WPI; 2001-061874/07.
XX DR
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 140; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 5 A; 1 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 938 AGAGTTTAT 947
DB 10 AAGATTAT 1

RESULT 234
AAF38607
ID AAF38607 standard; DNA; 10 BP.
AC AAF38607;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5346.
XX
XX Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;

```

```

KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PF 16-JUN-1999; 99US-00335032.
XX PF (UYJO ) UNIV JOHNS HOPKINS.
XX PA Velculescu V, Vogelstein B, Kinzler K;
XX PI WPI; 2001-061874/07.
XX DR
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 190; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 4 A; 0 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 AAATATTTT 330
DB 1 AAATATTTT 10

RESULT 235
AAF39560
ID AAF39560 standard; DNA; 10 BP.
AC AAF39560;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6299.
XX

```



KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 XX Saccharomyces cerevisiae.  
 XX WO200077214-A2.  
 XX 21-DEC-2000.  
 XX 14-JUN-2000; 2000WO-US016223.  
 XX 16-JUN-1999; 99US-00335032.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Example; Page 225; 419pp; English.  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1023 AGACCACTCC 1032  
 |||||  
 Db 1 AGACCACTCC 10

RESULT 236  
 AAF41556  
 ID AAF41556 standard; DNA; 10 BP.  
 XX  
 AC AAF41556;  
 XX  
 DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8295.  
 DE  
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 XX Saccharomyces cerevisiae.  
 XX WO200077214-A2.  
 XX 21-DEC-2000.  
 XX 14-JUN-2000; 2000WO-US016223.  
 XX 16-JUN-1999; 99US-00335032.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Example; Page 296; 419pp; English.  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX Sequence 10 BP; 4 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2018 CTTCAAAACCA 2027  
 |||||  
 Db 1 CTTCAAAACCA 10

RESULT 237  
 AAF43985/c  
 ID AAF43985 standard; DNA; 10 BP.  
 XX

AC	AAF43985;
XX	
DT	23-MAR-2001 (first entry)
XX	
DE	Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:12124.
XX	
KW	Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW	nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW	serial analysis of gene expression; antifungal; tag; identification;
KW	linker; PCR primer; ds.
XX	
OS	Saccharomyces cerevisiae.
XX	
PN	WO200077214-A2.
XX	
PD	21-DEC-2000.
XX	
PF	14-JUN-2000; 2000MO-US016223.
XX	
PR	16-JUN-1999; 99US-00335032.
XX	
PA	(UYJO ) UNIV JOHNS HOPKINS.
XX	
PI	Velculescu V, Vogelstein B, Kinzler K;
XX	
DR	WPI; 2001-061874/07.
XX	
PT	Yeast gene coding sequences comprising NORF genes with serial analysis of
PT	gene expression (SAGE) tags, useful for studying, monitoring and
PT	affecting phases of the cell cycle.
XX	
PS	Example; Page 383; 419pp; English.
XX	
CC	The present invention describes an isolated DNA molecule comprising a
CC	coding sequence of a yeast gene selected from a group of 745 NORF (not
CC	previously assigned open reading frame; or nonannotated ORF) genes
CC	comprising a SAGE (serial analysis of gene expression) tag. Also
CC	described are: (1) a method (M1) of using NORF genes to affect the cell
CC	cycle comprising administering a NORF gene whose expression varies by at
CC	least 10% between any two phases of the cell cycle selected from log
CC	phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC	antifungal drugs comprising: (a) contacting a test substance with a yeast
CC	cell; and (b) monitoring expression of a NORF gene whose expression
CC	varies as in M1, where a test substance which modifies the expression of
CC	the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC	identifying human genes which are involved in cell cycle progression
CC	comprising contacting human DNA with a probe which comprises at least 10
CC	contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC	and (4) a method (M4) for identifying a candidate drug as a member of a
CC	class of drugs having a characteristic effect on gene expression in a
CC	yeast cell comprising contacting a yeast cell with a candidate drug and
CC	monitoring expression in the yeast cell of at least 1 NORF gene whose
CC	expression is affected by the class of drugs. The NORF genes may be used
CC	to study, monitor and affect phases of the cell cycle, the differentially
CC	expressed genes may be used as markers of phases of the cell cycle. The
CC	methods may be used to identify candidate drugs which affect the cell
CC	cycle and for identification of antifungal drugs. AAF33288 to AAF44064
CC	represent SAGE tags used in the exemplification of the present invention.
CC	AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC	method, in the exemplification of the present invention
XX	
SQ	Sequence 10 BP; 1 A; 1 C; 1 G; 7 T; 0 U; 0 Other;
	Query Match 0.4%; Score 10; DB 1; Length 10;
	Best Local Similarity 100.0%; Pred. No. 1.9e+02;
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	2343 GAAATACAAA 2352
Db	10 GAAATACAAA 1
	RESULT 238

RESULT 239  
 AAF37506/c  
 ID AAF37506 standard; DNA: 10 BP.  
 XX AC AAF37506;  
 XX DT 23-MAR-2001 (first entry)  
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4245.  
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.  
 XX PN WO200077214-A2.  
 XX PD 21-DEC-2000.  
 XX PF 14-JUN-2000; 2000WO-US016223.  
 XX PR 16-JUN-1999; 99US-00335032.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Example; Page 151; 419pp; English.  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF3262 to AAF3267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX SQ Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1396 ATCAATAGAG 1405  
 Db |||||  
 10 ATCAATAGAG 1  
 RESULT 240  
 AAF38093  
 ID AAF38093 standard; DNA: 10 BP.  
 XX AC AAF38093;  
 XX DT 23-MAR-2001 (first entry)  
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4832.  
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.  
 XX PN WO200077214-A2.  
 XX PD 21-DEC-2000.  
 XX PF 14-JUN-2000; 2000WO-US016223.  
 XX PR 16-JUN-1999; 99US-00335032.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Example; Page 172; 419pp; English.  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF3262 to AAF3267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX SQ Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 945 TATCAGACGA 954  
|||||

Db 1 TATCAGACGA 10

## RESULT 241

AAF38320/c

ID AAF38320 standard; DNA; 10 BP.

XX AC AAF38320;

XX DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5059.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI Velculescu V, Vogelstein B, Kinzler K;

XX DR WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.

XX Example; Page 180; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention

SQ Sequence 10 BP; 4 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1391 TCATTATCAA 1400

Db 10 TCATTATCAA 1

## RESULT 242

AAF38644

ID AAF38644 standard; DNA; 10 BP.

XX AC AAF38644;

XX DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5143

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14 JUN 2000; 2000WO US016223.

XX PR 16-JUN-1999; 99US-00335032.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI Velculescu V, Vogelstein B, Kinzler K;

XX DR WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.

XX Example; Page 192; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 5 A; 1 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 337 AAATTTATAC 346  
 |||||  
 1 AAATTTATAC 10

Db

RESULT 243  
 AAF40279/C  
 ID AAF40279 standard; DNA; 10 BP.  
 XX  
 AC AAF40279;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7018.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 XX  
 DR WPI; 2001-061874/07.  
 XX  
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 PS Example; Page 250; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 4 A; 0 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1427 AATATATAAT 1436  
 |||||  
 10 AATATATAAT 1

Db

RESULT 244  
 AAF41775  
 ID AAF41775 standard; DNA; 10 BP.  
 XX  
 AC AAF41775;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8514.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 XX  
 DR WPI; 2001-061874/07.  
 XX  
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 PS Example; Page 304; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The

CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX

SQ Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 GAAGAAATCG 271

Db 1 GAAGAAATCG 10

RESULT 245

AAF43288

ID AAF43288 standard; DNA; 10 BP.

XX AAF43288;

AC AAF43288;

XX 23-MAR-2001 (first entry)

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11427.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX

OS Saccharomyces cerevisiae.

XX

XX WO200077214-A2.

XX

XX 21-DEC-2000.

XX

XX 14-JUN-2000; 2000WO-US016223.

XX

XX 16-JUN-1999; 99US-00335032.

XX

XX (UYJO ) UNIV JOHNS HOPKINS.

XX

XX Velculescu V, Vogelstein B, Kinzler K;

XX

XX WPI; 2001-061874/07.

XX

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX

XX Example; Page 358; 419pp; English.

XX

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF44064 to AAF44164  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX

SQ Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1166 TGGTAGAGAA 1175

Db 1 TGGTAGAGAA 10

RESULT 246

AAF35259

ID AAF35259 standard; DNA; 10 BP.

XX AAF35259;

AC AAF35259;

XX 23-MAR-2001 (first entry)

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1998.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX

XX Saccharomyces cerevisiae.

XX

XX WO200077214-A2.

XX

XX 21-DEC-2000.

XX

XX 14-JUN-2000; 2000WO-US016223.

XX

XX 16-JUN-1999; 99US-00335032.

XX

XX (UYJO ) UNIV JOHNS HOPKINS.

XX

XX Velculescu V, Vogelstein B, Kinzler K;

XX

XX WPI; 2001-061874/07.

XX

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX

XX Example; Page 71; 419pp; English.

XX

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 1 A; 1 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 325 ATTTTGCTG 334  
|||||  
1 ATTTTGCTG 10

## RESULT 247

AAAF39621  
ID AAF39621 standard; DNA; 10 BP.

AC AAF39621;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6360.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

16-JUN-1999; 99US-00335032.

(UYJO ) UNIV JOHNS HOPKINS.

Velculescu V, Vogelstein B, Kinzler K;

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 227; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression

varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 AGATTACGAC 174  
|||||  
1 AGATTACGAC 10

## RESULT 248

AAAF1338/C

ID AAF41338 standard; DNA; 10 BP.

AC AAF41338;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9077

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

16-JUN-1999; 99US-00335032.

(UYJO ) UNIV JOHNS HOPKINS.

Velculescu V, Vogelstein B, Kinzler K;

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 288; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 4 A; 1 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1394 TTATCAATAG 1403  
 DB 10 TTATCAATAG 1  
 |||||

RESULT 249  
 AAF42618/c  
 ID AAF42618 standard; DNA; 10 BP.  
 XX AAF42618;  
 AC AAF42618;  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10757.  
 XX

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX

OS Saccharomyces cerevisiae.

XX WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 334; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX

SQ Sequence 10 BP; 2 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 198 AAAATACATA 207  
 DB 10 AAAATACATA 1  
 |||||

RESULT 250

AAF34345

ID AAF34345 standard; DNA; 10 BP.

XX AAF34345;

AC AAF34345;

DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1084.

DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 38; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a



CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression of  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 2 A; 0 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 179 ATGTTTGTGA 189  
 |||||  
 Db 1 ATGTTTGTGA 10

RESULT 251  
 AAF36745/c  
 ID AAF36745 standard; DNA; 10 BP.  
 XX  
 AC AAF36745;  
 XX  
 XX 23-MAR-2001 (first entry)  
 DT  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3484.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 EN WO200077214-A2.  
 XX  
 XX 21-DEC-2000.  
 XX  
 XX 14-JUN-2000; 2000WO-US016223.  
 XX  
 XX 16-JUN-1999; 99US-00335032.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI WPI; 2001-061874/07.  
 DR

Yeast gene coding sequences comprising NORF genes with serial analysis of  
 gene expression (SAGE) tags, useful for studying, monitoring and  
 affecting phases of the cell cycle.

PS Example; Page 124; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 3 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1176 ATATAAATA 1185  
 |||||  
 Db 10 ATATAAATA 1

RESULT 252  
 AAF33555  
 ID AAF33555 standard; DNA; 10 BP.  
 XX  
 AC AAF33555;  
 XX  
 XX 23-MAR-2001 (first entry)  
 DT  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:294.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 EN WO200077214-A2.  
 XX  
 XX 21-DEC-2000.  
 XX  
 XX 14-JUN-2000; 2000WO-US016223.  
 XX  
 XX 16-JUN-1999; 99US-00335032.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI WPI; 2001-061874/07.  
 DR  
 XX  
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
PS Claim 1; Page 27; 419pp; English.  
XX  
XX The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
XX Sequence 10 BP; 9 A; 0 C; 1 G; 0 T; 0 U; 0 Other;  
SQ

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 AAAAAAGAAA 388  
Db 1 AAAAAAGAAA 10  
|||||

RESULT 253  
AAF34405  
ID AAF34405 standard; DNA; 10 BP.  
XX  
XX AAF34405;  
XX  
XX 23-MAR-2001 (first entry)  
XX  
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1144.  
XX  
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
XX Saccharomyces cerevisiae.  
XX  
XX WO200077214-A2.  
XX  
XX 21-DEC-2000.  
XX  
XX 14-JUN-2000; 2000WO-US016223.  
XX  
XX 16-JUN-1999; 99US-00335032.  
XX  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX Velculescu V, Vogelstein B, Kinzler K;

DR WPI; 2001-061874/07.  
XX  
XX Yeast gene coding sequences comprising NORF genes, useful for studying, monitoring and  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX Example; Page 40; 419pp; English.  
XX  
XX The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
XX Sequence 10 BP; 6 A; 0 C; 1 G; 3 T; 0 U; 0 Other;  
SQ

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 959 TGATTAAAAA 968  
Db 1 TGATTAAAAA 10  
|||||

RESULT 254  
AAF36200/C  
ID AAF36200 standard; DNA; 10 BP.  
XX  
XX AAF36200;  
XX  
XX 23-MAR-2001 (first entry)  
XX  
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2939.  
XX  
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
XX Saccharomyces cerevisiae.  
XX  
XX WO200077214-A2.  
XX  
XX 21-DEC-2000.  
XX  
XX 14-JUN-2000; 2000WO-US016223.  
XX  
XX 16-JUN-1999; 99US-00335032.  
XX  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX Velculescu V, Vogelstein B, Kinzler K;

```

XX PI Velculescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 105; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 0;
QY 1054 TCGTCCAATT 1063
DB 10 TCGTCCAATT 1
RESULT 255
AAF40125
ID AAF40125 standard; DNA; 10 BP.
XX AC AAF40125;
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6864.
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX KW serial analysis of gene expression; antifungal; tag; identification;
XX KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.

```

```

PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 245; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 6 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 0;
QY 2437 ATGAAGGAAA 2446
DB 1 ATGAAGGAAA 10
RESULT 256
AAF41100
ID AAF41100 standard; DNA; 10 BP.
XX AC AAF41100;
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7839.
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX KW serial analysis of gene expression; antifungal; tag; identification;
XX KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.

```

XX 14-JUN-2000; 2000WO-US016223.  
 XX 16-JUN-1999; 99US-00335032.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velulescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Example; Page 280; 419pp; English.  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX Sequence 10 BP; 2 A; 1 C; 2 G; 5 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 474 CGAATTTTGG 483  
 Db 1 CGAATTTTGG 10  
 |||||  
 RESULT 257  
 AAF33851/c  
 ID AAF33851 standard; DNA; 10 BP.  
 XX AAF33851;  
 AC AAF33851;  
 XX 23-MAR-2001 (first entry)  
 DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:590.  
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX Saccharomyces cerevisiae.  
 OS

PN WO200077214-A2.  
 XX 21-DEC-2000.  
 XX 14-JUN-2000; 2000WO-US016223.  
 XX 16-JUN-1999; 99US-00335032.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velulescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Claim 1; Page 396; 419pp; English.  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1396 ATCAATAGAG 1405  
 Db 10 ATCAATAGAG 1  
 |||||  
 RESULT 258  
 AAF39954  
 ID AAF39954 standard; DNA; 10 BP.  
 XX AAF39954;  
 AC AAF39954;  
 XX 23-MAR-2001 (first entry)  
 DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:604.  
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 KW

```

XX OS Saccharomyces cerevisiae.
XX KW WO200077214-A2.
XX PN 21-DEC-2000.
XX PD 14-JUN-2000; 2000WO-US016223.
XX PF 16-JUN-1999; 99US-00335032.
XX PR (UYJO ) UNIV JOHNS HOPKINS.
XX PA Velculescu V, Vogelstein B, Kinzler K;
XX PI WPI; 2001-061874/07.
XX DR
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 239; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 5 A; 0 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 754 ATAGTTGAAA 763
DB 1 ATAGTTGAAA 10
RESULT 259
AAF35394
ID AAF35394 standard; DNA; 10 BP.
XX AC AAF35394;
XX XX
XX 23-MAR-2001 (first entry)
XX DT
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2133.
XX XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

```

```

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX KW WO200077214-A2.
XX PN 21-DEC-2000.
XX PD 14-JUN-2000; 2000WO-US016223.
XX PF 16-JUN-1999; 99US-00335032.
XX PR (UYJO ) UNIV JOHNS HOPKINS.
XX PA Velculescu V, Vogelstein B, Kinzler K;
XX PI WPI; 2001-061874/07.
XX DR
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 76; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 4 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 900 TGATGAAGAT 909
DB 1 TGATGAAGAT 10
RESULT 260
AAF36420/C
ID AAF36420 standard; DNA; 10 BP.
XX AC AAF36420;
XX XX
XX 23-MAR-2001 (first entry)
XX DT
XX DE

```

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3159.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX WO200077214-A2.  
 XX  
 XX 21-DEC-2000.  
 XX  
 XX 14-JUN-2000; 2000WO-US016223.  
 PF  
 XX 16-JUN-1999; 99US-00335032.  
 PR  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI WPI; 2001-061874/07.  
 DR  
 XX  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 PT  
 XX Example; Page 112; 419pp; English.  
 PS  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF3262 to AAF3267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 3 A; 3 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 498 ATTGAAGG 507  
 Db |||||||||  
 10 ATTGAAGG 1  
 RESULT 261  
 ID AAF38893  
 XX AAF38893 standard; DNA; 10 BP.  
 AC AAF38893;

XX 23-MAR-2001 (first entry)  
 DT  
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5612  
 DE  
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX WO200077214-A2.  
 XX  
 XX 21-DEC-2000.  
 XX  
 XX 14-JUN-2000; 2000WO-US016223.  
 PF  
 XX 16-JUN-1999; 99US-00335032.  
 PR  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI WPI; 2001-061874/07.  
 DR  
 XX  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 PT  
 XX Example; Page 201; 419pp; English.  
 PS  
 XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF3262 to AAF3267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1259 AAGGACAAAG 1268  
 Db |||||||||  
 1 AAGGACAAAG 10  
 RESULT 262  
 AAF39096/c

ID XX AAF39096 standard; DNA; 10 BP.  
 AC AAF39096;  
 DT 23-MAR-2001 (first entry)  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5835.  
 XX  
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 XX Saccharomyces cerevisiae.  
 OS  
 XX WO200077214-A2.  
 PN  
 XX 21-DEC-2000.  
 XX  
 XX 14-JUN-2000; 2000WO-US016223.  
 PF  
 XX 16-JUN-1999; 99US-00335032.  
 PR  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI  
 XX WPI; 2001-061874/07.  
 DR  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 PS Example; Page 208; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1331 ACCGAAGAATT 1340  
 Db 10 ACCGAAGAATT 1

RESULT 263  
 AAF42788  
 ID AAF42788 standard; DNA; 10 BP.  
 XX  
 AC AAF42788;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10927.  
 XX  
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 XX Saccharomyces cerevisiae.  
 OS  
 XX WO200077214-A2.  
 PN  
 XX 21-DEC-2000.  
 PD  
 XX 14-JUN-2000; 2000WO-US016223.  
 PF  
 XX 16-JUN-1999; 99US-00335032.  
 PR  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI  
 XX WPI; 2001-061874/07.  
 DR  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 PS Example; Page 340; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1218 TCCACGGTTC 1227

```

Db      1  TCCACGGTTC 10
RESULT 264
AAF43422/c
ID  AAF43422 standard; DNA; 10 BP.
XX  AAF43422;
AC  AAF43422;
XX  23-MAR-2001 (first entry)
XX  Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11561.
XX  Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW  nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW  serial analysis of gene expression; antifungal; tag; identification;
KW  linker; PCR primer; ds.
XX  Saccharomyces cerevisiae.
OS  Saccharomyces cerevisiae.
XX  WO200077214-A2.
XX  21-DEC-2000.
XX  14-JUN-2000; 2000WO-US016223.
XX  16-JUN-1999; 99US-00335032.
XX  (UYJO ) UNIV JOHNS HOPKINS.
XX  Velculescu V, Vogelstein B, Kinzler K;
PI  WPI; 2001-061874/07.
XX  Yeast gene coding sequences comprising NORF genes with serial analysis of
PT  gene expression (SAGE) tags, useful for studying, monitoring and
PT  affecting phases of the cell cycle.
XX  Example; Page 362; 419pp; English.
XX  The present invention describes an isolated DNA molecule comprising a
CC  coding sequence of a yeast gene selected from a group of 745 NORF (not
CC  previously assigned open reading frame; or nonannotated ORF) genes
CC  comprising a SAGE (serial analysis of gene expression) tag. Also
CC  described are: (1) a method (M1) of using NORF genes to affect the cell
CC  cycle comprising administering a NORF gene whose expression varies by at
CC  least 10% between any two phases of the cell cycle selected from log
CC  phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC  antifungal drugs comprising: (a) contacting a test substance with a yeast
CC  cell; and (b) monitoring expression of a NORF gene whose expression
CC  varies as in M1, where a test substance which modifies the expression of
CC  the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC  identifying human genes which are involved in cell cycle progression
CC  comprising contacting human DNA with a probe which comprises at least 10
CC  contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC  and (4) a method (M4) for identifying a candidate drug as a member of a
CC  class of drugs having a characteristic effect on gene expression in a
CC  yeast cell comprising contacting a yeast cell with a candidate drug and
CC  monitoring expression in the yeast cell of at least 1 NORF gene whose
CC  expression is affected by the class of drugs. The NORF genes may be used
CC  to study, monitor and affect phases of the cell cycle, the differentially
CC  expressed genes may be used as markers of phases of the cell cycle, the
CC  methods may be used to identify candidate drugs which affect the cell
CC  cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC  represent SAGE tags used in the exemplification of the present invention.
CC  AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC  method, in the exemplification of the present invention
XX  Sequence 10 BP; 1 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

```

```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2482 TCCAAAAACA 2491
      |||||
DB      10 TCCAAAAACA 1
RESULT 265
AAF34490/c
ID  AAF34490 standard; DNA; 10 BP.
XX  AAF34490;
AC  AAF34490;
XX  23-MAR-2001 (first entry)
XX  Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1229.
XX  Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW  nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW  serial analysis of gene expression; antifungal; tag; identification;
KW  linker; PCR primer; ds.
XX  Saccharomyces cerevisiae
OS  Saccharomyces cerevisiae
XX  WO200077214-A2.
XX  21-DEC-2000.
XX  14-JUN-2000; 2000WO-US016223
XX  16-JUN-1999; 99US 00335032
XX  (UYJO ) UNIV JOHNS HOPKINS.
XX  Velculescu V, Vogelstein B, Kinzler K;
PI  WPI; 2001-061874/07.
XX  Yeast gene coding sequences comprising NORF genes with serial analysis of
PT  gene expression (SAGE) tags, useful for studying, monitoring and
PT  affecting phases of the cell cycle.
XX  Example; Page 43; 419pp; English.
XX  The present invention describes an isolated DNA molecule comprising a
CC  coding sequence of a yeast gene selected from a group of 745 NORF (not
CC  previously assigned open reading frame; or nonannotated ORF) genes
CC  comprising a SAGE (serial analysis of gene expression) tag. Also
CC  described are: (1) a method (M1) of using NORF genes to affect the cell
CC  cycle comprising administering a NORF gene whose expression varies by at
CC  least 10% between any two phases of the cell cycle selected from log
CC  phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC  antifungal drugs comprising: (a) contacting a test substance with a yeast
CC  cell; and (b) monitoring expression of a NORF gene whose expression
CC  varies as in M1, where a test substance which modifies the expression of
CC  the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC  identifying human genes which are involved in cell cycle progression
CC  comprising contacting human DNA with a probe which comprises at least 10
CC  contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC  and (4) a method (M4) for identifying a candidate drug as a member of a
CC  class of drugs having a characteristic effect on gene expression in a
CC  yeast cell comprising contacting a yeast cell with a candidate drug and
CC  monitoring expression in the yeast cell of at least 1 NORF gene whose
CC  expression is affected by the class of drugs. The NORF genes may be used
CC  to study, monitor and affect phases of the cell cycle, the differentially
CC  expressed genes may be used as markers of phases of the cell cycle, the
CC  methods may be used to identify candidate drugs which affect the cell
CC  cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC  represent SAGE tags used in the exemplification of the present invention.
CC  AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC  method, in the exemplification of the present invention
XX  Sequence 10 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

```



Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 475 GAATTTTGT 484  
 |||||  
 Db 10 GAATTTTGT 1

RESULT 266  
 ID AAF34724 standard; DNA; 10 BP.

XX AAF34724;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1463.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 serial analysis of gene expression; antifungal; tag; identification;  
 linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 gene expression (SAGE) tags, useful for studying, monitoring and  
 affecting phases of the cell cycle.

XX Example; Page 52; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 coding sequence of a yeast gene selected from a group of 745 NORF (not  
 previously assigned open reading frame; or nonannotated ORF) genes  
 comprising a SAGE (serial analysis of gene expression) tag. Also  
 described are: (1) a method (M1) of using NORF genes to affect the cell  
 cycle comprising administering a NORF gene whose expression varies by at  
 least 10% between any two phases of the cell cycle selected from log  
 phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 antifungal drugs comprising: (a) contacting a test substance with a yeast  
 cell; and (b) monitoring expression of a NORF gene whose expression  
 varies as in M1, where a test substance which modifies the expression of  
 the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 identifying human genes which are involved in cell cycle progression  
 comprising contacting human DNA with a probe which comprises at least 10  
 contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 and (4) a method (M4) for identifying a candidate drug as a member of a  
 class of drugs having a characteristic effect on gene expression in a  
 yeast cell comprising contacting a yeast cell with a candidate drug and  
 monitoring expression in the yeast cell of at least 1 NORF gene whose  
 expression is affected by the class of drugs. The NORF genes may be used  
 to study, monitor and affect phases of the cell cycle, the differentially  
 expressed genes may be used as markers of phases of the cell cycle. The  
 methods may be used to identify candidate drugs which affect the cell  
 cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 represent SAGE tags used in the exemplification of the present invention.  
 AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention  
 XX Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;  
 SQ

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1868 CTGAACAAG 1877  
 |||||  
 Db 1 CTGAACAAG 10

RESULT 267

AAF40070/C

ID AAF40070 standard; DNA; 10 BP.

XX AAF40070;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6809.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 serial analysis of gene expression; antifungal; tag; identification;  
 linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 gene expression (SAGE) tags, useful for studying, monitoring and  
 affecting phases of the cell cycle.

XX Example; Page 243; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 coding sequence of a yeast gene selected from a group of 745 NORF (not  
 previously assigned open reading frame; or nonannotated ORF) genes  
 comprising a SAGE (serial analysis of gene expression) tag. Also  
 described are: (1) a method (M1) of using NORF genes to affect the cell  
 cycle comprising administering a NORF gene whose expression varies by at  
 least 10% between any two phases of the cell cycle selected from log  
 phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 antifungal drugs comprising: (a) contacting a test substance with a yeast  
 cell; and (b) monitoring expression of a NORF gene whose expression  
 varies as in M1, where a test substance which modifies the expression of  
 the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 identifying human genes which are involved in cell cycle progression  
 comprising contacting human DNA with a probe which comprises at least 10  
 contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 and (4) a method (M4) for identifying a candidate drug as a member of a  
 class of drugs having a characteristic effect on gene expression in a  
 yeast cell comprising contacting a yeast cell with a candidate drug and  
 monitoring expression in the yeast cell of at least 1 NORF gene whose  
 expression is affected by the class of drugs. The NORF genes may be used  
 to study, monitor and affect phases of the cell cycle, the differentially  
 expressed genes may be used as markers of phases of the cell cycle. The  
 methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0;  
 QY 2268 GACCGGCGAT 2277  
 Db 10 GACCGGCGAT 1

RESULT 268  
 AAF40280/C  
 AC AAF40280;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7019.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 XX  
 DR WPI; 2001-061874/07.  
 XX

PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 250; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 3 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Mismatches 0;  
 QY 626 AAAATATAAT 635  
 Db 10 AAAATATAAT 1

RESULT 269  
 AAF41770/C  
 ID AAF41770 standard; DNA; 10 BP.  
 XX  
 AC AAF41770;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8509.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 XX  
 DR WPI; 2001-061874/07.  
 XX

PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 303; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2315 CTATCAGTTC 2324  
 Db |||||  
 10 CTATCAGTTC 1  
 RESULT 270  
 AAF33518/c  
 ID AAF33518 standard; DNA; 10 BP.  
 XX  
 AC AAF33518;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:257.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 DR WPI; 2001-061874/07.  
 XX  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 PS Claim 1; Page 27; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1396 ATCATAGAG 1405  
 Db |||||  
 10 ATCATAGAG 1  
 RESULT 271  
 AAF33852/c  
 ID AAF33852 standard; DNA; 10 BP.  
 XX  
 AC AAF33852;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:591.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 DR WPI; 2001-061874/07.  
 XX  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 PS Claim 1; Page 396; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate phases which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 ATCAATAGAG 1405  
 Db |||||  
 10 ATCAATAGAG 1

RESULT 272  
 AAF34992  
 ID AAF34992 standard; DNA; 10 BP.  
 AC AAF34992;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1731.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX

PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 PS Example; Page 61; 419pp; English.  
 XX

CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate phases which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX

SQ Sequence 10 BP; 4 A; 1 C; 0 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1563 TACATATTAT 1572  
 Db |||||  
 1 TACATATTAT 10

RESULT 273  
 AAF36344/G  
 ID AAF36344 standard; DNA; 10 BP.  
 AC AAF36344;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3083.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX

PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 PS Example; Page 110; 419pp; English.  
 XX

CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 1 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Gaps 0;  
 Matches 10; Conservative 0; Indels 0;

QY 1064 ACACAAAAT 1073  
 Db 10 ACACAAAAT 1

RESULT 274

AAF36972  
 ID AAF36972 standard; DNA; 10 BP.

XX AAF36972;

AC AAF36972;

DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3711.

DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 132; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 6 A; 0 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Gaps 0;  
 Matches 10; Conservative 0; Indels 0;

QY 446 AAGATGAAGA 455

Db 1 AAGATGAAGA 10

RESULT 275

AAF37749

ID AAF37749 standard; DNA; 10 BP.

XX AAF37749;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4488.

DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 160; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 4 A; 2 C; 1 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1558 GCTAATACAT 1567  
 Db 1 GCTAATACAT 10  
 RESULT 276  
 AAF39013/C  
 ID AAF39013 standard; DNA; 10 BP.  
 XX AAF39013;  
 AC AAF39013;  
 XX 23-MAR-2001 (first entry)  
 DT  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5752.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI WPI; 2001-061874/07.  
 XX  
 DR Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.  
 XX  
 PS Example; Page 205; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 6 A; 2 C; 0 G; 2 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 674 ATTTTGGATT 683  
 Db 10 ATTTTGGATT 1  
 RESULT 277  
 AAF39900  
 ID AAF39900 standard; DNA; 10 BP.  
 XX AAF39900;  
 AC AAF39900;  
 XX 23-MAR-2001 (first entry)  
 DT  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO.6619  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN WO200077214-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI WPI; 2001-061874/07.  
 XX  
 DR

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
XX Example; Page 237; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 4 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 ATAATGTTGA 365  
|||||||  
Db 1 ATAATGTTGA 10

RESULT 278  
AAF40110/c  
ID AAF40110 standard; DNA; 10 BP.

AC AAF40110;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6849.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX

XX Example; Page 244; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX

SQ Sequence 10 BP; 3 A; 2 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2161 GAATTAAGAT 2170  
|||||||  
Db 10 GAATTAAGAT 1

RESULT 279  
AAF40228

ID AAF40228 standard; DNA; 10 BP.

AC AAF40228;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6967.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Velculescu V, Vogelstein B, Kinzler K;  
 XX DR WPI; 2001-061874/07.  
 XX XX  
 XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX XX  
 XX PS Example; Page 248; 419pp; English.  
 XX CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX SQ Sequence 10 BP; 2 A; 0 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1748 ATGGTGTGAT 1757  
 Db 1 ATGGTGTGAT 10  
 RESULT 280  
 AAF42124/C  
 ID AAF42124 standard; DNA; 10 BP.  
 AC AAF42124;  
 XX XX  
 XX DT 23-MAR-2001 (first entry)  
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8863.  
 XX KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.  
 XX XX WO200077214-A2.  
 XX PN 21-DEC-2000.  
 XX PD  
 XX XX

PF 14-JUN-2000; 2000WO-US016223.  
 XX PR 16-JUN-1999; 99US-00335032.  
 XX XX  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX XX  
 XX PI Velculescu V, Vogelstein B, Kinzler K;  
 XX DR WPI; 2001-061874/07.  
 XX XX  
 XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX XX  
 XX PS Example; Page 316; 419pp; English.  
 XX CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX SQ Sequence 10 BP; 2 A; 1 C; 1 G; 6 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 594 AAGAAATATC 603  
 Db 10 AAGAAATATC 1  
 RESULT 281  
 AAF42175/C  
 ID AAF42175 standard; DNA; 10 BP.  
 XX AC AAF42175;  
 XX XX  
 XX DT 23-MAR-2001 (first entry)  
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8863.  
 XX KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.  
 XX XX WO200077214-A2.  
 XX PN



```

XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 318; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1933 GATCAGCATC 1942
Db 10 GATCAGCATC 1

RESULT 282
AAF43867/C
ID AAF43867 standard; DNA; 10 BP.
XX
XX AAF43867;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:12006.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX

```

```

OS Saccharomyces cerevisiae.
XX
XX PN WO200077214-A2.
XX
XX PD 21-DEC-2000.
XX
XX PF 14-JUN-2000; 2000WO-US016223.
XX
XX PR 16-JUN-1999; 99US-00335032.
XX
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX PI Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 378; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 3 A; 0 C; 1 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 CAATATTAAA 165
Db 10 CAATATTAAA 1

RESULT 283
AAF33364/C
ID AAF33364 standard; DNA; 10 BP.
XX
XX AAF33364;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10;
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX

```

KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX Saccharomyces cerevisiae.  
 OS  
 PN WO200077214-A2.  
 XX 21-DEC-2000.  
 PD 14-JUN-2000; 2000WO-US016223.  
 XX 16-JUN-1999; 99US-00335032.  
 PR (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI WPI; 2001-061874/07.  
 DR Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Claim 1; Page 24; 419pp; English.  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression  
 CC of the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on the expression of a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 SQ Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1056 GTCCCAATTAC 1065  
 DB 10 GTCCCAATTAC 1  
 RESULT 284  
 AAF34673  
 ID AAF34673 standard; DNA; 10 BP.  
 AC AAF34673;  
 XX  
 XX 23-MAR-2001 (first entry)  
 DT  
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1412.  
 DE

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF.  
 KW nor previously assigned open reading frame; nonannotated ORF. SAGE.  
 KW serial analysis of gene expression; antifungal; tag; linker; PCR primer; ds.  
 XX Saccharomyces cerevisiae.  
 OS  
 PN WO200077214-A2.  
 XX 21-DEC-2000.  
 PD 14-JUN-2000; 2000WO-US016223.  
 XX 16-JUN-1999; 99US-00335032.  
 PR (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 PI WPI; 2001-061874/07.  
 DR Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX Example; Page 50; 419pp; English.  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression  
 CC of the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on the expression of a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 SQ Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 CTGGCAAAA 134  
 DB 1 CTGGCAAAA 10  
 RESULT 285  
 AAF42142  
 ID AAF42142 standard; DNA; 10 BP.  
 XX  
 XX AAF42142;  
 AC  
 XX

DT	23-MAR-2001	(first entry)	
XX			
AC	AAF42886;		
DE			
XX			
XX	23-MAR-2001	(first entry)	
DT			
XX			
KW	Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;		
KW	not previously assigned open reading frame; nonannotated ORF; SAGE;		
KW	serial analysis of gene expression; antifungal; tag; identification;		
KW	linker; PCR primer; ds.		
XX			
OS	Saccharomyces cerevisiae.		
XX			
PN	WO200077214-A2.		
XX			
PD	21-DEC-2000.		
XX			
PF	14-JUN-2000; 2000WO-US016223.		
XX			
PR	16-JUN-1999; 99US-00335032.		
XX			
PA	(UYJO ) UNIV JOHNS HOPKINS.		
XX			
PI	Velculescu V, Vogelstein B, Kinzler K;		
XX			
DR	WPI; 2001-061874/07.		
XX			
PT	Yeast gene coding sequences comprising NORF genes with serial analysis of		
PT	gene expression (SAGE) tags, useful for studying, monitoring and		
PT	affecting phases of the cell cycle.		
XX			
PS	Example; Page 317; 419pp; English.		
XX			
CC	The present invention describes an isolated DNA molecule comprising a		
CC	coding sequence of a yeast gene selected from a group of 745 NORF (not		
CC	previously assigned open reading frame; or nonannotated ORF) genes		
CC	comprising a SAGE (serial analysis of gene expression) tag. Also		
CC	described are: (1) a method (M1) of using NORF genes to affect the cell		
CC	cycle comprising administering a NORF gene whose expression varies by at		
CC	least 10% between any two phases of the cell cycle selected from log		
CC	phase, S phase and G2/M; (2) a method (M2) for screening candidate		
CC	antifungal drugs comprising: (a) contacting a test substance with a yeast		
CC	cell; and (b) monitoring expression of a NORF gene whose expression		
CC	varies as in M1, where a test substance which modifies the expression of		
CC	the yeast gene is a candidate antifungal drug; (3) a method (M3) for		
CC	identifying human genes which are involved in cell cycle progression		
CC	comprising contacting human DNA with a probe which comprises at least 10		
CC	contiguous nucleotides of a NORF gene whose expression varies as in M1;		
CC	and (4) a method (M4) for identifying a candidate drug as a member of a		
CC	class of drugs having a characteristic effect on gene expression in a		
CC	yeast cell comprising contacting a yeast cell with a candidate drug and		
CC	monitoring expression in the yeast cell of at least 1 NORF gene whose		
CC	expression is affected by the class of drugs. The NORF genes may be used		
CC	to study, monitor and affect phases of the cell cycle, the differentially		
CC	expressed genes may be used as markers of phases of the cell cycle. The		
CC	methods may be used to identify candidate drugs which affect the cell		
CC	cycle and for identification of antifungal drugs. AAF33268 to AAF44064		
CC	represent SAGE tags used in the exemplification of the present invention.		
CC	AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE		
CC	method, in the exemplification of the present invention		
XX			
SQ	Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;		
	Query Match 0.4%; Score 10; DB 1; Length 10;		
	Best Local Similarity 100.0%; Pred. No. 1.9e+02;		
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1033 GATCGTACAG 1042		
Db	1 GATCGTACAG 10		
RESULT 286			
AAF42886/C			
ID	AAF42886 standard; DNA; 10 BP.		

```

RESULT 287
AAF34324/c
ID AAF34324 standard; DNA; 10 BP.
XX
XX AAF34324;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1063.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 38; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 288
AAF34785
ID AAF34785 standard; DNA; 10 BP.
XX
XX AAF34785;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1524.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K.
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 54; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 2069 CCGTTACTCTC 2078  
 Db 1 CCGTTACTCTC 10

RESULT 289  
 AAF36117/c  
 ID AAF36117 standard; DNA; 10 BP.  
 AC AAF36117;  
 XX 23-MAR-2001 (first entry)  
 DT  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2856.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX WO200077214-A2.  
 PN 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX  
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 PS Example; Page 102; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX Sequence 10 BP; 0 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 AACCAACAAA 98  
 Db 10 AACCAACAAA 1

RESULT 290  
 AAF38329/c  
 ID AAF38329 standard; DNA; 10 BP.  
 XX  
 AC AAF38329;  
 XX  
 DT 23-MAR-2001 (first entry)  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5068.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX WO200077214-A2.  
 PN 21-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016223.  
 XX  
 PR 16-JUN-1999; 99US-00335032.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX  
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 PS Example; Page 181; 419pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention

XX SQ Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 AAAGTGGCAA 131  
 |||||  
 Db 10 AAAGTGGCAA 1

RESULT 291  
 AAF38661/C  
 ID AAF38661 standard; DNA; 10 BP.  
 XX AAF38661;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5400.  
 DE  
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 XX Saccharomyces cerevisiae.  
 XX  
 XX WO200077214-A2.  
 XX  
 XX 21-DEC-2000.  
 XX  
 XX 14-JUN-2000; 2000WO-US016223.  
 XX  
 XX 16-JUN-1999; 99US-00335032.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 XX Example; Page 192; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 XX SQ Sequence 10 BP; 4 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 AAGAGTTGTT 83  
 |||||  
 Db 10 AAGAGTTGTT;

RESULT 292  
 AAF39083/C  
 ID AAF39083 standard; DNA; 10 BP.  
 XX AAF39083;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5822.  
 DE  
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 XX Saccharomyces cerevisiae.  
 XX  
 XX WO200077214-A2.  
 XX  
 XX 21-DEC-2000.  
 XX  
 XX 14-JUN-2000; 2000WO-US016223.  
 XX  
 XX 16-JUN-1999; 99US-00335032.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.  
 XX  
 XX Example; Page 207; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 CC  
 XX Sequence 10 BP; 4 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1897 TCACATAATT 1906  
 |||||  
 Db 10 TCACATAATT 1

## RESULT 293

AAF42120  
 ID AAF42120 standard; DNA; 10 BP.

XX AAF42120;

AC AAF42120;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8859.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velulescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 316; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
 CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 CC  
 XX Sequence 10 BP; 6 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 GATATTAAAA 229

Db 1 GATATTAAAA 10

## RESULT 294

AAF43670

ID AAF43670 standard; DNA; 10 BP.

XX AAF43670;

AC AAF43670;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11809.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Velulescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
 PT gene expression (SAGE) tags, useful for studying, monitoring and  
 PT affecting phases of the cell cycle.

XX Example; Page 371; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a  
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 CC previously assigned open reading frame; or nonannotated ORF) genes  
 CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 CC cycle comprising administering a NORF gene whose expression varies by at  
 CC least 10% between any two phases of the cell cycle selected from log  
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
 CC cell; and (b) monitoring expression of a NORF gene whose expression  
 CC varies as in M1, where a test substance which modifies the expression of  
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
 CC identifying human genes which are involved in cell cycle progression  
 CC comprising contacting human DNA with a probe which comprises at least 10  
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a  
 CC class of drugs having a characteristic effect on gene expression in a  
 CC yeast cell comprising contacting a yeast cell with a candidate drug and  
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
 CC expression is affected by the class of drugs. The NORF genes may be used  
 CC to study, monitor and affect phases of the cell cycle, the differentially  
 CC expressed genes may be used as markers of phases of the cell cycle. The  
 CC methods may be used to identify candidate drugs which affect the cell  
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
 CC represent SAGE tags used in the exemplification of the present invention.  
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
 CC method, in the exemplification of the present invention  
 CC  
 SQ Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0;

QY 758 TTGAAGAGAGA 767  
 Db 1 TTGAAGAGAGA 10  
 |||||

## RESULT 295

AAS19602  
 ID AAS19602 standard; DNA; 10 BP.

AC AAS19602;

DT 26-MAR-2002 (first entry)

DE Primer-extension oligonucleotide #33 to detect human MPL polymorphisms.  
 KW Human; single nucleotide polymorphism; SNP; MPL; chromosome 1p34;  
 KW myeloproliferative leukaemia virus oncogene; haplotyping; genotyping;  
 KW congenital amegakaryocytic thrombocytopaenia; CMT; primer; ss.

OS Homo sapiens.

PN WO200179232-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US012301.

PR 14-APR-2000; 2000US-0197839P.

PA (GENA-) GENAISSANCE PHARM INC.

PI Chew A, Choi JY, Koshy B, Stephens JC;

WPI; 2002-055251/07.

DR Nucleotide polymorphisms in the human myeloproliferative leukemia virus  
 XX oncogene (MPL) gene, useful for studying the function of and expressing  
 PT MPL protein for use in screening drugs for treating diseases related to  
 PT MPL activity.

PS Claim 17; Page 16; 85pp; English.

CC The present invention relates to novel single nucleotide polymorphisms  
 CC (SNPs) in the human myeloproliferative leukaemia virus oncogene (MPL)  
 CC gene located on chromosome 1p34, and methods for haplotyping and/or  
 CC genotyping the MPL gene. The methods of the invention make use of allele-  
 CC specific oligonucleotides (ASOs) as probes and primers and/or primer-  
 CC extension oligonucleotides for detecting MPL gene polymorphisms. The  
 CC polynucleotides and screened compounds are useful for the treatment of  
 CC diseases associated with MPL activity, such as congenital amegakaryocytic  
 CC thrombocytopaenia (CMT). AAS19570-AAS19607 represent primer-extension  
 CC oligonucleotides for detecting human MPL gene polymorphisms

XX Sequence 10 BP; 4 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0;

QY 2034 CACCACCAAC 2043

Db 1 CACCACCAAC 10  
 |||||

## RESULT 296

AAS19659  
 ID AAS19659 standard; DNA; 10 BP.

AC AAS19659;

DT 26-MAR-2002 (first entry)

DE Primer-extension oligonucleotide #12 to detect human GHRHR polymorphisms  
 KW Human; single nucleotide polymorphism; SNP; GHRHR; chromosome 7p14;  
 KW growth hormone releasing hormone receptor; haplotyping; genotyping;  
 KW isolated growth hormone deficiency; IGHD; pituitary adenoma; primer; ss.

OS Homo sapiens.

PN WO200179239-A2.

PD 25-OCT-2001.

PF 17-APR-2001; 2001WO-US012453.

PR 17-APR-2000; 2000US-0197978P.

PA (GENA-) GENAISSANCE PHARM INC.

PI Chew A, Choi JY, Denton RR, Nandabalan P, Sankar R.

WPI; 2002-066342/09.

DR Genotyping Human Growth hormone releasing hormone receptor gene of  
 XX individual for determining haplotype of individual by determining  
 PT identity of nucleotide pair at specific polymorphic sites for two copies  
 PT of gene.

PS Claim 18; Page 15; 90pp; English.

CC The present invention relates to novel single nucleotide polymorphisms  
 CC (SNPs) in the human growth hormone releasing hormone receptor (GHRHR)  
 CC gene located on chromosome 7p14, and methods for haplotyping and/or  
 CC genotyping the GHRHR gene. The methods of the invention make use of  
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or  
 CC primer-extension oligonucleotides for detecting the GHRHR gene  
 CC polymorphisms. The polynucleotides and screened compounds are useful for  
 CC the treatment of diseases associated with GHRHR activity, such as  
 CC isolated growth hormone deficiency (IGHD) and pituitary adenomas.  
 CC AAS19648-AAS19673 represent primer-extension oligonucleotides for  
 CC detecting human GHRHR gene polymorphisms

XX Sequence 10 BP; 6 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0;

QY 261 AGAAGAAATC 270

Db 1 AGAAGAAATC 10  
 |||||

## RESULT 297

AAS95353  
 ID AAS95353 standard; DNA; 10 BP.



```

XX AAS95353;
AC
XX
XX
DT 14-FEB-2002 (first entry)
DE Human Histamine H2 receptor ASO primer extension PCR primer #13.
XX
XX Human; histamine H2 receptor; HRH2; ss; PCR primer; polymorphic variant;
KW haplotyping; genotyping; acid-peptic disorder; mammary cancer;
KW gastric carcinoma; allele specific oligonucleotide; ASO;
XX primer extension.
XX
XX Homo sapiens.
OS
XX
XX WO200179220-A2.
PN
XX
XX 25-OCT-2001.
PD
XX
XX 12-APR-2001; 2001WO-US011941.
PF
XX
XX 12-APR-2000; 2000US-0196406P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Chew A, Choi JY, Koshiy B;
PI
XX
XX WPI; 2002-055249/07.
DR
XX
XX New human histamine H2 receptor (HRH2) isogene polymorphic variants,
PT useful in expressing HRH2 protein for use in screening for candidate
PT drugs to treat diseases related to HRH2 activity.
XX
XX Claim 17; Page 14; 62pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising a
CC polymorphic variant of a reference sequence for human Histamine H2
CC receptor (HRH2) gene, its fragment or complement, and the polymorphic
CC variant contains an HRH2 isogene defined by a haplotype listed in the
CC specification. Also disclosed are methods for haplotyping and genotyping
CC the HRH2 gene of an individual, a method for predicting a haplotype pair
CC for the HRH2 gene of an individual, identifying an association between a
CC trait and at least one haplotype or haplotype pair of HRH2 gene, allele
CC specific oligonucleotides (ASO) for performing the haplotyping/
CC genotyping, a recombinant nonhuman organisms transformed or transfected
CC with the polymorphic variant, the protein expressed by the polymorphic
CC variant, an antibody raised against the protein and screening for drugs
CC targeting the polypeptide by contacting HRH2 polymorphic variant with a
CC candidate agent and assaying for binding activity. The polymorphisms are
CC useful for studying the biological function of HRH2 gene, as well as in
CC identifying drugs targeting this protein for the treatment of disorder
CC related to its abnormal expression or function. The polymorphic variants
CC may be used in screening for compounds targeting CALM1 to treat a
CC specific condition or disease predicted to be associated with HRH2
CC activity, in studying the effect of the variation on the biological
CC activity of HRH2 as well as on the binding affinity of candidate drugs
CC targeting HRH2 for the treatment of acid-peptic disorders of the
CC gastrointestinal tract and also possibly human mammary cancer and gastric
CC carcinoma. The polymorphism and haplotype data can also be used for
CC validating whether HRH2 is a suitable drug target for drugs to treat acid
CC -peptic disorders of the gastrointestinal tract, screening of such drugs
CC and reducing bias in clinical trials of such drugs. The present sequence
CC is the 3' terminus of an ASO primer extension PCR primer used to detect
CC the polymorphisms of the invention
XX
XX Sequence 10 BP; 4 A; 1 C; 2 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2375 TCAATGAAGT 2384
Db 1 TCAATGAAGT 10

```

```

RESULT 298
ABL59309
ID ABL59309 standard; DNA; 10 BP.
XX
XX ABL59309;
AC
XX
XX 07-OCT-2002 (first entry)
DT
XX
XX Primer for platelet activating factor receptor gene polymorphisms.
DE
XX Human; platelet activating factor receptor; PTAFR; isogene; cancer;
KW chromosome 1; inflammatory disease; coronary disease; primer; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200251859-A2.
PN
XX
XX 04-JUL-2002.
PD
XX
XX 05-NOV-2001; 2001WO-US047441.
PF
XX
XX 03-NOV-2000; 2000US-0245633P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Chew A, Choi JY, Koshiy B;
PI
XX
XX WPI; 2002-566672/60.
DR
XX
XX New genetic variants comprising haplotypes of the human Platelet
PT Activating Factor Receptor (PTAFR) gene, useful for treating or screening
PT drugs for treating e.g. inflammatory diseases, coronary diseases or
PT cancer.
XX
XX Claim 17; Page 14; 59pp; English.
XX
XX The present sequence represents a primer which is used for detecting
CC polymorphisms in the human platelet Activating Factor Receptor (PTAFR)
CC gene. The gene comprises polymorphic sites referred to as PS1-5 to
CC designate the order in which they are located in the gene. Six isogenes
CC of the PTAFR gene exist. The PTAFR gene is located on chromosome 1, and
CC contains 1 exon. Polymorphisms PS3 and PS5 have previously been
CC identified. PS3 and PS5 occur in the coding region. The polynucleotide
CC comprising polymorphisms in the PTAFR gene is useful in screening
CC candidate drugs to treat diseases related to PTAFR activity, e.g.
CC inflammatory diseases, coronary diseases or cancer. The PTAFR isogenes
CC are especially useful for treating these diseases. The methods and
CC haplotypes are useful in improving the efficiency of drug discovery and
CC development processes, or for designing clinical trials of candidate
CC drugs for treating the specific condition or disease described above
XX
XX Sequence 10 BP; 2 A; 0 C; 2 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 475 GAATTTTCT 484
Db 1 GAATTTTCT 10

```

```

RESULT 299
AAS99954
ID AAS99954 standard; DNA; 10 BP.
XX
XX AAS99954;
AC
XX
XX 12-MAR-2002 (first entry)
DT
XX
XX Even-skipped homeobox 1 (EVX1) gene allele-specific oligonucleotide #31
DE

```

XX Even-skipped homeo box 1; EVX1; neurological disease; drug screening;  
 KW haplotyping; single nucleotide polymorphism; SNP; human; ss;  
 KW allele-specific oligonucleotide.  
 OS Homo sapiens.  
 XX WO200190120-A2.  
 XX 29-NOV-2001.  
 XX 21-MAY-2001; 2001WO-US016559.  
 XX 19-MAY-2000; 2000US-0205437P.  
 XX (GENA-) GENAISSANCE PHARM INC.  
 XX Duda A, Kliem SE, Kumar AM;  
 XX WPI; 2002-089913/12.  
 XX Novel genetic variants of even-skipped homeo box 1, EVX1 gene useful for  
 PT therapeutic purposes and for expressing EVX1 protein useful in  
 PT identifying drugs to treat neurological diseases.  
 XX  
 XX Claim 18; Page 13; 69pp; English.  
 XX The invention relates to an isolated polynucleotide (I), comprising a  
 CC nucleotide sequence which is a polymorphic variant of a reference  
 CC sequence for the even-skipped homeo box 1 (homologue of broscophila)  
 CC (EVX1) gene or its fragment, or a polymorphic variant of a reference  
 CC sequence for a EVX1 cDNA or its fragment. EVX1 polypeptide (II) is useful  
 CC for screening for drugs targeting the polypeptide, by contacting the EVX1  
 CC polymorphic variant with a candidate agent and assaying for binding  
 CC activity. A method is described for identifying an association between a  
 CC trait such as a clinical response to a drug targeting EVX1 and a  
 CC haplotype or haplotype pair of EVX1 gene. The methods are useful in  
 CC developing diagnostic tests and therapeutic treatments for neurological  
 CC diseases. (I) is useful for studying the expression and function of EVX1  
 CC and expressing EVX1 protein for use in screening for candidate drugs to  
 CC treat diseases related to EVX1 activity. The polymorphism and haplotype  
 CC data are useful for validating whether EVX1 is a suitable target for  
 CC drugs to treat neurological diseases, screening for such drugs and  
 CC reducing bias in clinical trials of such drugs. (I) is useful for  
 CC therapeutic purposes. (I) is useful for determining if an individual has  
 CC one of the haplotypes 1-4 or the haplotype pairs. Establishing the EVX1  
 CC haplotype or haplotype pair of an individual is useful for improving the  
 CC efficiency and reliability of several steps in the discovery and  
 CC development of drugs for treating diseases associated with EVX1 activity  
 CC e.g. neurological diseases. The haplotyping method is useful to validate  
 CC EVX1 as a candidate target for treating a specific condition or disease  
 CC predicted to be associated with EVX1 activity. (I) is useful for studying  
 CC expression of the EVX1 isogenes in vivo, for in vivo screening and  
 CC testing of drugs against EVX1 protein and for testing the efficacy of  
 CC therapeutic agents and compounds for neurological diseases in a  
 CC biological system. Antibody raised against (II) is useful for diagnostic  
 CC and prognostic formats and therapeutic methods, for immunoprecipitating  
 CC (II) from solution, for detecting EVX1 protein isoforms in biological  
 CC samples, frozen tissue sections, cells which have been fixed or unfixed  
 CC and prepared on slides, for use in immunocytochemical,  
 CC immunohistochemical and immunofluorescence techniques. AAS99924-AAS99958  
 CC represent human EVX1 gene allele-specific oligonucleotides of the  
 CC invention  
 XX  
 XX Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2005 AGCAGTTCGG 2014  
 |||||  
 DB 1 AGCAGTTCGG 10

## RESULT 300

ABK55548

ID ABK55548 standard; DNA; 10 BP.

XX AC ABK55548;

XX DT 18-JUN-2002 (first entry)

XX DE Selectin L Lymphocyte Adhesion Molecule, SEL

XX KW Human; Selectin L Lymphocyte Adhesion Molecule, SEL

XX KW neonatal pertussis; whooping cough; haplotype; allele-specific oligonucleotide, ss

XX OS Homo sapiens.

XX PN WO200216654-A1.

XX PD 28-FEB-2002.

XX PF 27-AUG-2001; 2001WO-US026675.

XX PR 25-AUG-2000; 2000US-0228262P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Anastasio AE, Bieglecki KM, Kliem SE, Koshy B, Kumar AM;

XX DR WPI; 2002-292071/33.

XX PT Novel genetic variants of selectin L lymphocyte adhesion molecule 1

XX PT (SELL) gene useful for therapeutic purposes and for expressing SELL

XX PT protein useful in identifying drugs to treat whooping cough.

XX PS Claim 19; Page 15; 137pp; English.

XX CC The invention relates to an isolated polynucleotide (I) comprising a

XX CC nucleotide sequence which is a polymorphic variant of a reference

XX CC sequence for Selectin L Lymphocyte Adhesion Molecule, SEL

XX CC polypeptide is useful for screening for drugs targeting the polypeptide

XX CC Oligonucleotides derived from (I) are used to determine the haplotype

XX CC or haplotype pair of SELL gene. These are useful to determine the

XX CC tests and therapeutic treatments for neonatal pertussis, whooping cough

XX CC (I) is useful for studying the expression and function of SELL and

XX CC expressing SELL protein for use in screening for candidate drugs

XX CC diseases related to SELL activity. The polymorphism and haplotype data

XX CC are useful for validating whether SELL is a suitable target for drugs

XX CC to treat whooping cough, screening for such drugs and reducing bias in

XX CC clinical trials of such drugs. Establishing the SELL haplotype or

XX CC haplotype pair of an individual is useful for improving the efficiency

XX CC and reliability of several steps in the discovery and development of

XX CC drugs for treating diseases associated with SELL activity. The

XX CC pertussis (whooping cough). The haplotyping method is useful to validate

XX CC SELL as a candidate target for treating a specific disease of interest

XX CC predicted to be associated with SELL activity. The method is also useful

XX CC in screening for compounds targeting SELL to treat a specific condition

XX CC or disease predicted to be associated with SELL activity, e.g. determining

XX CC which of the SELL haplotypes or haplotype pairs present in individual

XX CC members of a population with the specific disease of interest enables one

XX CC to screen for compounds that display the highest desired agonist or

XX CC antagonist activity for each of the most frequent SELL isoforms present

XX CC in the disease population. A polymorphic variant of SELL is useful in

XX CC studying the effect of the variation on the biological activity of SELL,

XX CC on the binding affinity of candidate drugs targeting SELL for the

XX CC treatment of neonatal pertussis (whooping cough) and in assays to measure

XX CC the binding affinities of one or more candidate drugs targeting the SELL

XX CC protein. ABK55465-ABK55559 represent SELL gene allele-specific

XX CC oligonucleotides of the invention

XX SQ Sequence 10 BP; 3 A; 2 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1229 TTATTAAGCC 1238  
 |||||  
 Db 1 TTATTAAGCC 10

RESULT 301  
 ABK55525  
 ID ABK55525 standard; DNA; 10 BP.  
 XX  
 AC ABK55525;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Selectin L Lymphocyte Adhesion Molecule 1 (SELL) oligonucleotide #61.  
 XX  
 KW Human; Selectin L Lymphocyte Adhesion Molecule 1; SELL;  
 KW neonatal pertussis; whooping cough; haplotyping; primer;  
 KW allele-specific oligonucleotide; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200216654-A1.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 27-AUG-2001; 2001WO-US026675.  
 XX  
 PR 25-AUG-2000; 2000US-0228262P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Anastasio AE, Bieglecki KM, Kliem SE, Koshy B, Kumar AM;  
 XX  
 DR WPI; 2002-292071/33.  
 XX  
 PT Novel genetic variants of selectin L lymphocyte adhesion molecule 1  
 (SELL) gene useful for therapeutic purposes and for expressing SELL  
 protein useful in identifying drugs to treat whooping cough.  
 XX  
 PS Claim 19; Page 15; 137pp; English.  
 XX

The invention relates to an isolated polynucleotide (I) comprising a  
 nucleotide sequence which is a polymorphic variant of a reference  
 sequence for Selectin L Lymphocyte Adhesion Molecule 1 (SELL) gene. SELL  
 polypeptide is useful for screening for drugs targeting the polypeptide.  
 CC  
 CC Oligonucleotides derived from (I) are used to target SELL and a haplotype  
 CC or haplotype pair of SELL gene. These are useful in developing diagnostic  
 CC tests and therapeutic treatments for neonatal pertussis (whooping cough).  
 CC (I) is useful for studying the expression and function of SELL and  
 CC expressing SELL protein for use in screening for candidate drugs to treat  
 CC diseases related to SELL activity. The polymorphism and haplotype data  
 CC are useful for validating whether SELL is a suitable target for drugs to  
 CC treat whooping cough, screening for such drugs and reducing bias in  
 CC clinical trials of such drugs. Establishing the SELL haplotype or  
 CC haplotype pair of an individual is useful for improving the efficiency  
 CC and reliability of several steps in the discovery and development of  
 CC drugs for treating diseases associated with SELL activity e.g. neonatal  
 CC pertussis (whooping cough). The haplotyping method is useful to validate  
 CC SELL as a candidate target for treating a specific condition or disease  
 CC predicted to be associated with SELL activity. The method is also useful  
 CC in screening for compounds targeting SELL to treat a specific condition  
 CC or disease predicted to be associated with SELL activity, e.g. detecting  
 CC which of the SELL haplotypes or haplotype pairs present in individual  
 CC members of a population with the specific disease of interest enables one  
 CC to screen for compounds that display the highest desired agonist or  
 CC antagonist activity for each of the most frequent SELL isoforms present  
 CC in the disease population. A polymorphic variant of SELL is useful in  
 CC studying the effect of the variation on the biological activity of SELL,  
 CC on the binding affinity of candidate drugs targeting SELL for the

CC treatment of neonatal pertussis (whooping cough) and in assays to measure  
 CC the binding affinities of one or more candidate drugs targeting the SELL  
 CC protein. ABK55465-ABK55559 represent SELL gene allele-specific  
 CC oligonucleotides of the invention  
 XX  
 SQ Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1942 CATTTCAGAC 1951  
 |||||  
 Db 1 CATTTCAGAC 10

RESULT 302  
 ABK81452  
 ID ABK81452 standard; DNA; 10 BP.  
 XX  
 AC ABK81452;  
 XX  
 DT 13-AUG-2002 (first entry)  
 XX  
 DE SCYA20 primer extension oligonucleotide #14.  
 XX  
 KW Small inducible cytokine subfamily A (Cys-Cys) member 20; SCYA20;  
 KW polymorphism; haplotype; psoriasis; gene expression;  
 KW primer extension oligonucleotide; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200232927-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 19-OCT-2001; 2001WO-US046093.  
 XX  
 PR 19-OCT-2000; 2000US-0241725P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Bieglecki KM, Chew A, Russo DP, Sausker EA;  
 XX  
 DR WPI; 2002-435525/46.  
 XX

New genetic variants comprising haplotypes of the small inducible  
 PT cytokine subfamily A, member 20 (SCYA20) gene, useful in improving the  
 PT efficiency drug screening protocols for compounds (e.g. antipsoriatic  
 PT drug) targeting SCYA20.  
 XX  
 PS Claim 16; Page 14; 62pp; English.  
 XX

The invention describes an isolated polynucleotide, which comprises genes  
 CC and haplotypes of the small inducible cytokine subfamily A (Cys-Cys),  
 CC member 20 (SCYA20) gene. The polynucleotide comprises polymorphic sites  
 CC referred to as PSI-9 to designate the order in which they are located in  
 CC the gene. The polymorphisms and haplotypes of SCYA20 gene are useful for  
 CC validating whether SCYA20 is a suitable target for drugs to treat  
 CC psoriasis and disorders associated with its abnormal expression or  
 CC function, screening for such drugs and reducing bias in clinical trials  
 CC of such drugs. Haplotype information would be useful in improving the  
 CC efficiency and output of several steps in the drug discovery and  
 CC development process, including target validation, identifying lead  
 CC compounds, early phase clinical trials. The methods are useful in  
 CC screening for compounds targeting SCYA20 to treat a specific condition or  
 CC disease predicted to be associated with SCYA20 activity, e.g. psoriasis.  
 CC This sequence represents a primer extension oligonucleotide used to  
 CC identify polymorphisms in the SCYA20 gene  
 XX  
 SQ Sequence 10 BP; 7 A; 0 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 626 AAAATATAAT 635  
|||||  
Db 1 AAAATATAAT 10

RESULT 303  
ABK17007  
ID ABK17007 standard; DNA; 10 BP.  
AC ABK17007;  
XX  
XX  
XX 26-MAR-2002 (first entry)  
XX  
XX Pyridoxal (Pyridoxine, vitamin B6) Kinase (PDXK) primer #30.  
XX  
KW Pyridoxal kinase; pyridoxine; vitamin B6;  
KW PDXK autoimmune polyglandular disease type 1; transgenic animal;  
KW gene therapy; primer extension; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200190125-A2.  
XX  
XX 29-NOV-2001.  
XX  
XX 24-MAY-2001; 2001WO-US016909.  
XX  
XX 24-MAY-2000; 2000US-0206664P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
XX  
XX Chew A, Duda A, Koshy B;  
XX  
XX WPI; 2002-106169/14.  
XX  
XX Isolated human pyridoxal (pyridoxine, vitamin B6) Kinase polyNTs, useful  
XX for therapeutic purposes, for studying the expression and function of the  
XX polyNT, and for expressing pyridoxal protein.  
XX  
XX Claim 19; Page 14; 135pp; English.  
XX  
XX The invention describes an isolated human pyridoxal (pyridoxine, vitamin  
XX B6) kinase, (PDXK) polynucleotide. The polynucleotide is useful in  
XX studying the expression and function of PDXK, and in expressing PDXK  
XX protein for use in screening for candidate drugs to treat PDXK related  
XX diseases and for therapeutic purposes. A transgenic animal is useful for  
XX studying expression of the PDXK isogenes in vivo, for in vivo screening  
XX and testing of drugs targeted against PDXK protein, and for testing the  
XX efficacy of therapeutic agents and compounds for autoimmune polyglandular  
XX disease type 1. The polypeptide is useful for studying the effect of the  
XX variation on the biological activity of PDXK and the binding affinity of  
XX candidate drugs targeting PDXK for the treatment of autoimmune  
XX polyglandular disease type 1. Genotyping and haplotyping is useful for  
XX improving the efficacy and reliability of several steps in the discovery  
XX and development of drugs for treating diseases associated with PDXK  
XX activity, e.g., autoimmune polyglandular disease type 1, to validate PDXK  
XX as a candidate agent for treating a specific condition or disease  
XX predicted to be associated with PDXK activity, and in the design of  
XX clinical trials of candidate drugs. This sequence is one of 38 (see  
XX ABK16978-ABK17015) primers used for detecting PDXK gene polymorphisms by  
XX primer extension terminations, described in the method of the invention  
XX  
XX Sequence 10 BP; 3 A; 6 C; 0 G; 1 T; 0 U; 0 Other;

QY 2030 CCATCACCAC 2039  
|||||

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CCATCACCAC 10

RESULT 304  
ABK16990  
ID ABK16990 standard; DNA; 10 BP.  
XX  
XX AC ABK16990;  
XX  
XX 26-MAR-2002 (first entry)  
XX  
XX DE Pyridoxal (Pyridoxine, vitamin B6) Kinase (PDXK) primer #13.  
XX  
KW Pyridoxal kinase; pyridoxine; vitamin B6;  
KW PDXK autoimmune polyglandular disease type 1; transgenic animal;  
KW gene therapy; primer extension; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200190125-A2.  
XX  
XX 29-NOV-2001.  
XX  
XX 24-MAY-2001; 2001WO-US016909  
XX  
XX 24-MAY-2000; 2000US-0206664P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
XX  
XX Chew A, Duda A, Koshy B;  
XX  
XX WPI; 2002-106169/14.  
XX  
XX Isolated human pyridoxal (pyridoxine, vitamin B6) Kinase polyNTs, useful  
XX for therapeutic purposes, for studying the expression and function of the  
XX polyNT, and for expressing pyridoxal protein.  
XX  
XX Claim 19; Page 14; 135pp; English.  
XX  
XX The invention describes an isolated human pyridoxal (pyridoxine, vitamin  
XX B6) kinase, (PDXK) polynucleotide. The polynucleotide is useful in  
XX studying the expression and function of PDXK, and in expressing PDXK  
XX protein for use in screening for candidate drugs to treat PDXK related  
XX diseases and for therapeutic purposes. A transgenic animal is useful for  
XX studying expression of the PDXK isogenes in vivo, for in vivo screening  
XX and testing of drugs targeted against PDXK protein, and for testing the  
XX efficacy of therapeutic agents and compounds for autoimmune polyglandular  
XX disease type 1. The polypeptide is useful for studying the effect of the  
XX variation on the biological activity of PDXK and the binding affinity of  
XX candidate drugs targeting PDXK for the treatment of autoimmune  
XX polyglandular disease type 1. Genotyping and haplotyping is useful for  
XX improving the efficacy and reliability of several steps in the discovery  
XX and development of drugs for treating diseases associated with PDXK  
XX activity, e.g., autoimmune polyglandular disease type 1, to validate PDXK  
XX as a candidate agent for treating a specific condition or disease  
XX predicted to be associated with PDXK activity, and in the design of  
XX clinical trials of candidate drugs. This sequence is one of 38 (see  
XX ABK16978-ABK17015) primers used for detecting PDXK gene polymorphisms by  
XX primer extension terminations, described in the method of the invention  
XX  
XX Sequence 10 BP; 8 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 968 ACAAGAGAAA 977  
|||||  
Db 1 ACAAGAGAAA 10

RESULT 305  
AAS95416/c

ID AAS95416 standard; DNA; 10 BP.  
 AC AAS95416;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Human ICAM2 gene allele-specific oligonucleotide PCR primer #21.  
 XX  
 KW Human; intercellular adhesion molecule 2; ICAM2; haplotyping; ss;  
 KW haplotype pair; single nucleotide polymorphism; genotyping; PCR primer;  
 KW gene therapy; drug screening; anti-HIV; anti-inflammatory; probe;  
 KW human immunodeficiency virus; sequencing primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200185918-A1.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 07-MAY-2001; 2001WO-US014714.  
 XX  
 PR 05-MAY-2000; 2000US-0201946P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Chew A, Choi JY, Denton RR, Kliem SE, Lee HH, Nandabalan K;  
 XX  
 DR WPI; 2002-055590/07.  
 XX  
 PT Novel polynucleotide containing polymorphisms in intercellular adhesion  
 PT molecule 2 gene, useful in developing drugs for treating human  
 PT immunodeficiency virus infection and inflammatory diseases.  
 XX  
 PS Claim 18; Page 14; 81pp; English.  
 XX  
 CC The invention relates to single nucleotide polymorphisms in the gene  
 CC encoding human intercellular adhesion molecule 2 (ICAM2). A method for  
 CC haplotyping the ICAM2 gene in an individual comprises identifying the  
 CC nucleotide at one or more polymorphic sites and determining whether one  
 CC of the copies of the gene is defined by one of the ICAM2 haplotypes given  
 CC in the specification or whether both copies are defined by a haplotype  
 CC pair. This method is useful in genotyping, whereby all possible haplotype  
 CC pairs can be assigned to specific genotypes. An association between a  
 CC trait and a haplotype or haplotype pair of the ICAM2 gene can be  
 CC identified by comparing the frequency of the haplotype or haplotype pair  
 CC in a population exhibiting the trait with the frequency of the haplotype  
 CC or haplotype pair in a reference population, where a higher haplotype  
 CC frequency in the trait population indicates the trait is associated with  
 CC the haplotype or haplotype pair. ICAM2 and its corresponding DNA are used  
 CC for studying the expression and function of ICAM2, for use in screening  
 CC for candidate drugs to treat diseases related to ICAM2 activity, such as  
 CC HIV infection and inflammatory diseases. The sequences are also useful  
 CC for studying the effect of variation on the biological activity of ICAM2  
 CC as well as on the binding affinity of candidate drugs targeting ICAM2.  
 CC Sequences AAS95362-AAS95417 and AAS95419-AAS95442 represent allele-  
 CC specific oligonucleotide probes, sequencing primers, PCR primers and cDNA  
 CC encoding human ICAM2  
 XX  
 SQ Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 444 CGAAGATGAA 453  
 Db 10 CGAAGATGAA 1  
 |||||  
 RESULT 306  
 AAS99202  
 ID AAS99202 standard; DNA; 10 BP.  
 XX

AC AAS99202;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE UDP glycosyltransferase 1 (UGT1A1) allele-specific oligonucleotide #69.  
 XX  
 KW UDP glycosyltransferase 1; UGT1A1; human; haplotyping; ss;  
 KW drug discovery; Gilbert's syndrome; Crigler-Najjar syndrome;  
 KW allele-specific oligonucleotide.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200179230-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 13-APR-2001; 2001WO-US012273.  
 XX  
 PR 18-APR-2000; 2000US-0197514P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Chew A, Choi JY, Koshy B, Rounds E;  
 XX  
 DR WPI; 2002-075063/10.  
 XX  
 PT Genotyping a human UDP glycosyltransferase 1 gene of an individual for  
 PT determining the haplotype of an individual, involves determining the  
 PT identity of a nucleotide pair at specific polymorphic sites for two  
 PT copies of the gene.  
 XX  
 PS Claim 18; Page 14; 81pp; English.  
 XX  
 CC The invention relates to genotyping a human UDP glycosyltransferase  
 CC (UGT1A1) gene of an individual, involving determining for the two copies  
 CC of the UGT1A1 gene present in the individual, the identity of the  
 CC nucleotide pair at one or more polymorphic sites. The new method is  
 CC useful for determining whether an individual has a haplotype or haplotype  
 CC pairs, given in the specification. It is useful for improving the  
 CC efficacy and reliability of several steps in the discovery and  
 CC development of drugs for treating diseases associated with UGT1A1  
 CC activity, e.g., Gilbert's syndrome and Crigler-Najjar syndrome, to  
 CC validate UGT1A1 as a candidate agent for treating a specific condition or  
 CC disease predicted to be associated with UGT1A1 activity, and in the  
 CC design of clinical trials of candidate drugs for treating a specific  
 CC condition or disease predicted to be associated with UGT1A1 activity. The  
 CC method is useful to screen for compounds targeting UGT1A1 to treat a  
 CC specific condition or disease associated with UGT1A1 activity. A nucleic  
 CC acid (I) comprising a polymorphic variant of a reference sequence for the  
 CC UGT1A1 gene or cDNA (II) or its fragment is useful in studying the  
 CC expression and function of UGT1A1, and in expressing UGT1A1 protein for  
 CC use in screening for candidate drugs to treat diseases related to UGT1A1  
 CC activity. (I) or (II) is useful for therapeutic purposes. (II) or a  
 CC recombinant organism comprising (II) is useful for studying expression of  
 CC the UGT1A1 isogenes in vivo, for in vivo screening and testing of drugs  
 CC targeted against UGT1A1 protein, and for testing the efficacy of  
 CC therapeutic agents and compounds for Gilbert's syndrome and Crigler-  
 CC Najjar syndrome, in a biological system. AAS99134-AAS99203 represent UDP  
 CC glycosyltransferase 1 gene allele-specific oligonucleotides used in the  
 CC method of the invention  
 XX  
 SQ Sequence 10 BP; 4 A; 1 C; 0 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1352 TTAATTCAT 1361  
 Db 1 TTAATTCAT 10  
 |||||  
 RESULT 307

```

ABV78495/c
ID ABV78495 standard; cDNA; 10 BP.
XX
AC ABV78495;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:206.
XX
KW SAGE tag; serial analysis of gene expression; human; Th1 cell;
KW activated T cell; T lymphocyte; immune response; expression pattern;
KW preferential expression; immune disorder; EST; expressed sequence tag;
KW ss.
XX
OS Homo sapiens.
XX
PN JP2002186482-A.
XX
PD 02-JUL-2002.
XX
PF 19-DEC-2000; 2000JP-00385816.
XX
PR 19-DEC-2000; 2000JP-00385816.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-594261/64.
XX
PT Human activated Th1 and Th2 cell expression gene group, useful for the
PT diagnosis and treatment of Th1 and Th2 related diseases.
XX
PS Claim 19; Page 11; 60pp; Japanese.
XX
CC The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are expressed in activated human Th1
CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC lying nearest to the polyA region of cDNAs derived from a variety of
CC genes. These tags serve to uniquely identify each transcript and can thus
CC be used to analyse the pattern of gene expression in particular cell
CC types. The invention also relates to proteins encoded by the genes
CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
CC inhibitors of the expression of groups of genes that are expressed in
CC either or both the two cell types. Groups of genes expressed in Th1
CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
CC representing 171 genes which are more highly expressed in Th1 cells
CC compared with Th2 cells
XX
SQ Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TCAGTTCATC 2327
DB 10 TCAGTTCATC 1

RESULT 308
ABV78476
ID ABV78476 standard; cDNA; 10 BP.
XX
AC ABV78476;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:187.
XX
KW SAGE tag; serial analysis of gene expression; human; Th1 cell;
KW activated T cell; T lymphocyte; immune response; expression pattern;
KW preferential expression; immune disorder; EST; expressed sequence tag;
KW ss.

Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2295 ATGGTTAAAG 2304
DB 1 ATGGTTAAAG 10

RESULT 309
ABV84738
ID ABV84738 standard; cDNA; 10 BP
XX
AC ABV84738;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human electron transfer flavoprotein beta subunit SAGE tag #548
XX
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C,
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC.
KW expression pattern; differential expression; ss.
XX
OS Homo sapiens.
XX
PN JP2002209591-A.
XX
PD 30-JUL-2002.
XX
PF 19-JAN-2001; 2001JP-00012328.
XX
PR 19-JAN-2001; 2001JP-00012328.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

```

```

XX WPI; 2002-631294/68.
XX
XX Human chronic hepatitis C tissue expression exasperating gene group
XX comprises 100 high-ranking genes.
XX
XX Claim 46; Page 26; 139pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
XX representing groups of genes which are differentially expressed in human
XX chronic hepatitis C (CH) liver tissue or hepatitis C-induced
XX hepatocellular carcinoma (HCC) compared with normal human liver tissue.
XX The SAGE tags of this invention consist of a sequence of 10 nucleotides
XX located downstream of the 5'-CATG-3' sequence motif lying nearest to the
XX polyA region of cDNAs derived from a variety of genes. These tags serve
XX to uniquely identify each transcript and can thus be used to analyse the
XX pattern of gene expression in particular cell types. The invention also
XX relates to proteins encoded by the genes expressed in chronic hepatitis C
XX liver tissue or HCC, antibodies against these proteins, and inhibitors of
XX the expression of groups of genes that are overexpressed in chronic
XX hepatitis C liver tissue or HCC. Groups of genes differentially expressed
XX in chronic hepatitis C tissue or HCC may be used for the diagnosis and
XX treatment of these diseases. Such genes, inhibitors of their expression
XX or activity, and antibodies against the gene products may be used in the
XX development of drugs to treat chronic hepatitis C and/or HCC. Sequences
XX ABV84691-ABV84790 are SAGE tags representing the 100 least highly
XX expressed genes out of those genes which are underexpressed in
XX hepatocellular carcinoma compared with chronic hepatitis C liver tissue
XX
XX Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1874 AAAGCCCAAGA 1883
XX DB 1 AAAGCCCAAGA 10
XX
XX RESULT 310
XX ABV84337/C
XX ID ABV84337 standard; cDNA; 10 BP.
XX AC ABV84337;
XX
XX 12-DEC-2002 (first entry)
XX
XX Human NADH-ubiquinone oxidoreductase AGGG subunit SAGE tag #147.
XX
XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
XX CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
XX expression pattern; differential expression; ss..
XX
XX Homo sapiens.
XX
XX JP2002209591-A.
XX
XX 30-JUL-2002.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-631294/68.
XX
XX Human chronic hepatitis C tissue expression exasperating gene group
XX comprises 100 high-ranking genes.
XX
XX Claim 10; Page 14; 139pp; Japanese.
XX

```

```

CC The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are differentially expressed in human
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC polyA region of cDNAs derived from a variety of genes. These tags serve
CC to uniquely identify each transcript and can thus be used to analyse the
CC pattern of gene expression in particular cell types. The invention also
CC relates to proteins encoded by the genes expressed in chronic hepatitis C
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC the expression of groups of genes that are overexpressed in chronic
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC treatment of these diseases. Such genes, inhibitors of their expression
CC or activity, and antibodies against the gene products may be used in the
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC ABV84291-ABV84390 are SAGE tags representing the 100 least highly
CC expressed genes out of those genes which are underexpressed in chronic
CC hepatitis C liver tissue compared with normal liver tissue
XX
XX Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 819 TCTTCTGAGT 828
XX DB 10 TCTTCTGAGT 1
XX
XX RESULT 311
XX ABV84317/C
XX ID ABV84317 standard; cDNA; 10 BP.
XX AC ABV84317;
XX
XX 12-DEC-2002 (first entry)
XX
XX Human multiple chronic hepatitis C underexpressed genes SAGE tag #127.
XX
XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
XX CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
XX expression pattern; differential expression; ss.
XX
XX Homo sapiens.
XX
XX JP2002209591-A.
XX
XX 30-JUL-2002.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-631294/68.
XX
XX Human chronic hepatitis C tissue expression exasperating gene group
XX comprises 100 high-ranking genes.
XX
XX Claim 10; Page 13; 139pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
XX representing groups of genes which are differentially expressed in human
XX chronic hepatitis C (CH) liver tissue or hepatitis C-induced
XX hepatocellular carcinoma (HCC) compared with normal human liver tissue.
XX The SAGE tags of this invention consist of a sequence of 10 nucleotides
XX located downstream of the 5'-CATG-3' sequence motif lying nearest to the
XX polyA region of cDNAs derived from a variety of genes. These tags serve
XX to uniquely identify each transcript and can thus be used to analyse the

```

CC pattern of gene expression in particular cell types. The invention also  
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
 CC the expression of groups of genes that are overexpressed in chronic  
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
 CC treatment of these diseases. Such genes, inhibitors of their expression  
 CC or activity, and antibodies against the gene products may be used in the  
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
 CC ABV84291-ABV84390 are SAGE tags representing the 100 least highly  
 CC expressed genes out of those genes which are underexpressed in chronic  
 CC hepatitis C liver tissue compared with normal liver tissue  
 XX  
 XX Sequence 10 BP; 2 A; 1 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1173 GAAATATATAA 1182  
 |||||  
 Db 10 GAAATATATAA 1

RESULT 312  
 ABK23803  
 ID ABK23803 standard; DNA; 10 BP.  
 AC ABK23803;  
 DT 09-APR-2002 (first entry)  
 DE Transcript tag DNA sequence #392 induced or suppressed by N-myc.  
 DE Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;  
 KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;  
 KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.  
 XX Homo sapiens.  
 XX WO200185941-A2.  
 PD 15-NOV-2001.

PF 11-MAY-2001; 2001WO-NL000361.  
 PR 11-MAY-2000; 2000EP-00201698.  
 PR 29-JUN-2000; 2000EP-00202284.  
 XX (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.  
 PA Versteeg R, Caron HN;  
 PI WPI; 2002-066603/09.  
 DR A new nucleic acid library of myc-dependent downstream genes capable of  
 XX supporting a neoplastic characteristic of cancer is useful to find new  
 PT therapies and diagnoses for cancer.  
 XX Disclosure; Page 60; 69pp; English.

PS The present invention relates to a nucleic acid library comprising myc-  
 CC dependent downstream genes or their functional fragments essentially  
 CC capable of supporting a neoplastic character of cancer such as growth,  
 CC invasion or spread. These myc target or tag sequences are identified by  
 CC SAGE (serial analysis of gene expression). The library is useful to find  
 CC new diagnoses and treatments for cancer. The invention is also useful to  
 CC enhance production of recombinant proteins in a production system with  
 CC high expression of endogenous or transfected myc oncogenes. ABK23412-  
 CC ABK23828 represent transcript tag DNA sequences that are activated or  
 CC repressed by N-myc in human neuroblastoma  
 XX  
 XX Sequence 10 BP; 8 A; 1 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 TAAAAACAAA 74  
 |||||  
 Db 1 TAAAAACAAA 10

RESULT 313  
 ABK23695/c  
 ID ABK23695 standard; DNA; 10 BP.  
 AC ABK23695;  
 DT 09-APR-2002 (first entry)  
 DE Transcript tag DNA sequence #284 induced or suppressed by N-myc.

DE Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;  
 KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;  
 KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.  
 XX Homo sapiens.  
 XX WO200185941-A2.  
 PD 15-NOV-2001.  
 PF 11-MAY-2001; 2001WO-NL000361  
 PR 11-MAY-2000; 2000EP-00201698  
 PR 29-JUN-2000; 2000EP-00202284.  
 XX (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.  
 PA Versteeg R, Caron HN;  
 PI WPI; 2002-066603/09.

DR A new nucleic acid library of myc-dependent downstream genes capable of  
 XX supporting a neoplastic characteristic of cancer is useful to find new  
 PT therapies and diagnoses for cancer.  
 XX Disclosure; Page 57; 69pp; English.

PS The present invention relates to a nucleic acid library comprising myc-  
 CC dependent downstream genes or their functional fragments essentially  
 CC capable of supporting a neoplastic character of cancer such as growth,  
 CC invasion or spread. These myc target or tag sequences are identified by  
 CC SAGE (serial analysis of gene expression). The library is useful to find  
 CC new diagnoses and treatments for cancer. The invention is also useful to  
 CC enhance production of recombinant proteins in a production system with  
 CC high expression of endogenous or transfected myc oncogenes. ABK23412-  
 CC ABK23828 represent transcript tag DNA sequences that are activated or  
 CC repressed by N-myc in human neuroblastoma  
 XX  
 XX Sequence 10 BP; 5 A; 0 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 ACATTTATTC 197  
 |||||  
 Db 10 ACATTTATTC 1

RESULT 314  
 ABK23740/c  
 ID ABK23740 standard; DNA; 10 BP  
 XX



AC ABK23740;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Transcript tag DNA sequence #329 induced or suppressed by N-myc.  
 XX  
 KW Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;  
 XX spread; myc target; myc tag; SAGE; serial analysis of gene expression;  
 KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200185941-A2.  
 XX  
 XX 15-NOV-2001.  
 XX  
 PF 11-MAY-2001; 2001WO-NL000361.  
 XX  
 PR 11-MAY-2000; 2000EP-00201698.  
 XX  
 XX 29-JUN-2000; 2000EP-00202284.  
 XX  
 PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.  
 XX  
 PI Versteeg R, Caron HN;  
 XX WPI; 2002-066603/09.  
 XX  
 DR A new nucleic acid library of myc-dependent downstream genes capable of  
 XX supporting a neoplastic characteristic of cancer is useful to find new  
 PT therapies and diagnoses for cancer.  
 XX  
 PS Disclosure; Page 58; 69pp; English.  
 XX  
 CC The present invention relates to a nucleic acid library comprising myc-  
 CC dependent downstream genes or their functional fragments essentially  
 CC capable of supporting a neoplastic character of cancer such as growth,  
 CC invasion or spread. These myc target or tag sequences are identified by  
 CC SAGE (serial analysis of gene expression). The library is useful to find  
 CC new diagnoses and treatments for cancer. The invention is also useful to  
 CC enhance production of recombinant proteins in a production system with  
 CC high expression of endogenous or transfected myc oncogenes. ABK23412-  
 CC ABK23828 represent transcript tag DNA sequences that are activated or  
 CC repressed by N-myc in human neuroblastoma  
 XX  
 XX Sequence 10 BP; 1 A; 0 C; 1 G; 8 T; 0 U; 0 Other;  
 SQ

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AAATACAAAA 2353  
 DB 10 AAATACAAAA 1  
 |||||  
 |||||

RESULT 315  
 ABK23772  
 ID ABK23772 standard; DNA; 10 BP.  
 XX  
 AC ABK23772;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Transcript tag DNA sequence #361 induced or suppressed by N-myc.  
 XX  
 KW Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;  
 XX spread; myc target; myc tag; SAGE; serial analysis of gene expression;  
 KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200185941-A2.  
 XX  
 XX 15-NOV-2001.  
 XX  
 PF 11-MAY-2001; 2001WO-NL000361.  
 XX  
 PR 11-MAY-2000; 2000EP-00201698.  
 XX  
 XX 29-JUN-2000; 2000EP-00202284.  
 XX  
 PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.  
 XX  
 PI Versteeg R, Caron HN;  
 XX WPI; 2002-066603/09.  
 XX  
 DR A new nucleic acid library of myc-dependent downstream genes capable of  
 XX supporting a neoplastic characteristic of cancer is useful to find new  
 PT therapies and diagnoses for cancer.  
 XX  
 PS Disclosure; Page 58; 69pp; English.  
 XX  
 CC The present invention relates to a nucleic acid library comprising myc-  
 CC dependent downstream genes or their functional fragments essentially  
 CC capable of supporting a neoplastic character of cancer such as growth,  
 CC invasion or spread. These myc target or tag sequences are identified by  
 CC SAGE (serial analysis of gene expression). The library is useful to find  
 CC new diagnoses and treatments for cancer. The invention is also useful to  
 CC enhance production of recombinant proteins in a production system with  
 CC high expression of endogenous or transfected myc oncogenes. ABK23412-  
 CC ABK23828 represent transcript tag DNA sequences that are activated or  
 CC repressed by N-myc in human neuroblastoma  
 XX  
 XX Sequence 10 BP; 1 A; 0 C; 1 G; 8 T; 0 U; 0 Other;  
 SQ

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AAATACAAAA 2353  
 DB 10 AAATACAAAA 1  
 |||||  
 |||||

RESULT 316  
 ABK28556  
 ID ABK28556 standard; DNA; 10 BP.  
 XX  
 AC ABK28556;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Paraoxonase 2 (PON2), primer extension oligonucleotide #29.  
 XX  
 KW Paraoxonase 2; PON2; coronary heart disease;  
 KW primer extension oligonucleotide; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200188202-A1.  
 XX  
 XX 22-NOV-2001.  
 XX  
 PF 18-MAY-2001; 2001WO-US016352.  
 XX  
 PR 18-MAY-2000; 2000US-0205145P.  
 XX  
 XX (GENA-) GENAISANCE PHARM INC.  
 XX  
 XX Anastasio AB, Chew A, Choi JY, Denton RR, Lee HH, Nandabalan K,  
 XX WPI; 2002-121985/16.  
 XX  
 XX An isolated polynucleotide comprising a paraoxonase 2 (PON2, isoyene  
 PT encodes a pharmaceutically important protein for the identification of  
 PT polymorphisms at the PON2 locus.

PD 15-NOV-2001.  
 XX  
 XX 11-MAY-2001; 2001WO-NL000361.  
 XX  
 PR 11-MAY-2000; 2000EP-00201698.  
 XX  
 XX 29-JUN-2000; 2000EP-00202284.  
 XX  
 PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.  
 XX  
 PI Versteeg R, Caron HN;  
 XX WPI; 2002-066603/09.  
 XX  
 DR A new nucleic acid library of myc-dependent downstream genes capable of  
 XX supporting a neoplastic characteristic of cancer is useful to find new  
 PT therapies and diagnoses for cancer.  
 XX  
 PS Disclosure; Page 59; 69pp; English.  
 XX  
 CC The present invention relates to a nucleic acid library comprising myc-  
 CC dependent downstream genes or their functional fragments essentially  
 CC capable of supporting a neoplastic character of cancer such as growth,  
 CC invasion or spread. These myc target or tag sequences are identified by  
 CC SAGE (serial analysis of gene expression). The library is useful to find  
 CC new diagnoses and treatments for cancer. The invention is also useful to  
 CC enhance production of recombinant proteins in a production system with  
 CC high expression of endogenous or transfected myc oncogenes. ABK23412-  
 CC ABK23828 represent transcript tag DNA sequences that are activated or  
 CC repressed by N-myc in human neuroblastoma  
 XX  
 XX Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;  
 SQ

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 487 GGAGGAGAGC 496  
 DB 1 GGAGGAGAGC 10  
 |||||  
 |||||

RESULT 316  
 ABK28556  
 ID ABK28556 standard; DNA; 10 BP.  
 XX  
 AC ABK28556;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Paraoxonase 2 (PON2), primer extension oligonucleotide #29.  
 XX  
 KW Paraoxonase 2; PON2; coronary heart disease;  
 KW primer extension oligonucleotide; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200188202-A1.  
 XX  
 XX 22-NOV-2001.  
 XX  
 PF 18-MAY-2001; 2001WO-US016352.  
 XX  
 PR 18-MAY-2000; 2000US-0205145P.  
 XX  
 XX (GENA-) GENAISANCE PHARM INC.  
 XX  
 XX Anastasio AB, Chew A, Choi JY, Denton RR, Lee HH, Nandabalan K,  
 XX WPI; 2002-121985/16.  
 XX  
 XX An isolated polynucleotide comprising a paraoxonase 2 (PON2, isoyene  
 PT encodes a pharmaceutically important protein for the identification of  
 PT polymorphisms at the PON2 locus.

```

XX PS Claim 19; Page 14; 125pp; English.
XX CC
XX CC The invention describes an isolated polynucleotide sequence comprising a
XX CC paroxonase 2 (PON2) isogene. Primers and probes allow identification of
XX CC this sequence and its polymorphisms and are useful for identifying which
XX CC isoform of paroxonase 2 a person carries. Identification of a PON2
XX CC isoform allows tailored pharmaceutical treatment to be designed and
XX CC administered. PON2 is a particularly important gene for the treatment of
XX CC coronary heart disease. This sequence represents a primer extension
XX CC oligonucleotide used for detecting PON2 gene polymorphisms, described in
XX CC the method of the invention
XX SQ Sequence 10 BP; 3 A; 1 C; 1 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 606 TCATTAGAT 615
DB 1 TCATTAGAT 10
XX
RESULT 317
ABK96317/c
ID ABK96317 standard; DNA; 10 BP.
XX
AC ABK96317;
XX
DT 24-SEP-2002 (first entry)
XX
DE EDG1 gene primer extension oligonucleotide #5.
XX
KW EDG1; human; haplotyping; vascular developmental disorder; PCR; primer;
KW endothelial differentiation sphingolipid G protein-coupled receptor 1;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200244200-A2.
XX
PD 06-JUN-2002.
XX
PF 03-DEC-2001; 2001WO-US046946.
XX
PR 01-DEC-2000; 2000US-0250606P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bieglecki KM, Kazemi A, Shah N;
XX WPI; 2002-519581/55.
XX
XX Novel genetic variants of Endothelial Differentiation, Sphingolipid G
XX Protein-Coupled Receptor 1 isogenes, useful for improving efficiency and
XX reliability in drug development for treating vascular developmental
XX disorders.
XX
XX Claim 16; Page 14; 68pp; English.
XX
XX The invention relates to an isolated polynucleotide (I) encoding
XX endothelial differentiation, sphingolipid G protein-coupled receptor 1
XX (EDG1) (II). Also described are methods for haplotyping or genotyping
XX EDG1 gene of an individual by identifying single nucleotide polymorphisms
XX (SNPs) of the gene. (II) is useful in screening for drugs targeting (II)
XX that are useful for treating vascular developmental disorders. The
XX methods are useful for improving the efficiency and reliability of
XX several steps in the discovery and development of drugs for treating
XX diseases associated with EDG1 activity. The haplotyping method is also
XX used in pharmaceutical research to validate EDG1 as a candidate target
XX for treating a specific condition or disease predicted to be associated
XX with EDG1 activity, e.g. vascular developmental disorders, and in the
XX
XX design of clinical trials for treating a specific condition of disease
XX associated with EDG1 activity. The methods are also useful for screening
XX compounds targeting EDG1. ABK96286-ABK96332 represent EDG1 gene allele
XX specific oligonucleotides, primer extension oligonucleotides and related
XX PCR primers of the invention
XX SQ Sequence 10 BP; 1 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 9.4e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 206 TACCACAACC 215
DB 10 TACCACAACC 1
XX
RESULT 318
AAD43420/c
ID AAD43420 standard; DNA; 10 BP.
XX
AC AAD43420;
XX
DT 14-NOV-2002 (first entry)
XX
DE Human CYP3A5 gene polymorphism detecting primer #6.
XX
KW Human; cytochrome P450; subfamily IIIA; polypeptide 5 isogene; CYP3A5;
KW drug screening; polymorphism; haplotype; drug metabolising disorder;
KW gene therapy; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200246209-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US047218.
XX
PR 08-DEC-2000; 2000US-0254367P.
XX
PR 03-MAY-2001; 2001US-0288470P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Han J, Kliem SE, Rounds E;
XX WPI; 2002-636448/68.
XX
XX Novel isolated polynucleotide which is a polymorphic variant of
XX cytochrome P450, subfamily IIIA, polypeptide 5 (CYP3A5) gene useful for
XX expressing CYP3A5 protein isoform used in drug screening techniques
XX Claim 17; Page 16; 127pp; English.
XX
XX The invention relates to isolated polynucleotide (I) encoding a variant of
XX subfamily IIIA, polypeptide 5 isogene (CYP3A5) gene useful for screening
XX for screening drugs. The invention is useful for identifying variants of the
XX function of CYP3A5 and expressing CYP3A5 protein for use in screening for
XX candidate drugs to treat diseases related to CYP3A5 activity. The
XX polymorphism and haplotype data is useful for validating whether CYP3A5
XX is a suitable target for drugs to treat drug metabolising disorders,
XX screening for such drugs and reducing bias in clinical trials of such
XX drugs. The invention is also useful for therapeutic purposes. The
XX invention is useful in studying the effect of variation on the biological
XX activity of CYP3A5 as well as on the binding affinity of candidate drugs
XX to CYP3A5, or for studying the enzymatic properties of such CYP3A5
XX variants using these candidate drugs as substrate. The invention is
XX useful in gene therapy. The present sequence is human CYP3A5 gene
XX polymorphism detecting primer
XX SQ Sequence 10 BP; 1 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;

```

Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1581 GAAGGAAAGT 1590  
Db. 10 GAAGGAAAGT 1  
|||||

RESULT 319  
ABL45894  
ID ABL45894 standard; DNA; 10 BP.  
XX AC ABL45894;  
XX 26-APR-2002 (first entry)  
XX Human EDG6 gene allele specific primer extension oligo SEQ ID NO: 88.  
DE Human; endothelial differentiation, G-protein coupled receptor 6; EDG6;  
KW haplotype; cancer; angiogenesis; inflammation; chromosome 19p13.3;  
KW cytotatic; antiinflammatory; gene therapy; SNP;  
KW single nucleotide polymorphism; primer; ss.  
XX Homo sapiens.  
XX WO200206446-A2.  
XX 24-JAN-2002.  
XX 17-JUL-2001; 2001WO-US022523.  
XX 17-JUL-2000; 2000US-0218727P.  
XX (GENA-) GENAISSANCE PHARM INC.  
XX Kliem SE, Koshy B;  
XX WPI; 2002-171804/22.  
XX New genetic variants of endothelial differentiation, G-protein coupled  
PT receptor-6 gene for studying expression, function of the gene and  
PT expressing EDG6 protein for use in screening drugs to treat cancer,  
PT inflammation.  
XX Claim 18; Page 14; 11pp; English.  
XX The present invention provides the gene, protein and cDNA sequences of  
CC the human endothelial differentiation, G-protein coupled receptor 6  
CC (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found  
CC within the sequences. The sequences can be used in the identification of  
CC the haplotype of an individual, and in the treatment of cancer,  
CC angiogenesis and inflammation. The present sequence is an allele specific  
CC primer extension oligonucleotide for the EDG6 gene, which is found on  
CC chromosome 19p13.3  
XX  
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2177 CCGATGAAGC 2186  
Db. 1 CCGATGAAGC 10  
|||||

RESULT 320  
AAS95562  
ID AAS95562 standard; DNA; 10 BP.  
XX AC AAS95562;  
XX 14-FEB-2002 (first entry)  
DT

XX Human IL8RB gene allele-specific oligonucleotide PCR primer #5.  
DE  
XX  
KW Human; interleukin 8 receptor beta; IL8RB; ss; antiinflammatory; probe;  
KW haplotyping; haplotype pair; single nucleotide polymorphism; genotyping;  
KW gene therapy; drug screening; chronic obstructive pulmonary disease;  
KW inflammatory disease; sequencing primer; PCR primer.  
XX  
OS Homo sapiens.  
XX WO200179221-A2.  
XX 25-OCT-2001.  
XX 12-APR-2001; 2001WO-US011942.  
XX 12-APR-2000; 2000US 0196734P.  
XX (GENA-) GENAISSANCE PHARM INC.  
XX Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;  
XX WPI; 2002-055250/07.  
XX New polymorphic variants comprising interleukin-8 receptor beta (IL8RB)  
PT isogene, useful in expressing IL8RB protein for use in screening for  
PT candidate drugs to treat diseases related to IL8RB activity, e.g.  
PT inflammatory disorders.  
XX Claim 18; Page 14; 74pp; English.  
XX The invention relates to single nucleotide polymorphisms in the human  
CC interleukin 8 receptor beta (IL8RB) gene. A method for haplotyping the  
CC IL8RB gene in an individual comprises identifying the nucleotide at one  
CC or more polymorphic sites and determining whether one of the copies of  
CC the gene is defined by one of the IL8RB haplotypes given in the  
CC specification or whether both copies are defined by a haplotype pair.  
CC This method is useful in genotyping, whereby all possible haplotype pairs  
CC can be assigned to specific genotypes. An association between a trait and  
CC a haplotype or haplotype pair of the IL8RB gene can be identified by  
CC comparing the frequency of the haplotype or haplotype pair in a  
CC population exhibiting the trait with the frequency of the haplotype or  
CC haplotype pair in a reference population, where a higher haplotype  
CC frequency in the trait population indicates the trait is associated with  
CC the haplotype or haplotype pair. IL8RB and its corresponding DNA are used  
CC for studying the expression and function of IL8RB, for use in screening  
CC for candidate drugs to treat diseases related to IL8RB activity, such as  
CC chronic obstructive pulmonary disease and other inflammatory disorders.  
CC The sequences are also useful for studying the effect of variation on the  
CC biological activity of IL8RB as well as on the binding affinity of  
CC candidate drugs targeting IL8RB. Sequences AAS95525-AAS95579 represent  
CC allele-specific oligonucleotide probes, sequencing primers and PCR  
CC primers used to detect IL8RB gene polymorphisms  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1658 GCTGTTTAAG 1667  
Db. 1 GCTGTTTAAG 10  
|||||

RESULT 321  
ABK54475/c  
ID ABK54475 standard; DNA; 10 BP.  
XX AC ABK54475;  
XX 05-JUN-2002 (first entry)  
DT  
XX

DE Primer-extension oligonucleotide #9 to detect human BMPR2 polymorphisms.  
 XX Human; single nucleotide polymorphism; SNP; BMPR2; chromosome 2q33-q34;  
 KW bone morphogenetic protein receptor type II; serine/threonine kinase;  
 KW haplotyping; genotyping; gene; primary pulmonary hypertension; PPH;  
 KW bone disorder; primer; ss.  
 XX Homo sapiens.  
 OS WO200216398-A2.  
 PN XX  
 XX  
 XX 28-FEB-2002.  
 PD XX  
 XX 27-AUG-2001; 2001WO-US026641.  
 PF XX  
 XX 25-AUG-2000; 2000US-0228272P.  
 PR XX  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA (LANZ/) LANZ E M.  
 XX  
 XX Chew A, Klem SE, Messer C, Sanchis A;  
 PI WPI; 2002-280906/32.  
 XX  
 XX Novel isolated polynucleotide which is a polymorphic variant of bone  
 PT morphogenetic protein receptor, type II (serine/threonine kinase) (BMPR2)  
 PT gene useful for expressing BMPR2 protein isoform used in drug screening.  
 XX  
 XX Claim 18; Page 15; 98pp; English.  
 PS  
 XX The present invention relates to novel single nucleotide polymorphisms  
 CC (SNPs) in the human bone morphogenetic protein receptor type II  
 CC (serine/threonine kinase) (BMPR2) gene located on chromosome 2q33-q34,  
 CC and methods for haplotyping and/or genotyping the BMPR2 gene. The methods  
 CC of the invention make use of allele-specific oligonucleotides (ASOs) as  
 CC probes and primers, and/or primer-extension oligonucleotides for  
 CC detecting the BMPR2 gene polymorphisms. The polynucleotides and screened  
 CC compounds are useful for the treatment of diseases associated with BMPR2  
 CC activity, such as primary pulmonary hypertension (PPH) and bone  
 CC disorders. ABK54467-ABK54482 represent primer-extension oligonucleotides  
 CC for detecting human BMPR2 gene polymorphisms  
 XX  
 SQ Sequence 10 BP; 4 A; 1 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 333 TGCCAAATTT 342  
 DB 10 TGCCAAATTT 1  
 RESULT 322  
 ID ABK64084 standard; DNA; 10 BP.  
 XX  
 AC ABK64084;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Human BF gene allele-specific oligonucleotide PCR primer #35.  
 XX  
 XX Human; B-factor; properdin; BF; primer; ss; gene therapy; drug screening;  
 KW antidiabetic; dermatological; diabetes; immunosuppressive;  
 KW antiinflammatory; systemic lupus erythematosus.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200218414-A2.  
 PN XX  
 XX 07-MAR-2002.  
 PD XX  
 XX

PF 29-AUG-2001; 2001WO-US027098.  
 XX  
 PR 29-AUG-2000; 2000US-0228940P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 XX Anastasio AE, Finkel K, Kazemi A, Koshy B;  
 PI WPI; 2002-304244/34.  
 XX  
 DR New genetic variants having polymorphisms in the B-Factor, Properdin (BF)  
 XX gene, useful for studying the function of BF, and for treating disorders  
 PT affected by expression or function of the BF isogene.  
 PT  
 XX Claim 19; Page 16; 151pp; English.  
 PS  
 XX The invention relates to single nucleotide polymorphisms in the gene  
 CC encoding the human B-factor properdin protein (BF). A method for  
 CC haplotyping the BF gene in an individual comprises identifying the  
 CC nucleotide at one or more polymorphic sites and determining whether one  
 CC of the copies of the gene is defined by one of the BF haplotypes given in  
 CC the specification or whether both copies are defined by a haplotype pair.  
 CC This method is useful in genotyping, whereby all possible haplotype pairs  
 CC can be assigned to specific genotypes. An association between a first and  
 CC a haplotype or haplotype pair of the BF gene can be identified by  
 CC comparing the frequency of the haplotype or haplotype pair in a  
 CC population exhibiting the trait with the frequency in the total population.  
 CC haplotype pair in a reference population, where a haplotype pair is a  
 CC frequency in the trait population indicates the trait is associated with  
 CC the haplotype or haplotype pair. BF and its corresponding DNA are used  
 CC for studying the expression and function of BF, for age in genotyping BF  
 CC candidate drugs to treat diseases related to BF activity, such as  
 CC diabetes and systemic lupus erythematosus. Sequences ABK64084, ABK64085  
 CC represent allele-specific PCR primers used to detect human BF gene  
 CC polymorphisms  
 XX  
 SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 544 GTGATCAACT 553  
 DB 1 GTGATCAACT 10  
 RESULT 323  
 ID ABL58357/c  
 XX ABL58357 standard; DNA; 10 BP.  
 XX  
 AC ABL58357;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE PNA label for CFTR gene.  
 XX  
 KW Single nucleotide polymorphism; SNP; atomic force microscope; AFM;  
 KW nucleic acid detection; cystic fibrosis transmembrane receptor; CFTR;  
 KW PNA; peptide nucleic acid; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200222889-A2.  
 PN  
 XX 21-MAR-2002.  
 PD  
 XX 12-SEP-2001; 2001WO-US042138.  
 XX  
 XX 11-SEP-2000; 2000US-0231608P.  
 PR  
 XX (HARD ) HARVARD COLLEGE  
 PA (MASI ) MASSACHUSETTS INST TECHNOLGY  
 XX



PT DNA using atomic force microscope by moving nanotube tip of microscope.  
 PT across gene sample and recording the image obtained with the microscope.  
 PS  
 PS  
 PS Example 14; Page 31; 56pp; English.

CC The invention relates to a method of detecting single nucleotide  
 CC polymorphisms (SNP) of gene samples using atomic force microscope (AFM).  
 CC The method involves providing AFM with at least one nanotube tip, moving  
 CC the nanotube tip across the gene sample and recording an image obtained  
 CC with the AFM. The method is useful for detecting SNPs of gene sample  
 CC e.g., a DNA fragment containing 10-10000 bases; or a DNA fragment  
 CC comprising a DNA fragment amplified using polymerase chain reaction,  
 CC which further comprises a probe. The method is also useful for detecting  
 CC SNPs in genomic DNA (comprising cystic fibrosis transmembrane receptor  
 CC gene). The method is also useful for detecting more than one SNP in a  
 CC gene, where the SNPs comprise probes comprising different peptide nucleic  
 CC acids (PNAs). It is also useful for detecting SNPs in gene sample which  
 CC comprises an array of gene samples, where the AFM comprises arrays of  
 CC single-walled nanotubes tips. The method allows direct visualization of  
 CC polymorphic sites on individual genes. The present sequence represents a  
 CC PNA label for the CFTR gene

SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2505 CTTGCTCTCA 2514  
 DB 1 CTTGCTCTCA 10

RESULT 326

ABK81525/c  
 ID ABK81525 standard; DNA; 10 BP.  
 AC ABK81525;  
 AC  
 DT 13-AUG-2002 (first entry)  
 DE Human CASP5 gene allele-specific oligonucleotide PCR primer #6.  
 KW Human; caspase 5; apoptosis-related cysteine protease; CASP5; primer; ss;  
 KW haplotyping; haplotype pair; cancer; single nucleotide polymorphism;  
 KW hereditary nonpolyposis colorectal cancer; gastrointestinal tumour;  
 KW endometrial tumour; chromosome 11q22.2-q22.3; PCR.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200226769-A2.  
 PN  
 PD 04-APR-2002.  
 XX  
 PF 01-OCT-2001; 2001WO-US030878.  
 XX  
 PR 29-SEP-2000; 2000US-0236568P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Choi JY, Klien SE, Russo DP;  
 XX  
 DR WPI; 2002-435191/46.  
 XX  
 PS Novel caspase 5 apoptosis-related cysteine protease, useful  
 PT therapeutically and in screening for drugs targeting protease  
 PT polypeptide.  
 PS  
 PS Claim 16; Page 15; 115pp; English.  
 CC The invention relates to single nucleotide polymorphisms in the gene  
 CC encoding the human caspase 5, apoptosis-related cysteine protease (CASP5)  
 CC polypeptide. A method for haplotyping the CASP5 gene in an individual

CC comprises identifying the nucleotide at one or more polymorphic sites and  
 CC determining whether one of the copies of the gene is defined by one of  
 CC the CASP5 haplotypes given in the specification or whether both copies  
 CC are defined by a haplotype pair. This method is useful in genotyping,  
 CC whereby all possible haplotype pairs can be assigned to specific  
 CC genotypes. An association between a trait and a haplotype or haplotype  
 CC pair of the CASP5 gene can be identified by comparing the frequency of  
 CC the haplotype or haplotype pair in a population exhibiting the trait with  
 CC the frequency of the haplotype or haplotype pair in a reference  
 CC population, where a higher haplotype frequency in the trait population  
 CC indicates the trait is associated with the haplotype or haplotype pair.  
 CC CASP5 and its corresponding DNA are used for studying the expression and  
 CC function of CASP5, for use in screening for candidate drugs for treating  
 CC diseases related to CASP5 activity, such as cancer (e.g. hepatocellular  
 CC nonpolyposis colorectal cancer, gastrointestinal tumours and endometrial  
 CC tumours). Sequences ABK81520 ABK81549 represent alleles specific  
 CC oligonucleotide PCR primers used to detect ASP5 gene polymorphisms.  
 XX  
 SQ Sequence 10 BP; 0 A; 2 C; 1 G; 3 T; 0 U; 0 Other.

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 GCACAAAAAA 136  
 DB 10 GCACAAAAAA 1

RESULT 327

AAL43018  
 ID AAL43018 standard; DNA; 10 BP.  
 XX  
 AC AAL43018;  
 XX  
 DT 08-AUG-2002 (first entry)  
 XX  
 DE Human cerberus 1 (CER1) gene primer-extension oligonucleotide 23.  
 XX  
 KW Human; PCR; ss; allele-specific; SNP; single nucleotide polymorphism;  
 KW cerberus 1 homologue; cysteine knot superfamily; CER1; drug screening;  
 KW developmental disorder; polymorphic site; CER1 haplotyping; primer  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200032929-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 19-OCT-2001; 2001WO-US046100.  
 XX  
 PR 19-OCT-2000; 2000US 0241634P  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC  
 XX  
 PI Kazemi A, Shah N;  
 XX  
 DR WPI; 2002-435527/46.  
 XX  
 XX Novel genetic variants of Cerberus 1 (Xenopus laevis) Homolog (Cysteine  
 PT Knot Superfamily) (CER1) isogenes, useful for improving efficiency and  
 PT reliability in drug development for treating developmental disorders  
 XX  
 PS Claim 16; Page 14; 75pp; English.  
 XX  
 CC The invention relates to the identification of 13 novel polymorphic sites  
 CC in the human cerberus 1 (Xenopus laevis) homologue (cysteine knot  
 CC superfamily) (CER1) gene. The invention also comprises the amino acid and  
 CC coding sequence of CER1. The CER1 protein is useful for screening drugs  
 CC that target CER1 - for the treatment of developmental disorders. The CER1  
 CC coding sequence is useful in studying the expression of CER1 isogenes,  
 CC for screening and testing of drugs targeted against CER1 protein, and in  
 CC testing the efficacy of therapeutic agents for treating developmental

CC disorders. The 13 novel polymorphic sites identified in the invention are  
 CC useful for haplotyping the CCR1 gene of an individual. The present DNA  
 CC sequence represents a human CCR1 gene primer-extension oligonucleotide  
 XX SQ Sequence 10 BP; 4 A; 1 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 17 CTGAATAATGT 26  
 |||||  
 Db 1 CTGAATAATGT 10

RESULT 328  
 AAD31786  
 ID AAD31786 standard; DNA; 10 BP.  
 AC AAD31786;  
 XX 18-JUN-2002 (first entry)  
 DT MR 8 arbitrary primer used for modified differential display.  
 XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;  
 KW vaccine; immune response; cytostatic; primer; ss.  
 XX Unidentified.  
 OS US2002018785-A1.  
 PN 14-FEB-2002.  
 PD 02-APR-2001; 2001US-00822250.  
 XX 22-SEP-1997; 97US-00935377.  
 PR (UVRP ) UNIV ROCHESTER.  
 PA Zauderer M;  
 PI WPI; 2002-239252/29.  
 DR Representational Difference Analysis method for identification of  
 XX antigens recognized by cytotoxic T cells and specific for human tumors,  
 PT comprises improved selection of genes encoding target antigens.  
 PS Example 4; Page 19; 54pp; English.

CC The present invention relates to novel methods for the identification of  
 CC antigens recognised by cytotoxic T cells (CTLs) and specific for human  
 CC tumours, cancers and infected cells. The method involves screening the  
 CC products of an expression library generated from DNA/RNA of a cell  
 CC expressing a target epitope with cytotoxic T cells generated against the  
 CC cell to identify DNA clones expressing target epitope or providing  
 CC cytotoxic T cells specific for a gene product differentially expressed by  
 CC a cell and measuring the cross-reactivity of the cytotoxic T cells for  
 CC cells expressing a target epitope in which the target epitope is  
 CC identified as a gene product inducing cytotoxic T cells. The method is  
 CC useful for identifying a target epitope or antigen specific for a tumour  
 CC cell. The target epitope is also useful for identifying target antigens  
 CC in other target cells against which it is desirable to induce cell-  
 CC mediated immunity. The antigen identified by the method is useful in  
 CC immunogenic compositions and vaccine preparations to induce the  
 CC regression of tumours, cancers and infections in mammals. The invention  
 CC also relates to vaccinia viral vectors which are useful for treating  
 CC tumour-bearing mammals, including humans to generate immune response  
 CC against the tumour cells. They are also useful for immunising or  
 CC vaccinating tumour-free subjects to prevent tumour formation. The present  
 CC DNA sequence is an arbitrary primer which is used for modified  
 CC differential display of genes encoding potential tumour immunogens. This  
 CC primer is used in the exemplification of the invention

XX SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1449 TACCTATGCG 1458  
 |||||  
 Db 1 TACCTATGCG 10

RESULT 329  
 ABS64267  
 ID ABS64267 standard; DNA; 10 BP.  
 XX  
 AC ABS64267;  
 XX 15-NOV-2002 (first entry)  
 DT Tachykinin receptor gene TACR2, primer extension oligo #21.  
 XX Human; single nucleotide polymorphism; SNP; TACR2; primer; probe; ss;  
 KW tachykinin receptor.  
 XX Homo sapiens.  
 OS WO200263046-A1.  
 PN 15-AUG-2002.  
 PD 09-NOV-2001; 2001WO-US047394.  
 XX 09-NOV-2000; 2000US-0247649P.  
 PR (GENA-) GENAISSANCE PHARM INC.  
 PA Cappola G, Chew A, Gilson CR, Koshy B;  
 PI WPI; 2002-636600/68.  
 DR New genetic variants having polymorphisms in the Tachykinin receptor  
 XX (TACR2) protein, useful for studying the function of TACR2, and for  
 PT treating disorders associated with abnormal expression of TACR2;  
 PT TACR2 isogene.  
 PS Claim 16; Page 15; 139pp; English.

CC The invention relates to an isolated polypeptide comprising a polymeric  
 CC variant of a reference sequence for the tachykinin receptor (TACR2)  
 CC protein. Also described is a method for: (1) haplotyping or genotyping  
 CC the TACR2 gene of an individual; (2) predicting a haplotype pair for the  
 CC TACR2 gene of an individual; (3) identifying an association between a  
 CC trait and at least one haplotype or haplotype pair of the TACR2 gene; and  
 CC (4) isolated oligonucleotide for detecting a single nucleotide  
 CC polymorphism in the TACR2 gene. Polymorphic variants of the TACR2 gene  
 CC are useful in studying the expression and biological function of TACR2,  
 CC and in identifying drugs targeting TACR2 protein for treating disorders  
 CC associated with abnormal expression or function of TACR2, e.g. asthma or  
 CC breast cancer. Polynucleotides comprising a polymorphic gene variant or  
 CC fragment may be used for therapeutic purposes, where a patient could  
 CC benefit from expression or increased expression of a particular TACR2  
 CC protein isoform, or an expression vector encoding the isoform may be  
 CC administered to the patient. Haplotype information is useful in improving  
 CC the efficiency and output of several steps in drug discovery and  
 CC development process, including target validation, identifying lead  
 CC compounds, and early phase clinical trials. Information on polymorphisms  
 CC may be applied in studying biological functions of TACR2 as well as in  
 CC identifying drugs targeting this protein for the treatment of disorders  
 CC related to its abnormal expression or function. ABS64163-ABS64302  
 CC represent human TACR2 gene allele-specific oligonucleotide probes and  
 CC primers used to detect haplotypes of the TACR2 gene of the invention  
 XX

```

SQ Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1400 ATAGAGCTAA 1409
Db 1 ATAGAGCTAA 10

RESULT 330
ABL45794/C
ID ABL45794 standard; DNA; 10 BP.
XX
AC ABL45794;
XX
XX 03-MAY-2002 (first entry)
XX
DE Human MMP13 gene allele specific primer extension oligo SEQ ID NO: 82.
XX
KW Human; matrix metalloproteinase 13 (collagenase 3); MMP13; cancer;
KW arthritis; haplotype; single nucleotide polymorphism; SNP; enzyme;
KW cytostatic; antiarthritic; gene therapy; chromosome 11q22.3; PCR primer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200206294-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-US022238.
XX
PR 13-JUL-2000; 2000US-0217950P.
PR 17-AUG-2000; 2000WO-US022693.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Finkel K, Kliem SE, Messer C, Tanguay DA;
XX
WPI; 2002-171797/22.
XX
XX Novel genetic variants of matrix metalloproteinase 13 (collagenase 3)
PT Gene useful in studying expression and function of the protein, and for
PT screening drugs to treat diseases e.g. cancer and arthritis.
XX
PS Claim 18; Page 15; 110pp; English.
XX
CC The present invention provides the cDNA, protein and gene fragments of
CC the human matrix metalloproteinase 13 (collagenase 3) (MMP13). Also
CC provided are single nucleotide polymorphisms (SNPs) identified within the
CC sequences. The sequences can be used to haplotype an individual and in
CC the treatment of cancer and arthritis, including metastatic cancers. The
CC present sequence is a primer extension oligonucleotide for the MMP13
CC gene, which is found on chromosome 11q22.3
XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1237 CCTCAAGTG 1246
Db 10 CCTCAAGTG 1

RESULT 331
AAS99221
ID AAS99221 standard; DNA; 10 BP.
XX
AC AAS99221;

SQ Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 762 AAGAGAACCA 771
Db 1 AAGAGAACCA 10

RESULT 332
ACC41747/C
ID ACC41747 standard; DNA; 10 BP.
XX
AC ACC41747;
XX

```

```

XX 12-MAR-2002 (first entry)
XX Human NAT1 gene allele-specific oligonucleotide PCR primer; #1
XX
XX Human; N-acetyltransferase 1; arylamine N-acetyltransferase; NAT1; ss;
KW haplotyping; cytostatic; haplotype pair; single nucleotide polymorphism;
KW genotyping; gene therapy; drug screening; lung cancer; sequencing primer;
KW PCR primer; probe.
XX
OS Homo sapiens.
XX
PN WO200179551-A1.
XX
PD 25-OCT-2001.
XX
PF 11-APR-2001; 2001WO-US011852.
XX
PR 12-APR-2000; 2000US-0196773P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
PA (SANC/) SANCHIS A.
XX
PI Bentivegna SC, Choi JY, Koshy B;
XX
WPI; 2002-075073/10.
XX
XX New polynucleotide, useful in developing diagnostic tests and treatments
PT treatments for lung cancer, comprises single nucleotide polymorphisms in
PT human N-acetyltransferase 1 (arylamine N-acetyltransferase; NAT1) gene.
XX
PS Claim 18; Page 14; 55pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in NAT1 gene
CC encoding the human N-acetyltransferase 1 (arylamine N-acetyltransferase
CC or NAT1) polypeptide. A method for haplotyping the NAT1 gene is also
CC individual comprises identifying the nucleotide at one or more
CC polymorphic sites and determining whether one of the copies of the gene
CC is defined by one of the NAT1 haplotypes given in the specification or
CC whether both copies are defined by a haplotype pair. This method is
CC useful in genotyping, whereby all possible haplotype pairs can be
CC assigned to specific genotypes. An association between a trait and a
CC haplotype or haplotype pair of the NAT1 gene can be identified by
CC comparing the frequency of the haplotype or haplotype pair in a
CC population exhibiting the trait with the frequency of the haplotype or
CC haplotype pair in a reference population, where a higher haplotype
CC frequency in the trait population indicates the trait is associated with
CC the haplotype or haplotype pair. NAT1 and its corresponding DNA are used
CC for studying the expression and function of NAT1, for use in screening
CC for candidate drugs to treat diseases related to NAT1 activity, such as
CC lung cancer. The sequences are also useful for studying the effect of
CC variation on the biological activity of NAT1 as well as on the binding
CC affinity of candidate drugs targeting NAT1. Sequences AAS99204-AAS99228
CC represent allele-specific oligonucleotide probes, sequencing primers and
CC PCR primers used to detect NAT1 gene polymorphisms
XX
SQ Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 762 AAGAGAACCA 771
Db 1 AAGAGAACCA 10

RESULT 332
ACC41747/C
ID ACC41747 standard; DNA; 10 BP.
XX
AC ACC41747;
XX

```



DT 21-MAY-2003 (first entry)  
 XX Zinc finger protein DNA-binding domain target sequence SEQ ID NO:294.  
 DE Zinc finger domain; zinc finger; zinc finger binding domain; probe;  
 XX chimeric nucleic acid; library; PCR primer; ss.  
 KW chimeric nucleic acid; library; PCR primer; ss.  
 XX Synthetic.  
 OS  
 XX WO2003016571-A1.  
 PN  
 XX 27-FEB-2003.  
 PD  
 XX 17-AUG-2002; 2002WO-KR001560.  
 PF  
 XX 17-AUG-2001; 2001US-0313402P.  
 PR 22-APR-2002; 2002US-0374355P.  
 XX (TOOL-) TOOLGEN INC.  
 PA  
 XX Kim J, Bae K, Park K, Kwon Y, Ryu E, Hwang M;  
 PI WPI; 2003-268344/26.  
 XX  
 DR New library comprising polypeptides having zinc finger domains, useful  
 PT for producing chimeric nucleic acids.  
 XX  
 PS Claim 40; Page 107; 234pp; English.  
 XX  
 CC The present invention describes a library comprising polypeptides. Each  
 CC polypeptide comprises a first or second zinc finger domain. The domains  
 CC of each polypeptide are identical to a zinc finger domain from a  
 CC naturally occurring protein and either do not occur in the same naturally  
 CC occurring protein or occur in the same naturally occurring protein in a  
 CC different configuration than in the polypeptide. The domains vary among  
 CC polypeptides. Also described: (1) producing chimeric nucleic acids; (2)  
 CC generating an artificial zinc finger polypeptide that specifically binds  
 CC to a target DNA site; and (3) identifying a nucleic acid encoding a zinc  
 CC finger polypeptide that specifically recognises a target DNA site. The  
 CC library can be used for producing chimeric nucleic acids. ACC41551 to  
 CC ACC41758 and ABR40919 to ABR41015 represent nucleotide and amino acid  
 CC sequences given in the exemplification of the present invention  
 XX  
 SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1211 AAGCAGCTCC 1220  
 DB |||||  
 10 AAGCAGCTCC 1  
 RESULT 333  
 ABT14371/C  
 ID ABT14371 standard; DNA; 10 BP.  
 XX  
 AC ABT14371;  
 XX  
 XX 20-FEB-2003 (first entry)  
 DT  
 XX Nucleic acid PCR amplification method-related RAPD PCR primer #141.  
 DE Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;  
 XX RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.  
 KW  
 XX Unidentified.  
 OS  
 XX WO200281743-A2.  
 PN  
 XX 17-OCT-2002.  
 PD  
 XX

PF 28-MAR-2002; 2002WO-GB001489.  
 XX  
 PR 02-APR-2001; 2001GB-00008182.  
 XX  
 PA (HAMI/) HAMILL B.  
 XX  
 PI Hamill B;  
 XX  
 DR WPI; 2003-075484/07.  
 XX  
 CC Amplification of nucleotide sequences from polynucleotides by chain  
 CC extension of oligonucleotide primers, comprises 2 oligonucleotides in  
 CC solution, 2 attached to supports and both share complementary sequences.  
 XX  
 PS Disclosure; Fig 17; 60pp; English.  
 XX  
 CC The invention comprises a method for the PCR amplification of nucleic  
 CC acids. The method involves a set of primers, where two of the primers are  
 CC in solution and at least two other primers are attached to a solid  
 CC support. The method of the invention can be used for the analysis of a  
 CC nucleic acid or a mixture of nucleic acids, including: single-stranded  
 CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The  
 CC present DNA sequence represents a random amplified polymorphic DNA (RAPD);  
 CC PCR primer of the invention.  
 XX  
 SQ Sequence 10 BP; 0 A; 3 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1698 CAGAGGAACC 1707  
 DB |||||  
 10 CAGAGGAACC 1  
 RESULT 334  
 AAD51658/C  
 ID AAD51658 standard; DNA; 10 BP.  
 XX  
 AC AAD51658;  
 XX  
 DT 16-APR-2003 (first entry)  
 XX  
 XX Human CYP2E gene polymorphism detecting primer #7.  
 DE  
 XX Human; cytochrome P450 subfamily 11E; CYP2E protein; haplotyping;  
 KW genotyping; gene therapy; cancer; polymorphism; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2002090597-A1.  
 PN  
 XX 14-NOV-2002.  
 PD  
 XX 07-MAY-2002; 2002WO-US014540.  
 PF  
 XX 07-MAY-2001; 2001US-0289330P.  
 PR  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA  
 XX Anastasio AE, Chew A, Gilson CR, Koshy B, Sauskar EA;  
 PI WPI; 2003-120563/11.  
 XX  
 XX New genetic variants comprising haplotypes of the cytochrome P450,  
 PT subfamily 11E (CYP2E) gene, useful for screening drugs for treating  
 PT cancer, validating CYP2E protein as a drug target, or reducing drug  
 PT clinical trials of such drugs.  
 XX  
 PS Claim 39; Page 16; 94pp; English.  
 XX  
 XX The invention relates to genetic variants of human cytochrome P450.  
 CC



XX PD 20-MAY-2003.  
 XX PF 26-JAN-2001; 2001US-00769482.  
 XX PR 28-JAN-2000; 2000US-0178772P.  
 XX PR 31-JAN-2000; 2000US-0179045P.  
 XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.  
 XX PI Srivastava S, Moul JW, Xu LL, Segawa T;  
 XX DR WPI; 2003-719644/68.  
 XX PT Novel isolated androgen-regulated gene designated as PMEPA1 useful for  
 PT selecting primers and probes for detecting prostate cancer cells in  
 PT biological samples by nucleic acid amplification techniques.  
 XX Example 7; Col 69; 58pp; English.  
 XX CC The invention relates to an isolated androgen-regulated gene (ARG)  
 CC designated as PMEPA1. The invention is useful for selecting primers and  
 CC probes for detecting prostate cancer cells in a biological sample by  
 CC using nucleic acid amplification techniques. The present sequence is  
 CC human ARG genomic maintenance and cell cycle regulation oligonucleotide  
 XX SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1837 GAAACACGCT 1846  
 DB ||||||||  
 10 GAAACACGCT 1  
 RESULT 338  
 AAL56064/c  
 ID AAL56064 standard; DNA; 10 BP.  
 AC AAL56064;  
 XX 11-MAR-2004 (first entry)  
 DT Human BAGE 5 intron/exon junction #3.  
 XX BAGE; tumour antigen; melanoma; cancer; cytostatic; gene therapy; gene;  
 KW ds.  
 XX Homo sapiens.  
 OS WO2003084990-A1.  
 PN 16-OCT-2003.  
 PD 05-APR-2002; 2002WO-EP003811.  
 PF 05-APR-2002; 2002WO-EP003811.  
 PR (CNRS ) CENT NAT RECH SCI.  
 PA De Sario A, Ruault M;  
 XX WPI; 2003-804293/75.  
 XX New BAGE proteins useful for manufacturing a medicament for diagnosing  
 PT and treating cancer, particularly melanoma.  
 XX Disclosure; Page 13; Opp; English.  
 XX CC The present invention provides the protein and coding sequences of a  
 CC number of members of the BAGE family of proteins from humans. The

CC proteins or their antibodies are useful for manufacturing a medicament  
 CC for the treatment of pathologies (e.g. tumours such as melanomas) linked  
 CC to the expression, at the surface of the cells of the organism, of  
 CC complexes between the peptide fragments and HLA molecules. The methods  
 CC may also be used for treating a subject with a tumour, such as melanoma  
 CC The nucleotide sequences, host cells, cytolytic cells or antibodies are  
 CC also useful for in vitro diagnosis of the disorders cited above. The  
 CC present sequence is a coding sequence/fragment of the invention  
 XX SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1120 CTACCACCTTG 1129  
 DB ||||||||  
 10 CTACCACCTTG 1  
 RESULT 339  
 ADH62228/c  
 ID ADH62228 standard; DNA; 10 BP.  
 XX AC ADH62228;  
 XX 25-MAR-2004 (first entry)  
 DT Human transcription regulator #8.  
 XX Androgen-regulated gene; ARG; PMEPA1; therapy; diagnosis; prognosis;  
 KW prostate cancer; hormonal therapy; human; ds.  
 XX Homo sapiens.  
 OS US2003170713-A1.  
 PN 11-SEP-2003.  
 PD 18-MAR-2003; 2003US-00390045.  
 PF 28-JAN-2000; 2000US-0178772P.  
 PR 31-JAN-2000; 2000US-0179045P.  
 PR 26-JAN-2001; 2001US-00769482.  
 XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.  
 XX Srivastava S, Moul JW, Xu LL, Segawa T;  
 XX WPI; 2003-898255/82.  
 XX Polynucleotide array, useful for diagnosing or prognosing prostate  
 PT cancer, comprises a planar, non-porous solid support and a set of  
 PT polynucleotide probes attached to the solid support.  
 XX Example 7; SEQ ID NO 20; 61pp; English.  
 XX The present invention relates to the identification and characterisation  
 CC of a novel androgen-regulated genes (ARGs) that exhibits abundant  
 CC expression in prostate tissue. The novel gene is designated PMEPA1. The  
 CC invention is useful for diagnosing and prognosing prostate cancer. The  
 CC invention is also useful in hormonal therapy. The present sequence is  
 CC androgen-regulated gene fragment.  
 XX SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 828 TGGGCTGTCA 837  
 DB ||||||||  
 10 TGGGCTGTCA 1

```

XX 11-SEP-2003.
XX PD
XX XX
XX PF 18-MAR-2003; 2003US-00390045.
XX XX
XX PR 28-JAN-2000; 2000US-0178772P.
XX PR 31-JAN-2000; 2000US-0179045P.
XX PR 26-JAN-2001; 2001US-00769482.
XX XX
XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX XX
XX PI Srivastava S, Moul JW, Xu LL, Segawa T;
XX XX WPI; 2003-898255/82.
XX DR
XX XX Polynucleotide array, useful for diagnosing or prognosing prostate
XX PT cancer, comprises a planar, non-porous solid support and a set of
XX PT polynucleotide probes attached to the solid support.
XX XX
XX PS Example 7; SEQ ID NO 56; 61pp; English.
XX XX
XX CC The present invention relates to the identification and characterisation
XX CC of a novel androgen-regulated genes (ARGs) that exhibits abundant
XX CC expression in prostate tissue. The novel gene is designated PMEPA1. The
XX CC invention is useful for diagnosing and prognosing prostate cancer. The
XX CC invention is also useful in hormonal therapy. The present sequence is
XX CC androgen-regulated gene fragment.
XX SQ Sequence 10 BP; 6 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1874 AAAGCCAAGA 1883
DB 1 AAAGCCAAGA 10
XX
RESULT 342
ADH78833/c
ID ADH78833 standard; DNA; 10 BP
XX
XX AC ADH78833;
XX XX
XX DT 22-APR-2004 (first entry)
XX XX
XX DE Human apical iodide transporter 5' intron extremity SEQ ID NO:21.
XX KW ds; human; apical iodide transporter; cytosolic; antithyroid;
XX KW gene therapy; hypersecretion of thyroid hormone; thyroid tumour;
XX KW radioactive iodine; intron.
XX OS Homo sapiens.
XX XX
XX PN FR2837492-A1.
XX XX
XX PD 26-SEP-2003.
XX XX
XX PF 21-MAR-2002; 2002FR-00003572.
XX XX
XX PR 21-MAR-2002; 2002FR-00003572.
XX XX
XX PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX XX
XX PI Leblanc G, Pourcher T;
XX XX
XX DR WPI; 2003-790461/75.
XX XX
XX PT New human apical iodide transporter useful for screening of compounds
XX PT able to modulate apical iodide transport in cells in treatment.
XX PT prevention or diagnosis of dysfunction, iodine deficiency.
XX XX

```

---

```

XX 11-SEP-2003.
XX PD
XX XX
XX PF 18-MAR-2003; 2003US-00390045.
XX XX
XX PR 28-JAN-2000; 2000US-0178772P.
XX PR 31-JAN-2000; 2000US-0179045P.
XX PR 26-JAN-2001; 2001US-00769482.
XX XX
XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX XX
XX PI Srivastava S, Moul JW, Xu LL, Segawa T;
XX XX WPI; 2003-898255/82.
XX DR
XX XX Polynucleotide array, useful for diagnosing or prognosing prostate
XX PT cancer, comprises a planar, non-porous solid support and a set of
XX PT polynucleotide probes attached to the solid support.
XX XX
XX PS Example 7; SEQ ID NO 36; 61pp; English.
XX XX
XX CC The present invention relates to the identification and characterisation
XX CC of a novel androgen-regulated genes (ARGs) that exhibits abundant
XX CC expression in prostate tissue. The novel gene is designated PMEPA1. The
XX CC invention is useful for diagnosing and prognosing prostate cancer. The
XX CC invention is also useful in hormonal therapy. The present sequence is
XX CC androgen-regulated gene fragment.
XX SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1837 GAAACCAAGCT 1846
DB 10 GAAACCAAGCT 1
XX
RESULT 341
ADH62264
ID ADH62264 standard; DNA; 10 BP.
XX
XX AC ADH62264;
XX XX
XX DT 25-MAR-2004 (first entry)
XX XX
XX DE Human energy metabolism, apoptosis and redox regulator #10.
XX XX
XX KW Androgen-regulated gene; ARG; PMEPA1; therapy; diagnosis; prognosis;
XX KW prostate cancer; hormonal therapy; human; ds.
XX OS Homo sapiens.
XX XX
XX PN US2003170713-A1.

```

PS Disclosure; SEQ ID NO 21; 46pp; French.

XX The invention relates to a novel isolated, purified protein related to a

CC apical iodide transporter protein. A protein of the invention has

CC cytosolic, and antithyroid activity. A protein of the invention is used

CC for screening of compounds able to modulate apical iodide transport in

CC cells. The nucleic acid encoding the protein can be used for production

CC of recombinant protein or to generate transgenic animals, useful in

CC screening for agents that modulate activity of the protein. The protein,

CC its peptides, nucleic acids encoding it, vectors containing the nucleic

CC acids and antibodies against the protein, are useful for prevention,

CC treatment (including gene therapy) of diseases that involve dysfunction

CC of apical iodide transport, e.g. hypersecretion of thyroid hormone or

CC development of thyroid tumours. The protein can also be used to counter

CC accumulation of, or contamination by, radioactive iodine, and its peptide

CC fragments are used to raise antibodies. The present sequence is used in

CC the exemplification of the invention.

XX

SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1864 GGTACTGAAC 1873

DB 10 GGTACTGAAC 1

RESULT 343

ACF57633

ID ACF57633 standard; DNA; 10 BP.

XX

AC ACF57633;

XX

DT 22-APR-2004 (first entry)

XX

DE Human ALDOB gene allele-specific primer SEQ ID NO: 84.

XX

KW Human; ALDOB; fructose-bisphosphate aldolase B; SNP;

KW single nucleotide polymorphism; primer; probe; ss.

XX

OS Homo sapiens.

XX

PN WO2003091454-A1.

XX

PD 06-NOV-2003.

XX

PF 26-APR-2002; 2002WO-US013328.

XX

PR 26-APR-2002; 2002WO-US013328.

XX

PA (GENA-) GENAISSANCE PHARM INC.

XX

PI Chew A, Kazemi A, Koshy B;

XX

DR WPI; 2003-877338/81.

XX

PS Claim 41; Page 15; Opp; English.

XX

CC The present invention provides the protein and coding sequences of human

CC fructose-bisphosphate aldolase B (ALDOB) and single nucleotide

CC polymorphisms (SNPs) which have been identified in each sequence. The

CC method of haplotyping the sequences is useful for haplotyping the

CC fructose-bisphosphate aldolase B (ALDOB) gene of an individual or for

CC validating the ALDOB protein as a candidate target for treating a medical

CC condition predicted to be associated with ALDOB activity. The present

CC sequence is an allele-specific primer/probe used to identify the

CC haplotype of the human ALDOB gene in the exemplification of the invention

XX

SQ Sequence 10 BP; 4 A; 0 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1595 CAAATTTTCAC 1604

DB 10 CAAATTTTCAC 1

RESULT 345

AD110084/C

ID AD110084 standard; cDNA; 10 BP.

XX

AC AD110084;

XX

DT 22-APR-2004 (first entry)

XX

DE IL-1 activated HUVEC differential display primer #6.

XX

KW ss; PCR; primer; human; cardiovascular disease; atherosclerosis;

KW ischaemia; reperfusion; hypertension; restenosis; arterial inflammation.

XX

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 ATATGATTAT 249

DB 1 ATATGATTAT 10

RESULT 344

ACA63212/C

ID ACA63212 standard; DNA; 10 BP.

XX

AC ACA63212;

XX

DT 22-APR-2004 (first entry)

XX

DE Human ALDOB gene allele-specific primer SEQ ID NO: 114.

XX

KW Human; ALDOB; fructose-bisphosphate aldolase B; SNP;

KW single nucleotide polymorphism; primer; probe; ss.

XX

OS Homo sapiens.

XX

PN WO2003091454-A1.

XX

PD 06-NOV-2003.

XX

PF 26-APR-2002; 2002WO-US013328.

XX

PR 26-APR-2002; 2002WO-US013328.

XX

PA (GENA-) GENAISSANCE PHARM INC.

XX

PI Chew A, Kazemi A, Koshy B;

XX

DR WPI; 2003-877338/81.

XX

PS Claim 41; Page 16; Opp; English.

XX

CC The present invention provides the protein and coding sequences of human

CC fructose-bisphosphate aldolase B (ALDOB) and single nucleotide

CC polymorphisms (SNPs) which have been identified in each sequence. The

CC method of haplotyping the sequences is useful for haplotyping the

CC fructose-bisphosphate aldolase B (ALDOB) gene of an individual or for

CC validating the ALDOB protein as a candidate target for treating a medical

CC condition predicted to be associated with ALDOB activity. The present

CC sequence is an allele-specific primer/probe used to identify the

CC haplotype of the human ALDOB gene in the exemplification of the invention

XX

SQ Sequence 10 BP; 3 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1595 CAAATTTTCAC 1604

DB 10 CAAATTTTCAC 1

RESULT 345

AD110084/C

ID AD110084 standard; cDNA; 10 BP.

XX

AC AD110084;

XX

DT 22-APR-2004 (first entry)

XX

DE IL-1 activated HUVEC differential display primer #6.

XX

KW ss; PCR; primer; human; cardiovascular disease; atherosclerosis;

KW ischaemia; reperfusion; hypertension; restenosis; arterial inflammation.

XX

```

OS Homo sapiens.
PN US2002170077-A1.
XX
XX 14-NOV-2002.
XX
XX 05-OCT-2001; 2001US-00970820.
XX
XX 10-FEB-1995; 95US-00386844.
XX 22-OCT-1998; 98US-00176330.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Falb DA, Gimbrone MA;
XX
XX WPI; 2003-370721/35.
XX
XX New fingerprint genes useful for treating and diagnosing cardiovascular
XX diseases, e.g. atherosclerosis, ischemia/reperfusion, or hypertension.
XX
XX Disclosure; SEQ ID NO 25; 93pp; English.
XX
XX The invention relates to a new isolated nucleic acid which comprises
XX rchd005, rchd024, rchd032, rchd036, rchd502, rchd523, rchd528, or rchd534
XX genes. The nucleic acids are useful for treating and diagnosing
XX cardiovascular diseases, such as atherosclerosis, ischemia/reperfusion,
XX hypertension, restenosis and arterial inflammation. The genes identified
XX may be used diagnostically or as targets for therapeutic intervention.
XX The present sequence represents a differential display primer.
XX
XX Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1 9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2031 CATCACCACC 2040
DB 10 CATCACCACC 1
RESULT 346
ADK65348/c
ID ADK65348 standard; DNA; 10 BP.
XX
XX ADK65348;
XX
XX 06-MAY-2004 (first entry)
XX
XX Mismatch 1 DNA for nucleic acid information recording method.
XX
XX ss; recording information; dissociation medium; hybridization medium;
XX electrical potential; detection; base-pair mismatch;
XX single-nucleotide polymorphism; diagnosis.
XX
XX Synthetic.
XX
XX WO2003089666-A2.
XX
XX 30-OCT-2003.
XX
XX 17-APR-2003; 2003WO-CA000574.
XX
XX 19-APR-2002; 2002US-0373644P.
XX
XX (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
XX Lee JS, Wettig SD, Kraatz H;
XX
XX WPI; 2003-845544/78.
XX
XX Recording information in nucleic acid polymer, useful e.g. for detecting
XX base-pair mismatches, based on intercalation of metal cations into a
duplex.
Example; Fig 7; 39pp; English.
The invention relates to a method of recording information in a nucleic
acid polymer comprising first modulating translation of two nucleic
acid strands (A) through a channel between a dissociation medium (DM) and
hybridization medium (HM) while varying an electrical potential across
the channel. The method is used (i) to record, read and write information
and (ii) to detect base-pair mismatches in a nucleic acid polymer. The
single-nucleotide polymorphisms for diagnosis of disease. The method
represents a mismatched DNA used in the method of recording information.
Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other.
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1 9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1522 CATGAAGTCC 1531
DB 10 CATGAAGTCC 1
RESULT 347
ADF91296/c
ID ADF91296 standard; DNA; 10 BP.
XX
XX ADF91296;
XX
XX 26-FEB-2004 (first entry)
XX
XX PCR primer for IL-1 induction/differential display OPI17.
XX
XX Human; ss; differential display; cardiovascular disease; interleukin-1;
XX IL-1; shear stress; high fat diet; high cholesterol diet;
XX multiple transmembrane domain receptor target; atherosclerosis;
XX ischaemia; reperfusion; hypertension; restenosis; inflammation; PCR;
XX primer.
XX
XX Homo sapiens.
XX
XX US2003188327-A1.
XX
XX 02-OCT-2003.
XX
XX 02-JUL-2002; 2002US-00186950
XX
XX 10-FEB-1995; 95US-00386844.
XX 07-JUN-1995; 95US-00485571.
XX 09-FEB-1996; 96US-00599654.
XX 06-OCT-1997; 97US-00944496.
XX 11-AUG-1999; 99US-00371900.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Falb DA, Gimbrone MA;
XX
XX WPI; 2004-041208/04.
XX
XX Isolated nucleic acid for use in treatment of cardiovascular diseases
XX e.g. atherosclerosis, contains nucleotide of sequences having specified
XX number of base pairs or nucleotide sequence of gene or gene fragment
XX contained in specified clones.
XX
XX Example; SEQ ID NO 25; 130pp; English.
XX
XX The invention relates to an isolated nucleic acid (appearing as ADF912/2-
XX ADF91278 and ADF91307 which are up regulated or down regulated
XX (differentially displayed) in individuals genetically predisposed to
XX cardiovascular disease. It may be up regulated by treatment with
XX interleukin (IL)-1 or treatment with shear stress. It may be down
XX regulated by treatment of individuals with high fat/high cholesterol

```

CC diet. Also included are a nucleotide vector containing the nucleotide  
 CC sequence, a genetically engineered host cell containing the nucleotide  
 CC sequence, a pure gene product encoded by the nucleic acid, an antibody  
 CC that immunospecifically binds the gene product, diagnosing cardiovascular  
 CC disease (comprising detecting a gene or its gene product that is  
 CC differentially expressed in cardiovascular disease states), treating  
 CC cardiovascular disease (comprising administering a compound that  
 CC modulates the synthesis or expression of a target gene or the activity of  
 CC the target gene product to a patient), monitoring the efficacy of a  
 CC compound in clinical trials for the treatment of cardiovascular disease  
 CC (comprising detecting a gene or its gene product, which is differentially  
 CC expressed in cardiovascular disease states), and identifying a compound  
 CC that modulates the activity of multiple transmembrane domain receptor  
 CC target gene product (comprising: contacting a first cell expressing the  
 CC multiple transmembrane domain receptor target gene product with a test  
 CC compound and activator of the multiple transmembrane domain receptor  
 CC target gene product; measuring the level of intracellular calcium release  
 CC within the first cell; and comparing the level to that of a second  
 CC multiple transmembrane domain receptor target gene product that expresses  
 CC the cell that has been contacted with the activator but not with the test  
 CC compound so that if the level of intracellular calcium release within the  
 CC first cell differs from that of the second cell, the compound that  
 CC modulates the activity of the multiple transmembrane domain receptor  
 CC target product has been identified). The invention is for use in the  
 CC treatment and diagnosis of cardiovascular disease e.g. atherosclerosis,  
 CC ischaemia/reperfusion, hypertension, or stenosis and arterial  
 CC inflammation. The invention permits the definition of disease pathways  
 CC and the identification of targets in the pathway that are useful both  
 CC diagnostically and therapeutically. It provides a simple and rapid  
 CC approach to the identification of useful therapeutics. The present  
 CC sequence is a PCR primer used to isolate cDNA differentially displayed  
 CC according to the invention.

XX SQ Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2031 CATCACACC 2040

DB 10 CATCACACC 1

RESULT 348

ADH14499/c

ID ADH14499 standard; DNA; 10 BP.

AC ADH14499;

DT 11-MAR-2004 (first entry)

XX Human retinoblastoma 1 (RB1CC1) genomic DNA 5' border of intron 12.

DE cell nucleus; transcription; gene expression; retinoblastoma-1; RB1CC1;  
 KW diagnosis; cancer; primer; ss.

XX Homo sapiens.

XX WO2003102028-A1.

XX 11-DEC-2003.

XX 30-JAN-2003; 2003WO-JP000882.

XX 03-JUN-2002; 2002JP-00161400.

XX 24-JUL-2002; 2002JP-00214978.

XX (OKAB// OKABE H.  
 PA (IKEG// IKEGAWA S.  
 PA (CHAN// CHANO T.

XX Chano T;

XX WPI; 2004-081932/08.

XX Protein in the nuclei of human and animal cells associated with  
 PT expression of retinoblastoma-1 gene for diagnosis of cancer.

XX Disclosure; Page 11; 113pp; Japanese.

XX The invention relates to a protein or polypeptide found in the nuclei of  
 CC human and animal cells that are associated with transcription and/or  
 CC induction of expression of retinoblastoma 1 gene (RB1CC1). The invention  
 CC of RB1CC1 gene and its protein is useful for the diagnosis of cancer. The  
 CC human RB1CC1 cDNA is 6.6 kb containing a 4782 bp ORF, encoding a 15  
 CC 1594 amino acid protein. This sequence corresponds to the sequence at the  
 CC junction between an intron and an exon in the human RB1CC1 genomic  
 CC sequence.

XX SQ Sequence 10 BP; 2 A; 0 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 AAATACATAC 208

DB 10 AAATACATAC 1

RESULT 349

AD126560/c

ID AD126560 standard; DNA; 10 BP.

XX AC AD126560;

XX -15-APR-2004 (first entry)

XX Rat PIM1 antisense K3 oligonucleotide i.

XX pain modulator; PIM kinase family; locked nucleic acid; LNA;  
 KW phosphorothioate; analgesic; uteropathic; antipruritic; cytostatic;  
 KW antiinflammatory; antilasthmatic; antitense; inhibition; gene therapy;  
 KW tactile allodynia; urinary incontinence; neurogenic bladder; pruritus;  
 KW tumour; asthma; primer; ss.

XX Rattus sp.

XX WO2003106681-A2.

XX 24-DEC-2003.

XX 12-JUN-2003; 2003WO-EP006158.

XX 14-JUN-2002; 2002DE-01026702.

XX (CHEF ) GRUENENTHAL GMBH.

XX Altan O, Kurreck J, Gruenweller A, Erdmann V;

XX WPI; 2004-142780/14.

XX New oligonucleotides directed against PIM1 kinase, useful for treating,  
 PT e.g. pain, urinary incontinence, tumors and inflammation, by gene  
 PT therapy.

XX Disclosure; Fig 1; 37pp; German.

XX This invention describes novel oligonucleotides or polynucleotide  
 CC constructs which are used in pharmaceutical or diagnostic compositions.  
 CC The oligonucleotides are used for identifying modulators of pain, based  
 CC on the ability of labelled oligonucleotides or polynucleotide constructs  
 CC to bind to an RNA. The oligonucleotides can also be used to diagnose  
 CC disease associated with altered expression of genes of the PIM kinase  
 CC family by measuring binding. The oligonucleotides have at least one

CC modified ribose, phosphodiester and/or base component. Particularly many,  
 CC of the nucleotides are 'locked nucleic acids' (LNA) or at least one  
 CC nucleotide is a phosphorothioate. The polynucleotide construct comprises  
 CC a ribozyme, DNA enzyme, vector (particularly for expression) or peptide  
 CC nucleic acid, most preferably a hammerhead ribozyme or Type 8-17 DNA  
 CC enzyme. It may be attached to a carrier (preferably the proteins tet,  
 CC transposin or ferritin) and/or encapsulated in a liposome. The products  
 CC of the invention have analgesic, uropathic, antipruritic, cytostatic,  
 CC antiinflammatory and antiasthmatic activity and can be used for antisense  
 CC and catalytic inhibition of PIM kinases and for antisense gene therapy.  
 CC The oligonucleotides are useful for treating (i) pain, especially  
 CC chronic, heat-induced or inflammatory pain, or tactile allodynia and (ii)  
 CC urinary incontinence, neurogenic bladder symptoms, pruritus, tumours and  
 CC inflammation, especially PIM1-kinase associated inflammation such as  
 CC asthma, or generally any PIM1-related disease symptoms. They can also be  
 CC used to screen for analgesic agents and for diagnosis of diseases  
 CC associated with expression of PIM family genes. AD126552-AD126627  
 CC represent antisense oligonucleotides described in the disclosure of the  
 CC invention.

XX Sequence 10 BP; 0 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1577 AAGAGAAGGA 1586

|||||||

DB 10 AAGAGAAGGA 1

RESULT 350

ADK13018/C

ID ADK13018 standard; DNA; 10 BP.

XX ADK13018;

XX 20-MAY-2004 (first entry)

XX Human glioma endothelial marker (GEM) standard tag SEQ ID NO:196.

XX glioma; brain tissue; neoplastic; glioma endothelial marker; GEM;

XX anticancer; antiglioma; immune response; cytostatic;

XX multi-drug sensitive glioma; human; standard tag: ss.

XX Homo sapiens.

XX Synthetic.

XX WO2004016758-A2.

XX 26-FEB-2004.

XX 15-AUG-2003; 2003WO-US025614.

XX 15-AUG-2002; 2002US-0403390P.

XX 01-APR-2003; 2003US-0458978P.

XX (GENZ ) GENZYME CORP.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Madden SI, Wang CJ, Cook BP, Latters J, Walter K;

XX WPI; 2004-247973/23.

XX Diagnosing glioma by detecting expression product of any one of 255  
 PT genes, glioma endothelial markers, in brain tissue sample suspected of  
 PT being neoplastic, and comparing the expression with expression in normal  
 PT brain tissue sample.

XX Example 2; SEQ ID NO 196; 114bp; English.

XX The present invention describes a method (M1) for aiding in the diagnosis  
 CC of glioma. (M1) involves detecting an expression product of at least one

CC gene (I) in a first brain tissue sample (T) suspected of being  
 CC neoplastic, where (I) is chosen from any one of 255 genes (glioma  
 CC endothelial markers (GEMs)) as given in specific table, and comparing the  
 CC expression of (I) in (T) with expression of (I) in a second tissue sample  
 CC tissue sample (R), where expression of (I) in a second tissue sample (R)  
 CC (R), identifies (T) as likely to be neoplastic. Also described: (1)  
 CC treating (M2) glioma involves contacting cells of the glioma with an  
 CC antibody that specifically binds to a extracellular epitope; (2)  
 CC identifying (M3) a test compound as potential anticancer or anti-glioma  
 CC drug involves contacting a test compound with the cell which expresses  
 CC (I), monitoring an expression product of the at least one gene and  
 CC identifying test compound as a potential anticancer drug if it decreases  
 CC the expression of at least one gene; (3) identifying (M4) a test compound  
 CC as potential anticancer or anti-glioma drug involves contacting a test  
 CC compound with the cell which expresses mRNA of at least one gene  
 CC identified by a tag as described above, monitoring mRNA of the gene, and  
 CC identifying the test compound as a potential anticancer drug if it  
 CC decreases the expression of at least one gene; and (4) inducing (M5) an  
 CC immune response to glioma involves administering to a mammal, a protein  
 CC or (I). (I) have cytostatic activities, and can be used to trigger immune  
 CC destruction of glioma cells, and as immune response inducers. (M1) is  
 CC useful for aiding in diagnosing glioma. (M2) is useful for treating multi-  
 CC drug sensitive glioma in a human. (M5) is useful for inducing an immune  
 CC response to a glioma in a mammal having glioma or in a mammal who has had  
 CC a glioma surgically removed. The present sequence represents a human cDNA  
 CC standard tag oligonucleotide, which is used in the example of the present  
 CC present invention.

XX Sequence 10 BP; 1 A; 0 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1065 CACAAAATC 1074

|||||||

DB 10 CACAAAATC 1

RESULT 351

ADL35951

ID ADL35951 standard; DNA; 10 BP

XX ADL35951;

XX 03-JUN-2004 (first entry)

XX Serial analysis of gene expression (SAGE) tag oligonucleotide.

XX gene data comparison; identification; gene sequence cluster identifier;  
 KW bioinformation data analysis; serial analysis of gene expression; SAGE;  
 KW tag; ss.

XX Synthetic.

XX WO2004023344-A1.

XX 18-MAR-2004.

XX 05-SEP-2003; 2003WO-SE001379.

XX 06-SEP-2002; 2002SE-00002667.

XX (AFFI-) AFFIBODY AB.

XX Larsson M, Wennborg A;

XX WPI; 2004-315607/29.

XX Comparison of two sets of gene data useful in analysis of the data  
 PT involves identifying gene data from each set that is also present in both  
 PT gene sequence cluster identifier.



PS Disclosure; Fig 7; 38pp; English.

XX The present invention describes the comparison of two sets of gene data, comprising associating each gene data of both the sets uniquely with a separate gene sequence cluster and identifying from respective sets, gene data that is associated to a same gene sequence cluster identifier. The data is represented by graphical symbols and correlated using computer based manipulations. Also described is a computer system for facilitating the comparison. The comparison can be used in the analysis of bioinformation data by facilitating the comparison of a set of gene data with a large number of different sets of gene data comprising results from experiments and functional descriptions. The gene sequence cluster identifier simplifies the comparison of gene data since it eliminates the difficulties caused by the use of different application specific identifiers of nucleic acid sequences pertaining to the same gene sequence cluster. The present sequence represents a serial analysis of gene expression (SAGE) tag oligonucleotide, which is used in the exemplification of the present invention.

XX SQ Sequence 10 BP; 6 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 AAAATTAGAG 142  
 |||||  
 Db 1 AAAATTAGAG 10

RESULT 352

ADL98325

ID ADL98325 standard; DNA; 10 BP.

XX AC ADL98325;

XX 17-JUN-2004 (first entry)

XX ttr-1 gene intron 4 alternate splice sequence, SEQ ID 5.

XX Nematode; Cytostatic; neoplasia; Class B synthetic multivulval gene; Class C synthetic multivulval gene; synMuv; Class B synMuv gene; Class C synMuv gene; KIAA1732; mep-1; lin(n3628); lin(n4256); lin-65; ttr-1; hat-1; epc-1; ssl-1; cell death; ds.

XX Caenorhabditis elegans.

XX WO2004024084-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028626.

XX 12-SEP-2002; 2002US-0410160P.

XX 02-JAN-2003; 2003US-0437821P.

XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.

XX Horvitz HRPD, Ceol C, Andersen E;

XX WPI; 2004-329386/30.

XX Identifying a candidate compound, for treating neoplasia, comprises contacting a cell having a mutation in a synthetic multivulval (synMuv) gene with a candidate compound, or providing a cell expressing a synMuv gene or polypeptide.

XX Disclosure; SEQ ID NO 5; 302pp; English.

XX The present invention relates to a method for identifying a candidate compound that treats a neoplasia. The method comprises contacting a cell having a mutation in a Class B synthetic multivulval (synMuv) gene with a candidate compound, or providing a cell expressing a Class B or C synMuv

CC gene or polypeptide, a KIAA1732 polypeptide, or a nucleic acid having at least 95% identity to a Class B or C synMuv gene or to a nucleic acid that encodes KIAA1732, and contacting the cell with a candidate compound. Exemplary Class B synMuv genes are mep-1, lin(n3628), lin(n4256) or lin-65, and exemplary Class C synMuv genes are ttr-1, hat-1, epc-1 or ssl-1. The methods, nucleic acids and polypeptides are useful for identifying candidate compounds that treat neoplasia or conditions characterized by inappropriate cell death. Alternative splice acceptors create small differences in the ttr-1 coding sequence. The present sequence is an alternative splice sequence for the fourth intron.

XX SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 921 AGTTTCAGAC 930  
 |||||  
 Db 1 AGTTTCAGAC 10

RESULT 353

ADL98324

ID ADL98324 standard; DNA; 10 BP.

XX AC ADL98324;

XX 17-JUN-2004 (first entry)

XX ttr-1 gene intron 4 alternate splice sequence, SEQ ID 4.

XX Nematode; Cytostatic; neoplasia; Class B synthetic multivulval gene; Class C synthetic multivulval gene; synMuv; Class B synMuv gene; Class C synMuv gene; KIAA1732; mep-1; lin(n3628); lin(n4256); lin-65; ttr-1; hat-1; epc-1; ssl-1; cell death; ds.

XX Caenorhabditis elegans.

XX WO2004024084-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028626.

XX 12-SEP-2002; 2002US-0410160P.

XX 02-JAN-2003; 2003US-0437821P.

XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.

XX Horvitz HRPD, Ceol C, Andersen E;

XX WPI; 2004-329386/30.

XX Identifying a candidate compound, for treating neoplasia, comprises contacting a cell having a mutation in a synthetic multivulval (synMuv) gene with a candidate compound, or providing a cell expressing a synMuv gene or polypeptide.

XX Disclosure; SEQ ID NO 4; 302pp; English.

XX The present invention relates to a method for identifying a candidate compound that treats a neoplasia. The method comprises contacting a cell having a mutation in a Class B synthetic multivulval (synMuv) gene with a candidate compound, or providing a cell expressing a Class B or C synMuv gene or polypeptide, or a KIAA1732 polypeptide, or a nucleic acid having at least 95% identity to a Class B or C synMuv gene or to a nucleic acid that encodes KIAA1732, and contacting the cell with a candidate compound. Exemplary Class B synMuv genes are mep-1, lin(n3628), lin(n4256) or lin-65, and exemplary Class C synMuv genes are ttr-1, hat-1, epc-1 or ssl-1. The methods, nucleic acids and polypeptides are useful for identifying candidate compounds that treat neoplasia or conditions characterized by inappropriate cell death. Alternative splice acceptors create small

CC differences in the trr-1 coding sequence. The present sequence is an  
 CC alternative splice sequence for the fourth intron.  
 XX  
 SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 921 AGTTTCAGAC 930  
 DB 1 AGTTTCAGAC 10  
 RESULT 354  
 ADN89109/c  
 ID ADN89109 standard; DNA; 10 BP.  
 XX  
 AC ADN89109;  
 XX  
 XX  
 XX 15-JUL-2004 (first entry)  
 XX  
 DE Hyperlipidemia treatment associated human ITGB3 haplotype probe #174.  
 XX  
 XX as; probe; antilipemic; gene therapy; allele; polymorphic site;  
 KW integrin beta 3; ITGB3; statin response marker; hyperlipidemia.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2004033710-A2.  
 PN  
 XX 22-APR-2004.  
 PD  
 XX 09-OCT-2003; 2003WO-US032361.  
 XX  
 PR 09-OCT-2002; 2002US-0417743P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Bentivegna SC, Bieglecki KM, Brain CD, Dain BJ, Cappola G;  
 PI Judson RS, Lachowicz M, Lee HH, Litvyn L, Messer C, Petersen N;  
 PI Reed CR, Rounds EM, Russo DP, Windemuth AK;  
 XX  
 DR WPI; 2004-340942/31.  
 XX  
 XX New kit comprising a set of oligonucleotides, useful for determining  
 PT whether an individual has a statin response marker I or II for preparing  
 PT a composition for treating hyperlipidemia.  
 PS  
 PS Claim 13; SEQ ID NO 177; 202pp; English.  
 XX  
 XX A kit comprising a set of oligonucleotides designed for identifying at  
 CC least one of the alleles at each polymorphic site (PS) in a set of 129  
 CC polymorphic sites (PSs) given in the specification, is new. The kit  
 CC identifies at least one of the alleles at each polymorphic site (PS) in a  
 CC set of 129 polymorphic sites (PSs) given in the specification, for  
 CC example: PS1 and PS42; PS19 and PS42; PS3, PS12, and PS42; a set of  
 CC polymorphic sites comprising a linked haplotype to any one of haplotypes  
 CC 101-194, 201-463 or 501-515 given in the specification; or a set of  
 CC polymorphic sites comprising a substitute haplotype for any one of  
 CC haplotypes 101-194, 201-463 or haplotypes 501-515 given in the  
 CC specification; where the nucleotide position of each polymorphic site  
 CC corresponds to the following nucleotide position in the 32577-bp  
 CC sequence: 1118 (PS1), 1773 (PS3), 1875 (PS4), 1911 (PS5), 1957 (PS6),  
 CC 2087 (PS10), 2157 (PS12), 13384 (PS15), 13405 (PS16), 16200 (PS19), 17194  
 CC (PS20), 17273 (PS21), 20035 (PS26), 20047 (PS28), 20615 (PS30), 21944  
 CC (PS33), 22155 (PS35), 25705 (PS37), 25921 (PS38), 27882 (PS39), and 30618  
 CC (PS42). INDEPENDENT CLAIMS are also included for: determining whether an  
 CC individual has a statin response marker I or a statin response marker II;  
 CC selecting a statin therapy to provide an optimal High Density Lipoprotein  
 CC Cholesterol (HDLc) response in an individual; predicting an individual's  
 CC High Density Lipoprotein Cholesterol (HDLc) response to treatment with a  
 CC statin; predicting an individual's High Density Lipoprotein Cholesterol

(HDLc) response to treatment with a statin; manufacturing a drug product;  
 CC seeking regulatory approval for marketing a pharmaceutical formulation  
 CC for treating a disease or condition in a population partially or wholly  
 CC defined by having a statin response marker I; marketing a drug product  
 CC comprising a statin as at least one active ingredient for treating a  
 CC disease or condition in a population partially or wholly defined by  
 CC having a statin response marker I; an isolated polynucleotide comprising  
 CC a first nucleotide sequence which comprises an integrin, beta 3 (ITGB3)  
 CC isogene encoding a ITGB3 polypeptide, where the ITGB3 isogene consists of  
 CC of isogenes 1-38 and 40-98 defined by a correspondingly numbered  
 CC haplotype, where each of the isogenes comprises nucleotides 1-32577,  
 CC 4256-4716, 1317913723, 14235-14858, 16126-16619, 16930-17414, 19141-  
 CC 19644, 19748-20177, 2053721009, 21731-22412, 24385-24930, 255926029,  
 CC 27822-28255, 30265-30754, and 31300-31718 of the 32577 bp sequence,  
 CC except where substituted by the sequence of alleles for the  
 CC correspondingly numbered haplotype at the polymorphic site, where  
 CC nucleotide positions in the 32577 bp sequence are indicated by a  
 CC sequence which is complementary to the sequence of the ITGB3 isogene  
 CC recombinant nonhuman organism, where the ITGB3 isogene encodes the  
 CC polypeptide encoded by the selected ITGB3 isogene, the ITGB3 isogene  
 CC of an integrin, beta 3 (ITGB3) isogene, where the ITGB3 isogene encodes  
 CC or more polymorphisms consisting of thymine at PS 1, adenine at PS 2,  
 CC cytosine at PS3, thymine at PS4, cytosine at PS5, adenine at PS6, thymine  
 CC at PS7, thymine at PS8, guanine at PS9, adenine at PS10, adenine at PS11,  
 CC thymine at PS12, adenine at PS13, guanine at PS 16, adenine at PS 18,  
 CC thymine at PS 19, guanine at PS2 1, guanine at PS22, cytosine at PS23,  
 CC cytosine at PS24, thymine at PS25; adenine at PS26, adenine at PS27,  
 CC thymine at PS29, adenine at PS30, cytosine at PS31, guanine at PS32,  
 CC adenine at PS33, adenine at PS35, cytosine at PS37, thymine at PS38,  
 CC cytosine at PS39, adenine at PS40, thymine at PS41, thymine at PS42,  
 CC guanine at PS43 and guanine at PS44; a genome anthology for the integrin,  
 CC beta 3 (ITGB3) gene which comprises two or more ITGB3 isogenes consisting  
 CC of isogenes 1-98, where each of the selected isogenes is defined by a  
 CC correspondingly numbered haplotype given in the specification, and where  
 CC each of the isogenes comprises nucleotides 1000-2235, 4256-4716, 13179-  
 CC 13723, 14235-14858, 16126-16619, 16930-17414, 19241-19644, 19748-20177,  
 CC 2053721009, 21731-22412, 24385-24930, 255926029, 27822-28255, 30265-  
 CC 30754, and 31300-31718 of the 32577-bp sequence except where substituted  
 CC by the sequence of alleles for the correspondingly numbered haplotype at  
 CC each of file polymorphic sites; haplotyping the integrin, beta 3 (ITGB3)  
 CC gene of an individual; assigning a haplotype pair for the integrin, beta  
 CC 3 (ITGB3) gene to an individual; reducing the potential for bias in a  
 CC clinical trial of a candidate drug for treating a disease or condition  
 CC predicted to be associated with ITGB3 activity; an isolated polypeptide  
 CC comprising a ITGB3 protein variant consisting of protein variants A, B,  
 CC C, D, E, F and G and comprising 788-amino acid sequence, except where  
 CC substituted by the corresponding sequence of amino acids whose positions  
 CC and alleles are given in the specification; an isolated monoclonal  
 CC antibody specific for and immunoreactive with the selected ITGB3 protein  
 CC variant comprising the isolated polypeptide; screening for a variant  
 CC targeting the selected ITGB3 protein variant comprising the isolated  
 CC polypeptide; an isolated fragment of an ITGB3 protein variant, where the  
 CC fragment is at least 6 amino acids in length and comprises one or more  
 CC variant amino acids consisting of methionine at a position corresponding  
 CC to amino acid position 14, arginine at a position corresponding to amino  
 CC acid position 66, methionine at a position corresponding to amino acid  
 CC position 445, and glutamine at a position corresponding to amino acid  
 CC position 515 the 788-amino acid sequence; screening for drugs targeting  
 CC the selected ITGB3 protein variant comprising the isolated polypeptide;  
 CC screening for compounds targeting the ITGB3 protein variant, where a drug  
 CC or disease predicted to be associated with ITGB3 activity, is a variant  
 CC ITGB3 protein as a candidate target for treatment of a disease or condition  
 CC predicted to be associated with ITGB3 activity, and an associated  
 CC oligonucleotide designed for detecting a polymorphism in the integrin,  
 CC beta 3 (ITGB3) gene at a polymorphic site (PS) consisting of PS1 PS44,  
 CC where the oligonucleotide contains or is located one to several  
 CC nucleotides downstream of the selected PS, where the oligonucleotide has  
 CC a length of about 15 to about 100 nucleotides; Preferred Kit: The kit  
 CC further comprises a manual with instructions for performing one or more  
 CC reactions on a human nucleic acid sample to identify the allele(s)  
 CC present in the individual at each polymorphic site in the set of  
 CC polymorphic sites and determining if the individual has a statin response

CC marker I or a statin response marker II based on the identified  
 CC allele(s). The set of oligonucleotides is designated for identifying both  
 CC alleles at each polymorphic site of the selected set of polymorphic  
 CC sites. The set of PSS comprises PS3, PS12 and PS42; PS 1, PS12 and PS42;  
 CC PS3 and PS42; PS1 and PS42; PS1, PS3, PS12 and PS42; or PS39. The set of  
 CC PS is PS3, PS12 or PS42. The individual is Caucasian. The linkage  
 CC disequilibrium between the linked haplotype and any one of haplotypes 101  
 CC -194, 201-463 or 501-515 has  $\Delta G_r$  2 consisting of at least 0.75, at least  
 CC 0.80, at least 0.85, at least 0.90, at least 0.95 or 1.0. At least one of  
 CC the oligonucleotides in the set of oligonucleotides is an allele-specific  
 CC oligonucleotide comprising a nucleotide sequence consisting of 10-15 bp.  
 CC The set of polymorphic sites is PS3, PS12, and PS42 and the set of  
 CC oligonucleotides comprises first, second and third allele-specific  
 CC oligonucleotide (ASO) probes, where the first ASO probe comprises 15-bp  
 CC sequence, or its complement, and S in the 15-bp sequence is guanine; the  
 CC second ASO probe comprises 15-bp sequence, or its complement, and Y in  
 CC the 15-bp sequence is cytosine, and the third ASO probe comprises 15 bp,  
 CC or its complement, and Y in the 15-bp sequence is cytosine. Preferred  
 CC Article: The article of manufacture comprises a pharmaceutical  
 CC formulation and at least one indicium identifying a population for whom  
 CC the pharmaceutical formulation is indicated, where the pharmaceutical  
 CC formulation comprises a statin as at least one active ingredient and the  
 CC identified population is partially or wholly defined by having a statin  
 CC response marker I, where a trial population having the statin response  
 CC marker I exhibits a better HDLC response to the pharmaceutical  
 CC formulation than to treatment with atorvastatin or salt of atorvastatin  
 CC acid. It also comprises packaging material and a pharmaceutical  
 CC formulation contained within the packaging material, where the  
 CC pharmaceutical formulation comprises a statin as at least one separate  
 CC active ingredient, and the packaging material comprises an approved label  
 CC which states that the pharmaceutical formulation is indicated for a  
 CC population partly or wholly defined by having a statin response marker I,  
 CC where a trial population having the statin response marker exhibits a  
 CC better HDLC response to the pharmaceutical formulation than to treatment  
 CC with atorvastatin or a salt of atorvastatin acid. Preferred  
 CC Oligonucleotide: The isolated oligonucleotide is an allele-specific  
 CC oligonucleotide that specifically hybridizes to an allele of the ITGB3  
 CC gene at a region containing the polymorphic site. The isolated  
 CC oligonucleotide is a primer-extension oligonucleotide. The kit is for  
 CC haplotyping the integrin, beta 3 (ITGB3) gene of all individual,  
 CC comprises a set of oligonucleotides designed for identifying at least one  
 CC of the alleles at each polymorphic site (PS) in a set of two or more  
 CC polymorphic sites. Preferred Method: Determining whether an individual  
 CC has a statin response marker I or a statin response marker II comprises  
 CC determining the copy number in the individual of the haplotype, where if  
 CC the selected haplotype is one of haplotypes given in the specification,  
 CC then the individual has a statin response marker I if the individual has  
 CC at least one copy of the selected haplotype and a statin response marker  
 CC II if the individual has zero copy of the selected haplotype; and the  
 CC individual has a statin response marker I if the individual has zero or  
 CC one copy of the selected haplotype and a statin response marker II if the  
 CC individual has two copies of the selected haplotype. The individual is a  
 CC candidate for treatment with a statin. The determining step comprises  
 CC genotyping each polymorphic site in a set of polymorphic sites comprising  
 CC the selected haplotype and using the results of the genotyping step to  
 CC identify, for the set of polymorphic sites the haplotype pair present in  
 CC the individual. The determining step comprises consulting a data  
 CC repository, that provides information on the copy number present in the  
 CC individual for the selected haplotype. The data repository is the  
 CC individual's medical records or a medical data card. Assigning an  
 CC individual to a first or second statin response marker group comprises  
 CC determining the copy number in the individual or a haplotype and  
 CC assigning the individual to the first statin response marker group if the  
 CC individual has at least one copy of the selected haplotype and to the  
 CC second statin response marker group if the individual has zero copy of  
 CC the selected haplotype; and assigning the individual to the first statin  
 CC response marker group if the individual has zero or one copy of the  
 CC selected haplotype and to the second statin response marker group if the  
 CC individual has two copies of the selected haplotype. The determining step  
 CC comprises genotyping each polymorphic site in a set of polymorphic sites

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 774 TGGTTTCTAT 783  
 Db 10 TGGTTTCTAT 1  
 RESULT 355  
 ADO39861/C  
 ID ADO39861 standard; DNA; 10 BP.  
 XX ADO39861;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Androgen-regulated gene (ARG) fragment #24.  
 XX  
 KW Androgen-regulated gene; ARG; PMEPA1; prostate cancer; Cap;  
 KW prostate-related disease; gene therapy; vaccine; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN US2004092469-A1.  
 XX  
 PD 13-MAY-2004.  
 XX  
 XX 09-MAY-2003; 2003US-00434479.  
 XX  
 PR 28-JAN-2000; 2000US-0178772P.  
 PR 31-JAN-2000; 2000US-0179045P.  
 PR 26-JAN-2001; 2001US-00769482.  
 PR 18-MAR-2003; 2003US-00390045.  
 XX  
 (SRIV/) SRIVASTAVA S.  
 PA (MOUL/) MOUL J W.  
 PA (XULL/) XU L L.  
 XX  
 XX Srivastava S, Moul JW, Xu LL;  
 WPI; 2004-374986/35.  
 XX  
 XX New PMEPA1 polypeptide that inhibits the growth of LN prostate cancer  
 (LNCaP) cells in a colony-forming assay, useful for detecting, preventing  
 and treating prostate cancer.  
 XX  
 XX Example 6; SEQ ID NO 36; 78pp; English.  
 XX  
 XX The invention relates to androgen-regulated gene (ARG). PMEPA1 and its  
 encoded protein. PMEPA1 polypeptide is useful in inhibiting the growth of  
 a prostate cancer (Cap) cell. It is also useful for reducing the  
 expression of an androgen receptor or modulating the expression of a gene  
 in a prostate cancer cell. PMEPA1 sequence is useful in gene therapy.  
 CC useful to prepare vaccines, useful as markers of prostate cancer and  
 CC other prostate-related diseases, and as targets for therapeutic  
 CC intervention in prostate cancer and other prostate-related diseases  
 CC PMEPA1, its encoding nucleic acid or the antibodies are useful for  
 CC detecting, preventing and treating prostate cancer. The present sequence  
 CC is an androgen-regulated gene fragment which has genomic maintenance and  
 CC cell cycle regulating activity.  
 XX  
 SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1837 GAACCCAGCT 1846  
 Db 10 GAACCCAGCT 1

RESULT 356  
 ADO39861

```

ID  ADO39881 standard; DNA; 10 BP.
XX
AC  ADO39881;
XX
XX  29-JUL-2004 (first entry)
XX
XX  Androgen-regulated gene (ARG) fragment #44.
XX
XX  Androgen-regulated gene; ARG; PMEPA1; prostate cancer; Cap;
XX  prostate-related disease; gene therapy; vaccine; ds.
XX
XX  Unidentified.
XX
XX  US2004092469-A1.
XX
XX  13-MAY-2004.
XX
XX  09-MAY-2003; 2003US-00434479.
XX
XX  28-JAN-2000; 2000US-0178772P.
XX  31-JAN-2000; 2000US-0179045P.
XX  26-JAN-2001; 2001US-00769482.
XX  18-MAR-2003; 2003US-00390045.
XX
XX  (SRIV/) SRIVASTAVA S.
XX  (MOUL/) MOUL J W.
XX  (XULL/) XU L L.
XX
XX  Srivastava S, Moul JW, Xu LL;
XX  WPI; 2004-374986/35.
XX
XX  New PMEPA1 polypeptide that inhibits the growth of LN prostate cancer
XX  (LNCap) cells in a colony-forming assay, useful for detecting, preventing
XX  and treating prostate cancer.
XX
XX  Example 6; SEQ ID NO 56; 78pp; English.
XX
XX  The invention relates to androgen-regulated gene (ARG), PMEPA1 and its
XX  encoded protein. PMEPA1 polypeptide is useful in inhibiting the growth of
XX  a prostate cancer (Cap) cell. It is also useful for reducing the
XX  expression of an androgen receptor or modulating the expression of a gene
XX  in a prostate cancer cell. PMEPA1 sequence is useful in gene therapy,
XX  useful to prepare vaccines, useful as markers of prostate cancer and
XX  other prostate-related diseases, and as targets for therapeutic
XX  intervention in prostate cancer and other prostate-related diseases.
XX  PMEPA1, its encoding nucleic acid or the antibodies are useful for
XX  detecting, preventing and treating prostate cancer. The present sequence
XX  is an androgen-regulated gene fragment which has energy metabolism,
XX  apoptosis and redox regulating activity.
XX
XX  Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
XX
XX  Query Match 0.4%; Score 10; DB 1; Length 10;
XX  Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 1874 AAAGCCNAGA 1883
XX  |||||
XX  1 AAAGCCNAGA 10
XX
XX  RESULT 357
XX  ADO39845/c
XX  ID ADO39845 standard; DNA; 10 BP.
XX
XX  AC ADO39845;
XX
XX  29-JUL-2004 (first entry)
XX
XX  Androgen-regulated gene (ARG) fragment #8.
XX
XX  Androgen-regulated gene; ARG; PMEPA1; prostate cancer; Cap;
XX
prostate-related disease; gene therapy; vaccine; ds.
Unidentified.
US2004092469-A1.
13-MAY-2004.
09-MAY-2003; 2003US-00434479.
28-JAN-2000; 2000US-0178772P.
31-JAN-2000; 2000US-0179045P.
26-JAN-2001; 2001US-00769482.
18-MAR-2003; 2003US-00390045.
(SRIV/) SRIVASTAVA S.
(MOUL/) MOUL J W.
(XULL/) XU L L.
Srivastava S, Moul JW, Xu LL;
WPI; 2004-374986/35.
New PMEPA1 polypeptide that inhibits the growth of LN prostate cancer
(LNCap) cells in a colony-forming assay, useful for detecting, preventing
and treating prostate cancer.
Example 6; SEQ ID NO 20; 78pp; English.
The invention relates to androgen-regulated gene (ARG), PMEPA1 and its
encoded protein. PMEPA1 polypeptide is useful in inhibiting the growth of
a prostate cancer (Cap) cell. It is also useful for reducing the
expression of an androgen receptor or modulating the expression of a gene
in a prostate cancer cell. PMEPA1 sequence is useful in gene therapy,
useful to prepare vaccines, useful as markers of prostate cancer and
other prostate-related diseases, and as targets for therapeutic
intervention in prostate cancer and other prostate-related diseases.
PMEPA1, its encoding nucleic acid or the antibodies are useful for
detecting, preventing and treating prostate cancer. The present sequence
is an androgen-regulated gene fragment which has energy metabolism,
apoptosis and redox regulating activity.
Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other.
Query Match 0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 828 TGGGCTGTCA 837
|||
10 TGGGCTGTCA 1
Db
RESULT 358
ADO39884
ID ADO39884 standard; DNA; 10 BP.
XX
XX  ADO39884;
XX
XX  09-SEP-2004 (first entry)
XX
XX  Human VR1 exon 1a transcription factor binding fragment #1.
XX
XX  ds; VR1 receptor; vanilloid receptor type 1; modulator;
XX  pain transmission; primary sensory neuron; transcription factor.
XX  detection; MZFL; NFKappaB; NFAT; GATA1; sensitivity; human;
XX  hypalgesia; hyperalgesia; neuralgia; myalgia; human;
XX
XX  Homo sapiens.
XX
XX  WO2004053120-A2.
XX
XX  24-JUN-2004.
XX

```

XX 01-DEC-2003; 2003WO-EP013522.  
 XX PF  
 XX 09-DEC-2002; 2002DE-01057421.  
 XX PF  
 XX (CHEF ) GRUENTHAL GMBH.  
 XX PA  
 XX Weihe E, Bieller A, Schaefer MKH;  
 XX PI  
 XX WPI; 2004-468868/44.  
 XX DR  
 XX New nucleic acid that modulates expression of the vanilloid receptor-1,  
 XX PT useful for control of pain or sensitivity disorders, comprises sequences  
 XX PT from control regions of the receptor gene.  
 XX PT  
 XX PS Disclosure; Page 44; 68pp; German.  
 XX PS  
 CC This invention describes a novel nucleic acid containing a specific  
 CC segment having at least one region that modulates expression of the VR1  
 CC (vanilloid receptor type 1) receptor, or a functional derivative, allele  
 CC or fragment of this region, or a sequence that hybridises to it under  
 CC standard conditions. The VR1 modulator is derived from one or more of  
 CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or  
 CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of  
 CC pain, particularly in primary sensory neurons. The invention also  
 CC describes a vector that contains the VR1 modulator, host cells containing  
 CC this vector (other than human germ or embryonal stem cells) and a method  
 CC for modulating expression of the VR1 receptor by introducing the  
 CC modulator or the vector into a cell that contains the VR1 gene. The  
 CC products of the invention are used for detecting a transcription factor  
 CC from its binding to a regulatory sequence (or a double-stranded  
 CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-  
 CC linked immunosorbent assay, particularly for diagnosis of diseases  
 CC associated with overexpression or underexpression of the transcription  
 CC factor. The region that modulates VR1 receptor expression includes a  
 CC binding site for a transcription factor, e.g. MZF1, NFkappaB, NFAT or  
 CC GATA1. The nucleic acids of the invention, or vectors containing them,  
 CC are used for prevention or treatment of pain, also for treating  
 CC sensitivity disorders, e.g. analgesia, hyperalgesia or hyperalgesia, also  
 CC neuralgia and myalgia, that are associated with activity of the VR1  
 CC receptor. This sequence represents a fragment of human VR1 exon 1a DNA  
 CC which is capable of binding to a transcription factor.  
 XX  
 SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1212 AGCAGCTCCA 1221  
 DB 1 AGCAGCTCCA 10  
 RESULT 359  
 ADR10674  
 ID ADR10674 standard; DNA; 10 BP.  
 XX AC  
 XX ADR10674;  
 XX AC  
 XX 21-OCT-2004 (first entry)  
 XX DT  
 XX Arbitrary decamer PCR primer MR\_8.  
 XX DE  
 XX Viral vector; thymidine kinase; cytotoxic T lymphocyte; CTL; tumour;  
 XX KW cancer; differential expression; trimolecular recombination; HLA;  
 XX KW human leukocyte antigen; autoimmune disease; viral infection;  
 XX KW fungal infection; mycobacterial infection; ss; PCR; primer.  
 XX OS  
 XX Synthetic.  
 XX PN  
 XX US2004151730-A1.

PD 05-AUG-2004.  
 XX PF  
 XX 03-JAN-2002; 2002US-00034350.  
 XX PF  
 XX 22-SEP-1997; 97US-00935377.  
 XX PR  
 XX (UYRP ) UNIV ROCHESTER.  
 XX PA  
 XX Zauderer M;  
 XX PI  
 XX WPI; 2004-592546/57.  
 XX DR  
 XX Identifying target epitope such as tumor specific target epitope by  
 XX PT screening expression library products from DNA or RNA of cell expressing  
 XX PT epitope with cytotoxic T cells generated against cell to identify clones  
 XX PT expressing epitope.  
 XX PT  
 XX PS Example 4; SEQ ID NO 15; 55pp; English.  
 XX PS  
 CC The invention relates to identifying a target epitope such as a tumour  
 CC specific target epitope or antigen, involving screening products of an  
 CC expression library generated from DNA or RNA (derived from a cell  
 CC expressing the target epitope) with cytotoxic T cells generated against  
 CC the cell to identify DNA clones expressing the target epitope. The method  
 CC optionally involves providing cytotoxic T cells specific for a gene  
 CC product differentially expressed by a cell expressing the target epitope,  
 CC and measuring crossreactivity of the cytotoxic T cells for the cell in  
 CC which target epitopes are identified as the gene product which induces  
 CC cytotoxic T cells. Also included are a viral vector (containing a DNA  
 CC insert flanked by unique sites for restriction enzymes positioned  
 CC so that religation of the viral vectors arms is prevented and the  
 CC orientation of the insert DNA is fixed and the DNA insert is operatively  
 CC associated with a strong regulatory element where the DNA insert encodes  
 CC a target epitope identified by the method. In the method, the expression  
 CC library is constructed in a viral vector (a vaccinia viral vector  
 CC constructed by trimolecular recombination) infectious for mammalian  
 CC cells. The cytotoxic T cells react with tumour cells derived from a non-  
 CC tumorigenic cell line and do not cross-react with the non-tumorigenic  
 CC cell line. The cytotoxic T cells are derived from animals tolerised with  
 CC a non-tumorigenic cell line and are then immunised with tumour cells  
 CC derived from the non-tumorigenic cell line. The cytotoxic T cells are  
 CC does not express costimulator activity and are subsequently stimulated  
 CC with a tumour cell line expressing costimulator activity. The genes  
 CC expressed in tumour cells are used to generate HLA (human leukocyte  
 CC antigen) restricted cytotoxic T cells, which are evaluated for activity  
 CC against tumour cells. The tumour cell is derived from a single  
 CC immortalised, non-tumorigenic cell line. The vector is derived by  
 CC recombination with plasmid p7.5/tk (thymidine kinase, pEL/tk or their  
 CC derivatives). The method is useful for identifying a target epitope  
 CC specific to tumours, cancers, autoimmune disease or to a cell infected  
 CC with a virus, fungus or mycobacteria. Differentially expressed tumour  
 CC antigen DNAs were amplified by a set of arbitrary decamer PCR primers.  
 CC The present sequence is one of the arbitrary decamer primers.  
 XX  
 SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1449 TACCTATGCC 1458  
 DB 1 TACCTATGCC 10  
 RESULT 360  
 ADR20697/C



```

XX WPI; 2004-728732/71.
XX
XX Diagnosing breast cancer comprises determining expression levels of a
XX gene selected from those differentially expressed in normal or cancerous
XX cells of a breast tissue sample including interleukin 1, thrombospondin 1
XX and cystatin C.
XX
XX Example 2; SEQ ID NO 49; 149pp; English.
XX
XX The invention relates to a method of diagnosis (M1) comprising: (a)
XX providing a test sample of breast tissue; (b) determining the level of
XX expression in the test sample of a gene (e.g. interleukin-8, superoxide
XX dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
XX specification, and (c) if the gene is expressed in the test sample at a
XX lower level than in a control normal breast tissue sample, diagnosing the
XX test sample as containing cancer cells. The method is used for diagnosing
XX breast cancer. This sequence corresponds to an oligonucleotide primer
XX used in the method of the invention.
XX
XX Sequence 10 BP; 1 A; 0 C; 1 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 65 TAAAAACAAA 74
XX 10 TAAAAACAAA 1
XX
XX RESULT 363
XX ADS78119
XX ID ADS78119 standard; DNA; 10 BP.
XX AC ADS78119;
XX DT 30-DEC-2004 (first entry)
XX DE Breast cancer detection oligonucleotide #1901.
XX
XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
XX antisense oligonucleotide inhibitor; cathepsin K inhibitor;
XX cathepsin L inhibitor; cathepsin F inhibitor;
XX metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
XX collagen antagonist; diagnosis; breast tissue; cancer.
XX
XX Homo sapiens.
XX
XX WO2004085621-A2.
XX
XX 07-OCT-2004.
XX
XX 22-MAR-2004; 2004WO-US008866.
XX
XX 20-MAR-2003; 2003US-0456735P.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX
XX Polyak K, Porter D, Allinen M;
XX
XX WPI; 2004-728732/71.
XX
XX Diagnosing breast cancer comprises determining expression levels of a
XX gene selected from those differentially expressed in normal or cancerous
XX cells of a breast tissue sample including interleukin 1, thrombospondin 1
XX and cystatin C.
XX
XX Example 6; SEQ ID NO 1901; 149pp; English.
XX
XX The invention relates to a method of diagnosis (M1) comprising: (a)
XX providing a test sample of breast tissue; (b) determining the level of
XX expression in the test sample of a gene (e.g. interleukin-8, superoxide

```

```

CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX
XX Sequence 10 BP; 5 A; 0 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 80 TGTGTGAAAA 89
XX 1 TGTGTGAAAA 10
XX
XX Db
XX
XX RESULT 364
XX ADS76819
XX ID ADS76819 standard; DNA; 10 BP.
XX AC ADS76819;
XX DT 30-DEC-2004 (first entry)
XX DE Breast cancer detection oligonucleotide #601.
XX
XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
XX antisense oligonucleotide inhibitor; cathepsin K inhibitor;
XX cathepsin L inhibitor; cathepsin F inhibitor;
XX metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
XX collagen antagonist; diagnosis; breast tissue; cancer.
XX
XX Homo sapiens.
XX
XX WO2004085621-A2.
XX
XX 07-OCT-2004.
XX
XX 22-MAR-2004; 2004WO-US008866.
XX
XX 20-MAR-2003; 2003US-0456735P.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX
XX Polyak K, Porter D, Allinen M;
XX
XX WPI; 2004-728732/71.
XX
XX Diagnosing breast cancer comprises determining expression levels of a
XX gene selected from those differentially expressed in normal or cancerous
XX cells of a breast tissue sample including interleukin 1, thrombospondin 1
XX and cystatin C.
XX
XX Example 2; SEQ ID NO 601; 149pp; English.
XX
XX The invention relates to a method of diagnosis (M1) comprising: (a)
XX providing a test sample of breast tissue; (b) determining the level of
XX expression in the test sample of a gene (e.g. interleukin-8, superoxide
XX dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
XX specification, and (c) if the gene is expressed in the test sample at a
XX lower level than in a control normal breast tissue sample, diagnosing the
XX test sample as containing cancer cells. The method is used for diagnosing
XX breast cancer. This sequence corresponds to an oligonucleotide primer
XX used in the method of the invention.
XX
XX Sequence 10 BP; 5 A; 2 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2109 CAATAAACTG 2118
Db      1 CAATAAACTG 10
|||||

RESULT 365
ADS77768/c
ID      ADS77768 standard; DNA; 10 BP.
XX
XX
AC      ADS77768;
XX
XX      30-DEC-2004 (first entry)
DT
XX
DE      Breast cancer detection oligonucleotide #1550.
XX
ss; primer; cytosstatic; RNA interference; RNAi; gene silencing;
KW      antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW      cathepsin L inhibitor; cathepsin F inhibitor;
KW      metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW      collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS      Homo sapiens.
XX
XX      WO2004085621-A2.
PN
XX      07-OCT-2004.
PD
XX
XX      22-MAR-2004; 2004WO-US008866.
PF
ss; primer; cytosstatic; RNA interference; RNAi; gene silencing;
KW      antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW      cathepsin L inhibitor; cathepsin F inhibitor;
KW      metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW      collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS      Homo sapiens.
XX
XX      WO2004085621-A2.
PN
XX      07-OCT-2004.
PD
XX
XX      22-MAR-2004; 2004WO-US008866.
PF
XX
XX      20-MAR-2003; 2003US-0456735P.
PR
(DAND ) DANA FARBER CANCER INST INC.
PA
Polyak K, Porter D, Allinen M;
PI
WPI; 2004-728732/71.
DR
Diagnosing breast cancer comprises determining expression levels of a
PT      gene selected from those differentially expressed in normal or cancerous
PT      cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT      and cystatin C.
XX
XX      Example 6; SEQ ID NO 1550; 149pp; English.
XX
CC      The invention relates to a method of diagnosis (M1) comprising: (a)
CC      providing a test sample of breast tissue; (b) determining the level of
CC      expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC      dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC      specification, and (c) if the gene is expressed in the test sample at a
CC      lower level than in a control normal breast tissue sample, diagnosing the
CC      test sample as containing cancer cells. The method is used for diagnosing
CC      breast cancer. This sequence corresponds to an oligonucleotide primer
CC      used in the method of the invention.
XX
XX      Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
SQ
Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TCAGTTCATC 2327
Db      10 TCAGTTCATC 1
|||||

RESULT 366
ADS76818
ID      ADS76818 standard; DNA; 10 BP.
XX
XX
AC      ADS76818;
XX
XX      30-DEC-2004 (first entry)
DT
XX

```

```

DE      Breast cancer detection oligonucleotide #600.
XX
XX      ss; primer; cytosstatic; RNA interference; RNAi; gene silencing;
KW      antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW      cathepsin L inhibitor; cathepsin F inhibitor;
KW      metalloprotease 2 inhibitor; thrombospondin 2 antagonist;
KW      collagen antagonist; diagnosis; breast tissue; cancer.
XX
XX      Homo sapiens.
XX
XX      WO2004085621-A2.
PN
XX      07-OCT-2004.
PD
XX
XX      22-MAR-2004; 2004WO-US008866.
PF
XX
XX      20-MAR-2003; 2003US-0456735P.
PR
(DAND ) DANA FARBER CANCER INST INC.
PA
Polyak K, Porter D, Allinen M;
PI
WPI; 2004-728732/71.
DR
Diagnosing breast cancer comprises determining expression levels of a
PT      gene selected from those differentially expressed in normal or cancerous
PT      cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT      and cystatin C.
XX
XX      Example 2; SEQ ID NO 600; 149pp; English.
XX
CC      The invention relates to a method of diagnosis (M1) comprising: (a)
CC      providing a test sample of breast tissue; (b) determining the level of
CC      expression in the test sample of a gene (e.g. interleukin 8, superoxide
CC      dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC      specification, and (c) if the gene is expressed in the test sample at a
CC      lower level than in a control normal breast tissue sample, diagnosing the
CC      test sample as containing cancer cells. The method is used for diagnosing
CC      breast cancer. This sequence corresponds to an oligonucleotide primer
CC      used in the method of the invention.
XX
XX      Sequence 10 BP; 5 A; 2 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2109 CAATAAACTG 2118
Db      1 CAATAAACTG 10
|||||

RESULT 367
ADS77329/c
ID      ADS77329 standard; DNA; 10 BP.
XX
XX      ADS77329;
XX
XX      30-DEC-2004 (first entry)
DT
XX
DE      Breast cancer detection oligonucleotide #1111.
XX
XX      ss; primer; cytosstatic; RNA interference; RNAi; gene silencing;
KW      antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW      cathepsin L inhibitor; cathepsin F inhibitor;
KW      metalloprotease 2 inhibitor; thrombospondin 2 antagonist;
KW      collagen antagonist; diagnosis; breast tissue; cancer.
XX
XX      Homo sapiens.
XX
XX      WO2004085621-A2.
PN
XX      07-OCT-2004.
PD

```



```

XX PF 22-MAR-2004; 2004WO-US008866.
XX PF 20-MAR-2003; 2003US-0456735P.
XX PA (DAND ) DANA FARBER CANCER INST INC.
XX PI Polyak K, Porter D, Allinen M;
XX DR WPI; 2004-728732/71.
XX PT Diagnosing breast cancer comprises determining expression levels of a
XX PT gene selected from those differentially expressed in normal or cancerous
XX PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
XX PT and cystatin C.
XX PS Example 4; SEQ ID NO 1111; 149pp; English.
XX CC The invention relates to a method of diagnosis (M1) comprising: (a)
XX CC providing a test sample of breast tissue; (b) determining the level of
XX CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
XX CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
XX CC specification, and (c) if the gene is expressed in the test sample at a
XX CC lower level than in a control normal breast tissue sample, diagnosing the
XX CC test sample as containing cancer cells. The method is used for diagnosing
XX CC breast cancer. This sequence corresponds to an oligonucleotide primer
XX CC used in the method of the invention.
XX SQ Sequence 10 BP; 1 A; 0 C; 1 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 65 TAAAAACAAA 74
XX Db 10 TAAAAACAAA 1
XX
XX RESULT 368
XX ADS77802
XX ID ADS77802 standard; DNA; 10 BP.
XX AC ADS77802;
XX XX
XX DT 30-DEC-2004 (first entry)
XX DE Breast cancer detection oligonucleotide #1584.
XX KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
XX KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
XX KW cathepsin L inhibitor; cathepsin F inhibitor;
XX KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
XX KW collagen antagonist; diagnosis; breast tissue; cancer.
XX OS Homo sapiens.
XX XX
XX PN WO2004085621-A2.
XX XX
XX PD 07-OCT-2004.
XX XX
XX PF 22-MAR-2004; 2004WO-US008866.
XX PR 20-MAR-2003; 2003US-0456735P.
XX PA (DAND ) DANA FARBER CANCER INST INC.
XX PI Polyak K, Porter D, Allinen M;
XX DR WPI; 2004-728732/71.
XX PT Diagnosing breast cancer comprises determining expression levels of a
XX PT gene selected from those differentially expressed in normal or cancerous

```

```

PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT and cystatin C.
XX Example 6; SEQ ID NO 1584; 149pp; English.
XX
XX The invention relates to a method of diagnosis (M1) comprising: (a)
XX CC providing a test sample of breast tissue; (b) determining the level of
XX CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
XX CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
XX CC specification, and (c) if the gene is expressed in the test sample at a
XX CC lower level than in a control normal breast tissue sample, diagnosing the
XX CC test sample as containing cancer cells. The method is used for diagnosing
XX CC breast cancer. This sequence corresponds to an oligonucleotide primer
XX CC used in the method of the invention.
XX SQ Sequence 10 BP; 5 A; 2 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2109 CAATAAACTG 2118
XX Db 1 CAATAAACTG 10
XX
XX RESULT 369
XX ADU18826
XX ID ADU18826 standard; DNA; 10 BP.
XX AC ADU18826;
XX XX
XX DT 13-JAN-2005 (first entry)
XX DE Hypoxia-related tumourigenesis-related SAGE tag #617.
XX KW screening; hypoxia-related tumourigenesis;
XX KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX OS Unidentified.
XX XX
XX PN WO2004092198-A2.
XX XX
XX PD 28-OCT-2004.
XX XX
XX PF 09-APR-2004; 2004WO-US011087.
XX XX
XX PR 09-APR-2003; 2003US-0461712P.
XX PA (GENZ ) GENZYME CORP.
XX XX
XX PI Nacht M;
XX DR WPI; 2004-758333/74.
XX XX
XX PT Identifying agents that alter biological activity of a polypeptide
XX PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis
XX PT comprises contacting an agent with a target cell and monitoring activity
XX PT of expressed product.
XX XX
XX PS Disclosure; Page 67; 100pp; English.
XX XX
XX The invention comprises a method of screening for candidate agents
XX CC capable of altering the biological activity of a protein encoded by a
XX CC nucleotide involved in hypoxia-related tumorigenesis. The method of the
XX CC invention involves: contacting a test agent with a target cell expressing
XX CC the nucleotide, and monitoring the activity of the expressed protein
XX CC product; if the test agent modifies the activity of the expressed protein
XX CC then this is a candidate agent. The method of the invention is useful for
XX CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing
XX CC or treating tumours. The present DNA sequence represents a SAGE tag that
XX CC was used in the exemplification of the invention.
XX

```



PF 09-APR-2004; 2004WO-US011087.  
 XX  
 PR 09-APR-2003; 2003US-0461712P.  
 XX  
 PA (GENZ ) GENZYME CORP.  
 XX  
 PI Nacht M;  
 XX  
 DR WPI; 2004-758333/74.  
 XX  
 PT Identifying agents that alter biological activity of a polypeptide  
 encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
 PT comprises contacting an agent with a target cell and monitoring activity  
 of expressed product.  
 PT  
 XX  
 PS Disclosure; Page 65; 100pp; English.  
 XX  
 CC The invention comprises a method of screening for candidate agents  
 capable of altering the biological activity of a protein encoded by a  
 CC nucleotide involved in hypoxia-related tumorigenesis. The method of the  
 CC invention involves: contacting a test agent with a target cell expressing  
 CC the nucleotide, and monitoring the activity of the expressed protein  
 CC product; if the test agent modifies the activity of the expressed protein  
 CC then this is a candidate agent. The method of the invention is useful for  
 CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
 CC or treating tumours. The present DNA sequence represents a SAGE tag that  
 CC was used in the exemplification of the invention.  
 XX  
 SQ Sequence 10 BP; 1 A; 3 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 759 TGAAGAGAA 768  
 Db 10 TGAAGAGAA 1  
 RESULT 373  
 ADU19029/c  
 ID ADU19029 standard; DNA; 10 BP.  
 AC ADU19029;  
 XX  
 XX 13-JAN-2005 (first entry)  
 DT  
 DE Hypoxia-related tumorigenesis-related SAGE tag #820.  
 XX  
 KW screening; hypoxia-related tumorigenesis;  
 KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2004092198-A2.  
 XX  
 PD 28-OCT-2004.  
 XX  
 PF 09-APR-2004; 2004WO-US011087.  
 XX  
 PR 09-APR-2003; 2003US-0461712P.  
 XX  
 PA (GENZ ) GENZYME CORP.  
 XX  
 PI Nacht M;  
 XX  
 DR WPI; 2004-758333/74.  
 XX  
 PT Identifying agents that alter biological activity of a polypeptide  
 encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
 PT comprises contacting an agent with a target cell and monitoring activity  
 of expressed product.  
 PT  
 XX

PS Disclosure; Page 71; 100pp; English.  
 XX  
 CC The invention comprises a method of screening for candidate agents  
 capable of altering the biological activity of a protein encoded by a  
 CC nucleotide involved in hypoxia-related tumorigenesis. The method of the  
 CC invention involves: contacting a test agent with a target cell expressing  
 CC the nucleotide, and monitoring the activity of the expressed protein  
 CC product; if the test agent modifies the activity of the expressed protein  
 CC then this is a candidate agent. The method of the invention is useful for  
 CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
 CC or treating tumours. The present DNA sequence represents a SAGE tag that  
 CC was used in the exemplification of the invention.  
 XX  
 SQ Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1231 ATTAAGCCTC 1240  
 Db 10 ATTAAGCCTC 1  
 RESULT 374  
 ADU40784  
 ID ADU40784 standard; DNA; 10 BP.  
 AC ADU40784;  
 XX  
 XX 27-JAN-2005 (first entry)  
 DT  
 DE Novel nucleotide analysis method-related DNA sequence SeqID153.  
 XX  
 KW microarray; DNA sequencing; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN JP2004318840-A.  
 XX  
 PD 11-NOV-2004.  
 XX  
 PF 08-MAR-2004; 2004JP-00064494.  
 XX  
 PR 02-APR-2003; 2003JP-00099464.  
 XX  
 PA (CANO ) CANON KK.  
 XX  
 DR WPI; 2004-807907/80.  
 XX  
 PT DNA probe design information-processing method in nucleic acid sequence  
 analysis system, involves extracting probe candidate based on extracted  
 PT partial base sequence with respect to obtained self/competition frequency  
 PT tables.  
 XX  
 PS Disclosure; SEQ ID NO 153; 30pp; Japanese.  
 XX  
 CC This invention relates to a novel method which involves obtaining  
 CC self/competition frequency tables (105,106) by counting each appearance  
 CC number of partial base sequences maintained with respect to  
 CC self/competition base sequence data (101,103). A probe candidate is  
 CC derived based on extracted partial base sequence with respect to the  
 CC obtained frequency tables. The method is useful for processing  
 CC information of DNA probe design used in nucleic acid sequence analysis  
 CC system. The method enables exact and reproducible DNA probe design,  
 CC reliably. The present sequence is that of a DNA sequence which was used  
 CC in the illustration of the method of the invention.  
 XX  
 SQ Sequence 10 BP; 6 A; 1 C; 2 G; 1 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 AACTGGAAA 323  
 Db 1 AACTGGAAA 10

RESULT 375  
 ADU78451  
 ID ADU78451 standard; DNA; 10 BP.  
 XX  
 AC ADU78451;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE Rice oligonucleotide #65.  
 XX  
 KW Gene expression; ss.  
 XX  
 OS Oryza sativa.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004099445-A1.  
 XX  
 PD 18-NOV-2004.  
 XX  
 XX 09-MAY-2003; 2003WO-JP005840.  
 XX  
 PR 09-MAY-2003; 2003WO-JP005840.  
 XX  
 XX (IWAT-) IWATE PREFECTURAL GOVERNMENT.  
 PA (KAHL/) KAHL G.  
 PA (WINT/) WINTER P.  
 PA (KRUE/) KRUEGER D.  
 PA (REIC/) REICH S.  
 XX  
 PI Kahl G, Winter P, Krueger D, Reich S, Matsumura H, Terauchi R;  
 XX  
 DR WPI; 2004-821696/81.  
 XX  
 XX Use of type III restriction enzyme to isolate from cDNA of an expressed  
 PT gene, a tag comprising more than 25 nucleotides and capable of  
 PT identifying the expressed gene.  
 XX  
 PS Example 1; Page 22; 53pp; English.  
 XX  
 CC The invention relates to the use of a type III restriction enzyme to  
 CC isolate from cDNA of an expressed gene, a tag comprising more than 25  
 CC nucleotides and capable of identifying the expressed gene, where the 3'  
 CC end of the tag is defined by a cleavage site of the type III restriction  
 CC enzyme and the 5' end of the tag is defined by the cleavage site of  
 CC another restriction enzyme that is closest to the 3' end of the cDNA of  
 CC the expressed gene. The invention also relates to a ditag-oligonucleotide  
 CC comprising two tags each of which is derived from a different expressed  
 CC gene, where each tag comprises more than 25 nucleotides and is capable of  
 CC identifying an expressed gene, where the 3' end of the tag is defined by  
 CC a cleavage site of the type III restriction enzyme and the 5' end of the  
 CC tag is defined by the cleavage site of another restriction enzyme that is  
 CC closest to the 3' end of the cDNA of the expressed gene, a polynucleotide  
 CC comprising two ditag oligonucleotides, and a gene expression analysis  
 CC method comprising synthesizing a cDNA pool from mRNA of expressed genes  
 CC using a primer comprising oligo-dT and a recognition sequence of a type  
 CC III restriction enzyme, followed by digestion of the cDNA pool with  
 CC another restriction enzyme, purifying fragments comprising a poly A  
 CC sequence from the cDNA pool, and ligating the fragments to either linker-  
 CC A or linker-B, both of which comprise the recognition sequence of the  
 CC type III restriction enzyme, digesting the above fragments with the type  
 CC III restriction enzyme, and ligating the resulting fragment comprising  
 CC linker-A to the resulting fragment comprising linker-B after performing a  
 CC 3'-filling reaction, digesting the ligated fragments with the other  
 CC restriction enzyme to cleave off the linker sequence, and therefore  
 CC obtaining a ditag-oligonucleotide comprising two tags of more than 25  
 CC nucleotides and capable of identifying the expressed gene, ligating the  
 CC ditag-oligonucleotides to produce a polynucleotide, analyzing the

CC nucleotide sequence of the polynucleotide, and quantifying the expression  
 CC level of an expressed gene based on the number of tags corresponding to  
 CC the expressed gene included in the polynucleotide. The polynucleotide  
 CC is useful for gene expression analysis which involves analyzing the  
 CC polynucleotide sequence and quantifying the expression level of an  
 CC expressed gene based on the number of tags corresponding to the expressed  
 CC gene included in the polynucleotide. The isolated tag allows accurate  
 CC quantitative gene expression analysis and rapid gene expression profiling  
 CC in any organism for which no expressed sequence tag (EST) database is  
 CC available. This sequence represents a rice oligonucleotide used in the  
 CC method of the invention.

XX  
 SQ Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2308 GGAAAAGCTA 2317  
 Db 1 GGAAAAGCTA 10

RESULT 376  
 ADW38541  
 ID ADW38541 standard; DNA; 10 BP.  
 XX  
 AC ADW38541;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Immunomodulatory gene FLJ22875 oligonucleotide.  
 XX  
 KW cytostatic; immunosuppressive; virucide; diagnosis; prognosis;  
 KW pharmaceutical; immunotherapy; cancer; cytostatic; immunosuppressive;  
 KW autoimmune disease; immunosuppressive; immune inhibitor; anti-cancer  
 KW infection; FLJ22875; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005000099-A2.  
 XX  
 PD 06-JAN-2005.  
 XX  
 PF 09-JUN-2004; 2004WO US018461.  
 XX  
 PR 09-JUN-2003; 2003US-0477291P.  
 XX  
 PA (GENZ ) GENZYME CORP.  
 XX  
 PI Roberts BL;  
 XX  
 DR WPI; 2005-058046/06.  
 XX  
 XX New isolated blood factor domain polynucleotides having immunomodulatory  
 PT activity useful for aiding in the diagnosis or treating disorders  
 PT relating to the immune responses, e.g. cancers, autoimmune diseases, or  
 PT viral infections.  
 XX  
 PS Disclosure; SEQ ID NO 50; 141pp; English.  
 XX  
 CC The invention describes an isolated polynucleotide (I) encoding a peptide  
 CC selected from 21 polynucleotides fully given in the specification, or the  
 CC complement of the polynucleotide. Also described are: an isolated peptide  
 CC selected from 21 peptides fully given in the specification; a host cell  
 CC comprising (I) or the peptide; an antibody that specifically recognizes  
 CC and binds the peptide; a composition comprising the host cell, the  
 CC peptide, or the antibody, and a pharmaceutical carrier; an immune  
 CC effector cell raised in the presence and at the expense of a host cell;  
 CC and a method for eliciting a cytolytic response in a subject. Also  
 CC disclosed are: a method for monitoring gene expression, a method for  
 CC modulating the expression of the immunomodulatory polynucleotides, and  
 CC expression products; a method for screening for candidate agents that

CC modulate the expression of the polynucleotide or the expression products  
 CC of the polynucleotide; assays for the identification, assessment, and  
 CC development of candidate agents capable of modulating the activity of the  
 CC polynucleotides or polypeptides; a method for monitoring an immune  
 CC response in a subject; and a method for active immunotherapy. The  
 CC polynucleotides (e.g., blood factor domains) having immunomodulatory  
 CC activity are useful for detecting, diagnosing, prognosing, or monitoring  
 CC the progression of a disease. They are useful for aiding in the diagnosis  
 CC or treating disorders relating to the immune responses, e.g. cancers,  
 CC autoimmune diseases, or viral infections. This sequence represents a  
 CC oligonucleotide associated with immunomodulatory gene FLJ22875.  
 XX  
 SQ Sequence 10 BP; 4 A; 1 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 999 TTTAATACAT 1008  
 DB 1 TTTAATACAT 10  
 |||||

RESULT 377  
 ADM38501/c  
 ID ADM38501 standard; DNA; 10 BP.

XX AC ADM38501;

XX DT 24-MAR-2005 (first entry)

XX DE Immunomodulatory gene FAM3C oligonucleotide.

XX KW cytostatic; immunosuppressive; virucide; diagnosis; prognosis;  
 KW pharmaceutical; immunotherapy; cancer; cytostatic; neoplasm;  
 KW autoimmune disease; immunosuppressive; immune disorder; viral infection;  
 XX infection; FAM3C; ss.

XX OS Homo sapiens.

XX PN WO200500099-A2.

XX PD 06-JAN-2005.

XX PF 09-JUN-2004; 2004WO-US018461.

XX PR 09-JUN-2003; 2003US-0477291P.

XX PA (GENZ ) GENZYME CORP.

XX PI Roberts BL;

XX DR WPI; 2005-058046/06.

XX PT New isolated blood factor domain polynucleotides having immunomodulatory  
 PT activity, useful for aiding in the diagnosis or treating disorders  
 PT relating to the immune responses, e.g. cancers, autoimmune diseases, or  
 PT viral infections.

XX PS Disclosure; SEQ ID NO 10; 141pp; English.

XX CC The invention describes an isolated polynucleotide (I) encoding a peptide  
 CC selected from 21 polynucleotides fully given in the specification, or the  
 CC complement of the polynucleotide. Also described are: an isolated peptide  
 CC selected from 21 peptides fully given in the specification; a host cell  
 CC comprising (I) or the peptide; an antibody that specifically recognizes  
 CC and binds the peptide; a composition comprising the host cell, the  
 CC peptide, or the antibody, and a pharmaceutical carrier; an immune  
 CC effector cell raised in the presence and at the expense of a host cell;  
 CC and a method for eliciting a cytolytic response in a subject. Also  
 CC disclosed are: a method for monitoring gene expression; a method for  
 CC modulating the expression of the immunomodulatory polynucleotides and  
 CC expression products; a method for screening for candidate agents that

CC modulate the expression of the polynucleotide or the expression products  
 CC of the polynucleotide; assays for the identification, assessment, and  
 CC development of candidate agents capable of modulating the activity of the  
 CC polynucleotides or polypeptides; a method for monitoring an immune  
 CC response in a subject; and a method for active immunotherapy. The  
 CC polynucleotides (e.g., blood factor domains) having immunomodulatory  
 CC activity are useful for detecting, diagnosing, prognosing, or monitoring  
 CC the progression of a disease. They are useful for aiding in the diagnosis  
 CC or treating disorders relating to the immune responses, e.g. cancers,  
 CC autoimmune diseases, or viral infections. This sequence represents a  
 CC oligonucleotide associated with immunomodulatory gene FAM3C.  
 XX  
 SQ Sequence 10 BP; 2 A; 0 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 TCAAAATACA 205  
 DB 10 TCAAAATACA 1  
 |||||

RESULT 378

ID ADM64666/c  
 ID ADM64666 standard; RNA; 10 BP.

XX AC ADM64666;

XX DT 24-MAR-2005 (first entry)

XX DE Sendai virus E sequence, SEQ ID NO 79.

XX KW ss; gene therapy; E sequence.

XX OS Sendai virus.

XX OS Synthetic.

XX PN WO2005001082-A1.

XX PD 06-JAN-2005.

XX PF 30-JUN-2004; 2004WO-JP009617.

XX PR 30-JUN-2003; 2003JP-00187312.

XX PA (DNAV-) Dनावेक रेस इन्क.

XX PI You J, Iida A, Hasegawa M;

XX DR WPI; 2005-091512/10.

XX PT Novel minus strand RNA virus comprising gene modified in high mutation

XX PS region, useful as gene therapy vector.

XX DR Disclosure; SEQ ID NO 79; 92pp; Japanese.

XX CC The invention relates to a minus strand RNA virus having a foreign gene  
 CC in which a partial sequence in the E sequence of a minus strand RNA virus  
 CC contained in its gene sequence has been modified, where the sense strand  
 CC of the wild type foreign gene is replaced by another sequence such that  
 CC the identity with the E sequence is lowered. The minus strand RNA virus  
 CC is useful as a gene therapy vector for in vivo or ex vivo  
 CC administrations. The minus strand RNA virus enables stable expression of  
 CC a foreign gene e.g. CFTR in the target tissue. The present sequence  
 CC represents a Sendai virus E sequence.

XX SQ Sequence 10 BP; 3 A; 0 C; 0 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 TAAATTAATA 383  
 Db 10 TAAATTAATA 1

RESULT 379  
 ADW12379  
 ID ADW12379 standard; DNA; 10 BP.  
 XX  
 AC ADW12379;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE MR\_8 PCR arbitrary primer used for modified differential display method.  
 XX  
 KW Screening; cytotoxic T-lymphocyte; CTL; tumor marker; DNA vaccine;  
 KW immune response; genetic engineering; PCR; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US2004265900-A1.  
 XX  
 PD 30-DEC-2004.  
 XX  
 PF 29-JUL-2004; 2004US-00901415.  
 XX  
 PR 22-SEP-1997; 97US-00935377.  
 PR 03-JAN-2002; 2002US-00034350.  
 XX  
 PA (ZAUD/) ZAUDERER M.  
 XX  
 PI Zauderer M;  
 XX  
 DR WPI; 2005-064900/07.  
 XX

Identifying target epitope, by screening products of expression library generated from DNA or RNA derived from cell expressing target epitope with cytotoxic T cells generated against cell to identify DNA clones expressing target epitope.

Example 8; SEQ ID NO 15; 56pp; English.

The present invention relates to a method for identifying a target epitope. The method involves screening products of an expression library generated from DNA or RNA derived from a cell expressing the target epitope with cytotoxic T lymphocytes (CTL) generated against the cell to identify DNA clones expressing the target epitope. The invention further relates to the engineering of recombinant viruses as expression vectors for tumor, cancer or infected cell-specific antigens. The invention is useful for treating tumor bearing mammals and for preventing progression of tumor markers. The target antigen is used for the preparation of vaccines to induce a cell-mediated immune response. The present sequence is an arbitrary primer used for modified differential display method. This sequence is used in the identification of potential tumor-specific antigens.

XX  
 SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 TACCTATGGC 1458  
 Db 1 TACCTATGGC 10

RESULT 380  
 ADV92175/c  
 ID ADV92175 standard; DNA; 10 BP.  
 XX  
 AC ADV92175;  
 XX

DT 07-APR-2005 (first entry)  
 XX  
 DE Universal bacterial 16S rRNA BSR1541/20-based probe.  
 XX  
 KW DNA detection; ss; rRNA; probe.  
 XX  
 OS Bacteria.  
 XX  
 PN WO2005003384-A1.  
 XX  
 PD 13-JAN-2005.  
 XX  
 PF 05-JUL-2004; 2004WO-DK000480.  
 XX  
 PR 03-JUL-2003; 2003DK-00001018.  
 PR 03-JUL-2003; 2003US 04849264.  
 XX  
 PA (DAOG-) DANMARKS OG GRONLANDS GEOLOGISKE UNIVERS  
 XX  
 PI Bender M, Jacobsen CS;  
 XX  
 DR WPI; 2005-101503/11.  
 XX

Selective detection of target nucleic acid sequence in a sample comprising contacting the sample with nucleic acid probe.

Disclosure; Page 19; 67pp; English.

The invention relates to detecting the presence or absence of at least one target nucleic acid sequence in a sample (that further contains a nucleic acid molecule comprising a sequence corresponding to the target nucleic acid sequence) comprises contacting the sample with at least one nucleic acid probe that is capable of selectively binding to a continuum of at least a part of the nucleic acid molecule corresponding to the target nucleic acid sequence and a part of the nucleic acid molecule adjacent to the corresponding sequence. Also included are a composition or a kit, used in the method above each comprising at least one nucleic acid probe that is capable of selectively binding to a continuum of at least a part of the nucleic acid molecule corresponding to the target nucleic acid sequence and a part of the nucleic acid molecule adjacent to the corresponding sequence. The method further comprises contacting the sample with a first extendable primer. Binding of the nucleic acid probe to the nucleic acid molecule comprising a sequence corresponding to the target nucleic acid sequence prevents annealing of the extendable primer and/or extension of the primer (i.e. is a blocking probe). The continuum of at least a part of the nucleic acid molecule corresponding to the target nucleic acid sequence and a part of the nucleic acid molecule adjacent to the corresponding sequence comprises a transcription initiation site and its upstream sequence. The method, composition, and kit are useful for detecting the presence or absence of at least one target nucleic acid sequence in a sample that further contains a nucleic acid molecule comprising a sequence corresponding to the target nucleic acid sequence. The present sequence is probe for a universal bacterial rRNA gene (based on prior art primers deposited in the European Patent Office RNA database), used in the method of the invention.

XX  
 SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 GGATCACCTC 515  
 Db 10 GGATCACCTC 1

RESULT 381  
 ADZ36254/c  
 ID ADZ36254 standard; RNA; 10 BP.  
 XX  
 AC ADZ36254;  
 XX

```

DT 30-JUN-2005 (first entry)
DE Rat PIM-1 RNA fragment #11.
XX
XX
KW ss; siRNA; small interfering RNA; gene silencing; RNAi; PIM-1; analgesic;
KW antiinflammatory; antiallergic; antiasthmatic; uropathic; antipruritic;
KW cytosolic; PIM-1 kinase; pain; allergy; asthma; micronutrient disorder;
KW bladder disease; pruritus; tumor; inflammation; gene therapy;
KW RNA interference.
XX
XX Rattus sp.
OS
XX
XX WO2005033310-A1.
PN
XX
XX 14-APR-2005.
PD
XX
XX 24-SEP-2004; 2004WO-EP010757.
PF
XX
XX 01-OCT-2003; 2003DE-01045773.
PR
XX
XX 28-OCT-2003; 2003DE-01050256.
PR
XX
XX (CHEF ) GRUENENTHAL GMBH.
PA
XX
XX Erdmann V, Gruenweller A, Kurreck J, Christoph T, Gillen C;
PI
XX
XX WPI; 2005-285430/29.
DR
XX
XX New double-stranded RNA complementary to the sequence encoding PIM-1
PT kinase, useful for treating e.g. chronic pain, inflammation or allergy,
PT also related expression vectors and transformed cells.
XX
XX Disclosure; Page 7; 56pp; German.
XX
XX This invention describes a novel double-stranded RNA which is at least
CC 90% complementary to a segment of the RNA sequence for kinase PIM-1 and
CC can be used as a small interfering RNA (siRNA) in a method to inhibit
CC expression of PIM-1 in a cell. The RNA fragment is completely
CC complementary to a segment of PIM-1 RNA and includes a 5'-AA motif, has a
CC GC content at least 38%, contains no more than 2 consecutive G residues,
CC has a target sequence present in PIM-1 nucleic acid but nowhere else in
CC the host genome and can optionally be chemically modified. The RNA
CC fragment can reduce PIM-1 expression in a cell by at least 50% and is
CC directed against mammalian, especially human, PIM-1. For therapeutic use
CC the RNA fragment may be incorporated into micellar structures (preferably
CC liposomes) or into capsids. The double stranded RNA fragments have
CC analgesic, anti-inflammatory, antiallergic, antiasthmatic, uropathic,
CC antipruritic and cytosolic activity and can be used for treating any
CC disease associated with PIM-1 kinase, especially chronic pain; tactile
CC anodynia; heat-induced or inflammatory pain; allergy; asthma; urinary
CC incontinence; neurogenic bladder problems; pruritis; tumors and
CC inflammation, including use of the vectors for in vivo or in vitro gene
CC therapy. The invention also describes a method of identifying RNA
CC fragments with pain-modulating activity by determining the binding
CC constant of the fragment, preferably labeled, to the mRNA of PIM-1 in a
CC binding assay and for identifying substances that modulate PIM-1
CC expression. This sequence represents a fragment of rat PIM-1 kinase which
CC can be targeted by siRNA's.
XX
XX Sequence 10 BP; 5 A; 0 C; 4 G; 0 T; 1 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1601 TCACCTTCTT 1610
DB 10 TCACCTTCTT 1
XX
RESULT 382
AEC81842/c
ID AEC81842 standard; RNA; 10 BP.
XX
AC AEC81842;
XX
XX 01-DEC-2005 (first entry)
XX
XX Muscblind-like MBNL-1 binding site in chicken cTCT.
XX
XX Neuromuscular disease; neurological disease; muscular-gen.;
XX neuroprotective; muscular dystrophy; growth disorder;
XX musculoskeletal disease; gene therapy; drug screening;
XX animal disease model; gene therapy; muscblind-like 1; MBNL1; ss.
XX
XX Gallus gallus.
OS
XX
XX WO2005086825-A2.
PN
XX
XX 22-SEP-2005.
PD
XX
XX 10-MAR-2005; 2005WO-US007631.
PF
XX
XX 10-MAR-2004; 2004US-0551748P.
PR
XX
XX (UYFL ) UNIV FLORIDA.
PA
XX
XX Swanson MS, Kanadia RN, Thornton CA;
PI
XX
XX WPI; 2005-630793/64.
DR
XX
XX Treating disease associated with aberrant microsatellite expansion, e.g.
PT myotonic dystrophy, by administering an amount of recombinant adeno-
PT associated virus (RAAV) containing a transgene that encodes a muscblind
PT -like protein.
XX
XX Disclosure; SEQ ID NO 53; 119pp; English.
XX
XX The present invention provides a claimed method of treating a disease
CC associated with aberrant microsatellite expansion. This comprises
CC administering to a mammal in need of treatment a recombinant adeno-
CC associated virus (RAAV) containing a transgene that encodes a protein
CC selected from muscblind-like proteins MBNL1, MBNL2, MBNL3, or its
CC combinations. The treatment comprises ameliorating or eliminating the
CC symptoms of a neuromuscular or neurological condition caused by aberrant
CC microsatellite expansion. The neuromuscular condition is especially
CC myotonic dystrophy (DM). In other embodiments, the treatment comprises
CC reversing the mis-splicing of: the Cln1 skeletal muscular chloride
CC channel; the NMDA receptor NR1 (GRIN1); the microtubule-associated
CC protein tau (MAPT); or the TNNT2 (cTNT) protein. The mammal is preferably
CC human. The mammal in need of treatment may have RNA inclusions in
CC neuronal cells. A claimed mouse model for disease associated with
CC aberrant microsatellite expansion comprises a mouse having a substantial
CC deletion of Mbml1 exon 3 in the mouse genome. The mouse exhibits symptoms
CC typical of a disease associated with aberrant microsatellite expansion in
CC humans, such as muscle weakness and ocular cataracts. In a preferred
CC mouse model, the microsatellite repeat expansion disease is caused by a
CC microsatellite expansion in a coding or non-coding region of DNA; the
CC mouse exhibits abnormal muscblind proteins; the disease is myotonic
CC dystrophy; and the mouse has loss of functional Cln1 protein, amyloid
CC beta (A4) precursor protein, NMDA receptor NR1, microtubule-associated
CC protein tau, TNNT2 protein or TNNT3 protein. The mouse model is used in a
CC claimed method of identifying a compound useful in the treatment of
CC disease (especially myotonic dystrophy) associated with aberrant
CC microsatellite expansion. The present sequence is that of a MBNL1 binding
CC motif in chicken cTCT RNA.
XX
XX Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 0.4%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1500 AAAAGCAGCA 1509
DB 10 AAAAGCAGCA 1
XX

```

RESULT 383  
 AEE26650  
 ID AEE26650 standard; DNA; 10 BP.  
 AC AEE26650;  
 XX  
 DT 09-FEB-2006 (first entry)  
 XX  
 DE LNA-modified detection probe, axkOL140, EQ16580, SEQ ID 19.  
 XX  
 KW RNA amplification; RNA detection; RNA purification; probe; ss;  
 KW locked nucleic acid.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1 /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Labelled with 6-FITC, fluorescein"  
 FT modified\_base 2  
 FT /\*tag= d  
 FT /mod\_base= OTHER  
 FT /note= "LNA"  
 FT modified\_base 3  
 FT /\*tag= b  
 FT /mod\_base= 5-methylcytidine  
 FT modified\_base 4  
 FT /\*tag= e  
 FT /mod\_base= OTHER  
 FT /note= "LNA"  
 FT modified\_base 5  
 FT /\*tag= c  
 FT /mod\_base= 5-methylcytidine  
 FT modified\_base 6..10  
 FT /\*tag= f  
 FT /mod\_base= OTHER  
 FT /note= "LNA. Also 3' end labelled with 5-nitroindole"  
 XX  
 US2005272075-A1.  
 XX  
 XX 08-DEC-2005.  
 XX  
 XX 07-APR-2005; 2005US-00100897.  
 XX  
 XX 07-APR-2004; 2004US-0560148P.  
 XX 23-JUL-2004; 2004US-0590856P.  
 XX 12-AUG-2004; 2004US-0600961P.  
 XX 15-OCT-2004; 2004US-0619291P.  
 XX 28-JAN-2005; 2005US-0648221P.  
 XX (JACO/) JACOBSEN N.  
 XX (KONG/) KONGSEN L.  
 XX (KAUF/) KAUPPINEN S.  
 XX (ECHW/) ECHWALD S M.  
 XX (MOUR/) MOURITZEN P.  
 XX (NIEL/) NIELSEN P S.  
 XX (NORH/) NORHOLM M.  
 XX Jacobsen N, Kongbak L, Kauppinen S, Schwald SM, Mouritzen P;  
 PI Nielsen PS, Norholm M;  
 XX WPI; 2006-037202/04.  
 XX  
 XX Isolating, purifying, amplifying, detecting identifying, quantifying, or  
 XX capturing non-coding RNAs, such as microRNA or small interfering RNA  
 XX (siRNA) by using an oligonucleotide containing a number of nucleoside  
 XX analogues.  
 XX  
 XX Example 10; SEQ ID NO 19; 113pp; English.  
 XX  
 XX The present invention relates to novel methods for quantifying non-coding

CC RNAs, such as microRNA or short interfering RNA (siRNA). The methods  
 CC comprises using an oligonucleotide containing a number of nucleoside  
 CC analogues e.g LNA analogues. The methods are useful for detecting and  
 CC quantifying individual small RNA molecules in complex mixtures composed  
 CC of hundreds of thousands of different nucleic acids. The present sequence  
 CC was used to illustrate the invention.  
 XX  
 SQ Sequence 10 BP; 5 A; 2 C; 1 G; 2 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 351 AGCACATAAT 360  
 Db 1 AGCACATAAT 10  
 RESULT 384  
 AEE81259  
 ID AEE81259 standard; DNA; 10 BP.  
 XX  
 AC AEE81259;  
 XX  
 DT 23-FEB-2006 (first entry)  
 XX  
 DE Cystic disorder diagnosis associated CACNB3 tag.  
 XX  
 KW nephrotropic; cytostatic; hepatotropic; cerebrotropic; cerebrotective;  
 KW antitubercular; tuberculostatic; gene therapy; diagnosis; therapeutic;  
 KW polycystic kidney disease; genetic disorder; brain malformation;  
 KW neurological disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005117941-A2.  
 XX  
 PD 15-DEC-2005.  
 XX  
 XX 29-APR-2005; 2005WO-US014982.  
 XX  
 XX 29-APR-2004; 2004US 0566670P.  
 XX 22-JUL-2004; 2004US 0590385P.  
 XX  
 XX (GENZ ) GENZYME CORP.  
 XX  
 XX Beskronnaya O, Husson H;  
 XX  
 WPI; 2006-078693/08.  
 XX  
 XX Inhibiting cystic disorders or abnormalities in a tissue, for treating of  
 XX polycystic disorders, comprises contacting the tissue with a modulator of  
 XX the biological activity of a gene or polynucleotide.  
 XX  
 XX Disclosure; Page 58; 69pp; English.  
 XX  
 XX The invention describes a method of inhibiting cystic disorders or  
 XX abnormalities in a tissue by contacting the tissue with an agent that  
 XX modulates the biological activity of a gene or polynucleotide, given in  
 XX the specification, thus inhibiting cystic abnormalities. Also described  
 XX are: a method for inhibiting the formation of polycystic lesions in a  
 XX subject; and a method for preventing or treating Autosomal Dominant  
 XX Polycystic Kidney Disease (ADPKD) in a suitable subject. The method is  
 XX useful for treating renal cystic disorders such as polycystic kidney  
 XX disorders, vonHippel-Lindau, tuberosclerosis, nephronophthisis, autosomal  
 XX dominant polycystic kidney disease, autosomal recessive polycystic kidney  
 XX disease, acquired cystic kidney disease, and autosomal dominant  
 XX polycystic liver disease. This sequence represents a polynucleotide  
 XX from a gene up-regulated in cystic kidney epithelial libraries. The  
 XX biological activity of the gene can be modulated in order to diagnose and  
 XX treat renal cystic disorders.  
 XX  
 XX Sequence 10 BP; 5 A; 3 C; 1 G; 1 T; 0 U; 0 Other;



```

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2460 CACAGTCAAA 2469
      |||||
      1 CACAGTCAAA 10

Db

RESULT 385
ABF25435
ID AEF25435 standard; DNA; 10 BP.
XX
AC AEF25435;
XX
DT 09-MAR-2006 (first entry)
XX
DE Let-7a-related oligonucleotide - SEQ ID 49.
XX
KW RNA detection; ss; Let-7a.
XX
OS Unidentified.
XX
PN US2006003337-A1.
XX
PD 05-JAN-2006.
XX
PF 30-JUN-2004; 2004US-00881362.
XX
PR 30-JUN-2004; 2004US-00881362.
XX
PA (BRAN/) BRANDIS J.
PA (BOLC/) BOLCHAKOVA E V.
PA (KARG/) KARGER A E.
XX
PI Brandis J, Bolchakova EV, Karger AE;
XX
DR WPI; 2006-077942/08.
XX
PT Detecting small RNA, by forming detection mixture having sample, PCR
PT primers, ligating agent and target probe set that hybridize and ligate to
PT form probe set ligation sequence, amplifying ligation sequence by PCR,
PT detecting sequence.
XX
PS Disclosure; SEQ ID NO 49; 30pp; English.
XX
CC The invention comprises a method of detecting small RNA molecules. The
CC method involves forming a mixture consisting of a sample, a ligating
CC agent and target probe set that hybridizes to RNA and ligates to form a
CC probe set ligation sequence; forming a detection mixture having probe set
CC ligation sequence, first and second PCR primers; amplifying the probe set
CC ligation sequence by PCR; and detecting amplification of probe set
CC ligation sequence in the mixture. The method of the invention is useful
CC for detecting small RNA molecules, such as mRNA, siRNA, and snRNA. The
CC present nucleic acid represents a let-7a-related oligonucleotide that was
CC used in the exemplification of the invention.
XX
SQ Sequence 10 BP; 6 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1683 AACTATACAA 1692
      |||||
      1 AACTATACAA 10

Db

RESULT 386
ABF19990
ID AEF19990 standard; DNA; 10 BP.
XX

```

```

AC AEF19990;
XX
DT 09-MAR-2006 (first entry)
XX
DE Cystic kidney up-regulated gene tag sequence #49.
XX
KW nephrotropic; gene therapy; gene expression; diagnosis; therapeutic;
KW substrate inhibition; polycystic kidney disease; genetic disorder; ds.
XX
OS Homo sapiens.
XX
PN WO2006002203-A2.
XX
PD 05-JAN-2006.
XX
PF 23-JUN-2005; 2005WO-US021994.
XX
PR 23-JUN-2004; 2004US-0582673P.
XX
PR 25-JUN-2004; 2004US-0582875P.
XX
PA (GENZ ) GENZYME CORP.
XX
PI Mcpherson JM, Beskrovnaya O;
XX
DR WPI; 2006-079830/08.
XX
PT Inhibiting cystic disorders or abnormalities in a suitable tissue
PT comprising contacting the tissue with an agent that modulates the
PT biological activity of a gene or polynucleotide given in the
PT specification.
XX
PS Disclosure; Page 60; 78pp; English.
XX
CC The invention describes a method of inhibiting cystic disorders or
CC abnormalities in a suitable tissue comprising contacting the tissue with
CC an agent that modulates the biological activity of a gene or
CC polynucleotide given in the specification. Also described are: a method
CC for inhibiting the formation of polycystic lesions in a subject; and a
CC method for preventing or treating autosomal dominant polycystic kidney
CC disease (ADPKD) in a suitable subject. The method is useful in inhibiting
CC cystic disorders or abnormalities in a suitable tissue or preventing or
CC treating autosomal dominant polycystic kidney disease. This sequence
CC represents a tag from a human gene up-regulated in cystic kidney.
XX
SQ Sequence 10 BP; 5 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

Query Match      0.4%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2460 CACAGTCAAA 2469
      |||||
      1 CACAGTCAAA 10

Db

RESULT 387
ABF42318
ID AEF42318 standard; DNA; 10 BP.
XX
AC AEF42318;
XX
DT 23-MAR-2006 (first entry)
XX
DE Mutant loxp site spacer region SEQ ID NO:184.
XX
KW recombination; recombinant protein; ss.
XX
OS Synthetic.
XX
PN US2006014264-A1.
XX
PD 19-JAN-2006.
XX

```

PF 15-DEC-2004; 2004US-00012522.  
XX  
PR 13-JUL-2004; 2004US-0587399P.  
XX  
PA (STOW-) STOWERS INST MEDICAL RES.  
XX  
PI Sauer BL, Petyuk VA;  
XX  
DR WPI; 2006-099427/10.  
XX  
XX  
PT New Cre mutant polypeptide comprising a sequence that catalyzes site  
PT specific recombination at a lox site having at least one additional  
PT nucleotide in the spacer region, useful in genetic manipulations.  
XX  
XX  
PS Disclosure; SEQ ID NO 184; 126pp; English.  
XX  
XX  
CC The invention relates to a novel purified Cre mutant polypeptide  
CC comprising a sequence that specifically binds to an antibody that binds  
CC specifically to a Cre wild-type polypeptide comprising a fully defined  
CC 343-amino acid sequence (AEF42135) and catalyzes site specific  
CC recombination at a lox site having at least one additional nucleotide in  
CC the spacer region. The purified Cre mutant polypeptide is useful in  
CC genetic manipulations. The present sequence represents a spacer region  
CC used in a mutant loxP site of the invention.  
XX  
SQ Sequence 10 BP; 6 A; 0 C; 0 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 371 AATTAATTAA 380  
DB 1 AATTAATTAA 10  
  
RESULT 388  
AEF42322  
ID AEF42322 standard; DNA; 10 BP.  
XX  
AC AEF42322;  
XX  
DT 23-MAR-2006 (first entry)  
XX  
DE Mutant loxP site spacer region SEQ ID NO:188.  
XX  
KW recombination; recombinant protein; ss.  
XX  
OS Synthetic.  
XX  
PN US2006014264-A1.  
XX  
PD 19-JAN-2006.  
XX  
PF 15-DEC-2004; 2004US-00012522.  
XX  
PR 13-JUL-2004; 2004US-0587399P.  
XX  
PA (STOW-) STOWERS INST MEDICAL RES.  
XX  
PI Sauer BL, Petyuk VA;  
XX  
DR WPI; 2006-099427/10.  
XX  
PT New Cre mutant polypeptide comprising a sequence that catalyzes site  
PT specific recombination at a lox site having at least one additional  
PT nucleotide in the spacer region, useful in genetic manipulations.  
XX  
XX  
PS Disclosure; SEQ ID NO 188; 126pp; English.  
XX  
XX  
CC The invention relates to a novel purified Cre mutant polypeptide  
CC comprising a sequence that specifically binds to an antibody that binds  
CC specifically to a Cre wild-type polypeptide comprising a fully defined

CC 343-amino acid sequence (AEF42135) and catalyzes site specific  
CC recombination at a lox site having at least one additional nucleotide in  
CC the spacer region. The purified Cre mutant polypeptide is useful in  
CC genetic manipulations. The present sequence represents a spacer region  
CC used in a mutant loxP site of the invention.  
XX  
SQ Sequence 10 BP; 6 A; 0 C; 0 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 373 TTAATTAAAA 382  
DB 1 TTAATTAAAA 10  
  
RESULT 389  
AEF42389/c  
ID AEF42389 standard; DNA; 10 BP.  
XX  
AC AEF42389;  
XX  
DT 23-MAR-2006 (first entry)  
XX  
DE Mutant loxP site spacer region SEQ ID NO:255  
XX  
KW recombination; recombinant protein; ss.  
XX  
OS Synthetic.  
XX  
PN US2006014264-A1.  
XX  
PD 19-JAN-2006.  
XX  
PF 15-DEC-2004; 2004US-00012522.  
XX  
PR 13-JUL-2004; 2004US-0587399P.  
XX  
PA (STOW-) STOWERS INST MEDICAL RES.  
XX  
PI Sauer BL, Petyuk VA;  
XX  
DR WPI; 2006-099427/10.  
XX  
PT New Cre mutant polypeptide comprising a sequence that catalyzes site  
PT specific recombination at a lox site having at least one additional  
PT nucleotide in the spacer region, useful in genetic manipulations.  
XX  
XX  
PS Disclosure; SEQ ID NO 255; 126pp; English.  
XX  
XX  
CC The invention relates to a novel purified Cre mutant polypeptide  
CC comprising a sequence that specifically binds to an antibody that binds  
CC specifically to a Cre wild-type polypeptide comprising a fully defined  
CC 343-amino acid sequence (AEF42135) and catalyzes site specific  
CC recombination at a lox site having at least one additional nucleotide in  
CC the spacer region. The purified Cre mutant polypeptide is useful in  
CC genetic manipulations. The present sequence represents a spacer region  
CC used in a mutant loxP site of the invention.  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 2 G; 5 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2288 AAATCACATG 2297  
DB 10 AAATCACATG 1  
  
RESULT 390  
AEF42341

ID AEF42341 standard; DNA; 10 BP.  
 AC AEF42341;  
 XX  
 DT 23-MAR-2006 (first entry)  
 XX  
 DE Mutant loxP site spacer region SEQ ID NO:207.  
 XX  
 KW recombination; recombinant protein; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US2006014264-A1.  
 XX  
 PD 19-JAN-2006.  
 XX  
 PF 15-DEC-2004; 2004US-00012522.  
 XX  
 PR 13-JUL-2004; 2004US-0587399P.  
 XX  
 PA (STOW-) STOWERS INST MEDICAL RES.  
 XX  
 PI Sauer BL, Petyuk VA;  
 XX  
 DR WPI; 2006-099427/10.  
 XX  
 DE New Cre mutant polypeptide comprising a sequence that catalyzes site specific recombination at a lox site having at least one additional nucleotide in the spacer region, useful in genetic manipulations.  
 PT  
 PT specific recombination at a lox site having at least one additional nucleotide in the spacer region, useful in genetic manipulations.  
 PT  
 PS Disclosure; SEQ ID NO 207; 126pp; English.  
 XX  
 CC The invention relates to a novel purified Cre mutant polypeptide comprising a sequence that specifically binds to an antibody that binds specifically to a Cre wild-type polypeptide comprising a fully defined 343-amino acid sequence (AEF42135) and catalyzes site specific recombination at a lox site having at least one additional nucleotide in the spacer region. The purified Cre mutant polypeptide is useful in genetic manipulations. The present sequence represents a spacer region used in a mutant loxP site of the invention.  
 CC  
 XX  
 SQ Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1332 CGAAGAATTA 1341  
 DB 1 CGAAGAATTA 10  
 |||||  
 RESULT 391  
 AEF42319/c  
 ID AEF42319 standard; DNA; 10 BP.  
 XX  
 AC AEF42319;  
 XX  
 DT 23-MAR-2006 (first entry)  
 XX  
 DE Mutant loxP site spacer region SEQ ID NO:185.  
 XX  
 KW recombination; recombinant protein; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US2006014264-A1.  
 XX  
 PD 19-JAN-2006.  
 XX  
 PF 15-DEC-2004; 2004US-00012522.  
 XX  
 PR 13-JUL-2004; 2004US-0587399P.  
 XX

XX  
 PA (STOW-) STOWERS INST MEDICAL RES.  
 XX  
 PI Sauer BL, Petyuk VA;  
 XX  
 DR WPI; 2006-099427/10.  
 XX  
 DE New Cre mutant polypeptide comprising a sequence that catalyzes site specific recombination at a lox site having at least one additional nucleotide in the spacer region, useful in genetic manipulations.  
 PT  
 PT specific recombination at a lox site having at least one additional nucleotide in the spacer region, useful in genetic manipulations.  
 PT  
 PS Disclosure; SEQ ID NO 185; 126pp; English.  
 XX  
 CC The invention relates to a novel purified Cre mutant polypeptide comprising a sequence that specifically binds to an antibody that binds specifically to a Cre wild-type polypeptide comprising a fully defined 343-amino acid sequence (AEF42135) and catalyzes site specific recombination at a lox site having at least one additional nucleotide in the spacer region. The purified Cre mutant polypeptide is useful in genetic manipulations. The present sequence represents a spacer region used in a mutant loxP site of the invention.  
 CC  
 XX  
 SQ Sequence 10 BP; 4 A; 0 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 371 AATTAATTAA 380  
 DB 10 AATTAATTAA 1  
 |||||  
 RESULT 392  
 AEF42367  
 ID AEF42367 standard; DNA; 10 BP.  
 XX  
 AC AEF42367;  
 XX  
 DT 23-MAR-2006 (first entry)  
 XX  
 DE Mutant loxP site spacer region SEQ ID NO:233.  
 XX  
 KW recombination; recombinant protein; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US2006014264-A1.  
 XX  
 PD 19-JAN-2006.  
 XX  
 PF 15-DEC-2004; 2004US-00012522.  
 XX  
 PR 13-JUL-2004; 2004US-0587399P.  
 XX  
 PA (STOW-) STOWERS INST MEDICAL RES.  
 XX  
 PI Sauer BL, Petyuk VA;  
 XX  
 DR WPI; 2006-099427/10.  
 XX  
 DE New Cre mutant polypeptide comprising a sequence that catalyzes site specific recombination at a lox site having at least one additional nucleotide in the spacer region, useful in genetic manipulations.  
 PT  
 PT specific recombination at a lox site having at least one additional nucleotide in the spacer region, useful in genetic manipulations.  
 PT  
 PS Disclosure; SEQ ID NO 233; 126pp; English.  
 XX  
 CC The invention relates to a novel purified Cre mutant polypeptide comprising a sequence that specifically binds to an antibody that binds specifically to a Cre wild-type polypeptide comprising a fully defined 343-amino acid sequence (AEF42135) and catalyzes site specific recombination at a lox site having at least one additional nucleotide in the spacer region. The purified Cre mutant polypeptide is useful in

CC genetic manipulations. The present sequence represents a spacer region  
 CC used in a mutant loxP site of the invention.

XX  
 SQ Sequence 10 BP; 4 A; 1 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 10; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred.No. 1.9e+02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 585 TATGCATGAA 594  
 |||||  
 Db 1 TATGCATGAA 10

Search completed: January 17, 2007, 09:05:16  
 Job time : 8 secs